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                                                                                 August 9, 2004, 16:51:52; Search time 11 Seconds (without alignments) 3.623 Million cell updates/sec
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Sequence 13
Sequence 13
Sequence 13
Sequence 23
Sequence 23
Sequence 23
Sequence 24
Sequence 25
Sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                              us-10-664-775-4
2279
1 gatcactcctctagtgaaag......ttgtaattctaggtgctgat
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 250 summaries
                                                            nucleic search, using sw model
                                                                                                                                                                                 IDENTITY_NUC Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                    20 segs, 9225 residues
                                                                                                                                                                                                                                                                   length: 0
length: 2000000000
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Match 1
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                                                                                                                                     Title:
Perfect score:
                                                               1
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Maximum DB
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                                                              nucleic
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No.
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Sequence 22, Appl Sequence 20, Appl Sequence 22, Appl Sequence 20, Appl Sequence 20, Appl Sequence 9, Appl Sequence 10, Appl		with Modified nation with FVIIa  #1.25  on of human  on of human  on of human	4; Indels TGAAATATGTATT CCACATGGATATT
US-08-293-778-22 US-08-293-778-20 US-08-295-636-8 US-08-293-778-22 US-08-293-778-20 US-08-293-778-20 US-08-955-636-10	ALIGNMENTS	i. of Bleeding actor in Combinator in Combinator in Combinator in Combinator in the 4500 mmr B82,202A  6 mmr B34290  6 mmr B34290  1. Coding porti	Pred. No. 0.99; 0; Mismatches 24 GTCGAGACTTGCTTTGTTTT
ਜ਼ਿਜ਼ਜ਼ਜ਼ਜ਼ਜ਼		sey, James H.  Philip C.  Treatment  Treatment  Tresue Fac  Tresue, Aedlock  ARESS:  ARESS:  ARESS:  ARESS:  ARESS:  ARESS:  ARESS:  BRESS:  B	TATCE
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0000000		A-3/C Application U Application U Application U FECRMATION: T: Comp. Phill T: Comp. Phill T: Comp. Phill T: Comp. Phill T: NOVENTION: T TINVENTION: T TOWNENTION: T TOWNENTION: T TEXAS SEE: Richards SEE: Richards SEE: Richards TYPE: Floppy TYPE: Floppy TYPE: Floppy TYPE: Floppy TYPE: Floppy TYPE: Pach INFORM TAMEN AMPLICATION UMBER: TAMEN TAMEN TAMEN TAMEN TAMEN TAMEN TOWNES T	ilari Cons CAATT
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	H	382-2024-3 anne 3, Appare 1, Appare 1, Appare 1, Appare 2, Appare 3, Appare 2, Appare 3, Appare	maccal S ses 35 440 659
0 0 00 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT	CONTRACTOR OF THE PARTY OF THE	Guery Best 1 Matche Qy Db
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Tissue Factor in Combination with FVIIa
                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,777
                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OMRF B34290C
                                                                                                                         STATE: Texas
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882202
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: OMI
TELECOMMUNICATION:
TELEPHONE: 214-939-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLGGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AYPULLE.
ANTI-SENSE: NU
ORIGINAL SOURCE:
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35; Conservative
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FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                 STREET: 1201
CITY: Dallas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houston
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Tissue Factor in Combination with an Activator of
FVII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-08-231-777-3/c
US-08-231-777-3/c
Sequence 3, Application US/08321777
Fatent No. 5504067
GENERAL INFORMATION:
APPLICANT: Morrissey, James H.
APPLICANT: Comp, Philip C.
TITLE OF INVENTION: Treatment of Bleeding with Modified
                                                                                                                                                                                                                                                                                                                                   COUNTRY: 105AS

COUNTRY: US

COMPUTER READABLE FORM:

MEDIUW TYPE: EIDPPY disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/021,615A

FILING DATE: 19-FEB-1993

CLASSIFICATION 1514

PRIOR APPLICATION BTA:

APPLICATION NUMBER: US 07/882,202

FILING DATE: 13-MAY-1992

ATRONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
COCATION: 36..1433
OTHER INFORMATION: /note= "Coding portion of human OTHER INFORMATION: factor VII cDNA"
                         Sequence 3, Application US/08021615A
Patent No. 5504064
GENERAL INFORMATION:
APPLICANT: Morrissey, James H.
APPLICANT: Comp, Philip C.
TITLE OF INVENTION: Treatment of Bleeding w
ITILE OF INVENTION: Treatment of Combin
ITILE OF INVENTION: PVII
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
STREET: 1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REGISTRATION NUMBER: OMRF B34290CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IELEFRANS 214-393-4600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
ORGANISM: Homo sap
TISSUE TYPE: Blood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                  Dallas
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         US-08-021-615A-3/c
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Sequence 13, Application US/09009217

Patent No. 6132729
GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: King, Steven W.
APPLICANT: Gao, Boning
TITLE OF INVENTION: COMBINED TISSUE FACTOR AND
TITLE OF INVENTION: CHEMOTHERAPEUTIC METHODS AND COMPOSITIONS FOR COAGULATION
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, white & Durkee
                                                                                                                                                                                                                                                                                                          440 TICAATIGICITITAICIGICGAGACTIGCITIGITITIGAAATAIGIATICAATITIGG 498
                                                                                                                                                                                                                                                                                                                                                      659 TITGCTGGCATTICTTTTTTTTAGATAGGTATTTTTCCACATGGATATTCAACTGTGG 601
                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                               0.9%; Score 20.6; DB 1; Length 1440;
59.3%; Pred. No. 0.99;
tive 0; Mismatches 24; Indels 0
) NAME/KEY: CDS

) LOCATION: 36.1433

) OTHER INPORMATION: /note= "Coding portion of human

) OTHER INFORMATION: factor VII cDNA"

US-08-321-777-3
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440 TICAATIGICITITAICIGICGAGACTIGCTITIGITITIGAAATAIGIATICAATITIGG 498
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PCT-US93-04493-3/c
; Sequence 3, Application PC/TUS9304493
; GENERAL INFORMATION:
    APPLICANT: Morrissey, James H.
    APPLICANT: Comp, Philip C.
    TITLE OF INVENTION: Truncated Tissue Factor and FVIIa or TITLE OF INVENTION: FVII Activator for Blood Coagulation NUMBER OF SEQUENCES: 4
    CORRESPONDENCE ADDERSS: 5
    ADDRESSEE: Richards, Medlock & Andrews STREET: 1201 Elm Street, Suite 4500
    CITY: Dallas
    STREE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; DB 1; Length 1440; 0.99;
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ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYEE: FIDOPPY disk
COMPUTER: IBM PC COMPATIBLE
OMPRATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04493
FILING DATE: 19930512
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35,719
ER: OMRF B34290CIPC/PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20.6; DB; Pred. No. 0.99; 0; Mismatches
APPLICATION NUMBER: US 60/042,427
FILING DATE: 27-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,920
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGERENCEY/DOCKET NUMBER: UTSD:537
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION ON INFORMATION:
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TELECOMMUNICATION ON INFORMATION:
TELECOMMUNICATION INFORM
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APPLICATION NUMBER: US 07/882202
FILING DATE: 13-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021615
FILING DATE: 19-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: TELLYON NUMBER: 35,719
REGISTRATION NUMBER: 35,719
REGISTRATION NUMBER: 35,719
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.9%;
Best Local Similarity 59.3%;
Matches 35; Conservative
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APPLICANT: Thorpe, Philip E.
APPLICANT: King, Steven W.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR COGGLIATION AND TUMOR TITLE OF INVENTION: TREATMENT
NUMBER OF SEQUENCES: 27
CORRESSONDENCE ADDRESS: ADDRESS: ADDRESSE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: HOUSTON STREET: P.O. Box 4433
CITY: HOUSTON STREET: DOS 4433
COMPUTER: READABLE FORM:
MEDIUM TYPE: PatentIn Release #1.0, Version #1.30
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                               COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
COMPUTER: IBM PC COMPATIBLE
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,217
FILING APPLICATION DATA:
APPLICATION NUMBER: US 60/042,427
FILING DATE: 27-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-JAN-1997
PRIOR APPLICATION NUMBER: US 60/035,920
FILING DATE: 22-JAN-1997
PRIOR APPLICATION NUMBER: US 60/035,920
FILING DATE: 22-JAN-1997
ATPOREY INFORMATION:
APPLICATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: 41,071
REFERENCE/DOCKET NUMBER: 41,071
REFERENCE/DOCKET NUMBER: 41,071
REFERENCE/DOCKET NUMBER: 41,071
REGISTRATION NUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.9%; Score 20.6; DB Best Local Similarity 59.3%; Pred. No. 0.99; Matches 35; Conservative 0; Mismatches
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Patent No. 6132730
GENERAL INFORMATION:
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US-09-009-656-13/c
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1440 base pairs

FILING DATE: Concurr CLASSIFICATION: PRIOR APPLICATION DATA:

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; OTHER INF(
US-07-882-202A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Dal
STATE: Te
COUNTRY:
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                                                                                                                                                                                                                                                    /product= "Tissue Factor"
/note= "Coding portion of human factor VIII cDNA"
/citation= ([1])
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                                                                                                                                                                                                                                                                                                                                                        Query Match
0.9%; Score 20.6; DB 1; Length 1440;
Best Local Similarity 59.3%; Pred. No. 0.99;
Matches 35; Conservative 0; Mismatches 24; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/07882202A
Patent No. 5374617
GENERAL INFORMATION:
APPLICANT: Morrissey, James H.
APPLICANT: Comp. Philip C.
TITLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Tissue Factor in Combination with FVIIa
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: 103

ZIP: 75270-2197

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOSPY disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/882,202A

FILING DATE: 13-MAY-1992

CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Richards, Medlock & Andrews
1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OMRF B34290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REPERENCE/DOCKET NUMBER: OMRF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
TISSUE TYPE: Blood
FEATURE:
                          double
                                                                                                                                                                                  FEATURE:
NAME/KEY.
CDS
ICCATION: 36.1433
OTHER INFORMATION:
OTHER INFORMATION:
COTHER INFORMATION:
PCT-US93-04493-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
TYPE: NUCLEIC ACID
STRANDEDNESS: doub]
TOPOLOGY: linear
                                                                                                                                             ORGANISM: Homo sap
TISSUE TYPE: Blood
                                                               CDNA
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                                                             MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: lines
MOLECULE TYPE: CI
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1201 | CITY: Dallas STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
ORIGINAL SOURCE
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Patent No. 5504064
GENERAL INFORMATION:
APPLICANT: Workissy, James H.
APPLICANT: Comp, Philip C.
TITLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Tissue Factor in Combination with an Activator of
TITLE OF INVENTION: FVII
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                                                                                         DB 1; Length 1440;
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                                                                                                                         14; Indels
LOCATION: 36.1433
OTHER INFORMATION: factor VII cons portion of human OTHER INFORMATION: factor VII cona"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: 36..1433
; OTHER INFORMATION: /note= "Coding portion of human; OTHER INFORMATION: factor VII cDNA"
US-08-021-615-1
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                                                                                     Query Match
0.7%; Score 16.6; D
Best Local Similarity 64.1%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBËR: 31,966
REFRENCE/DOCKET NUMBER: OMRF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hansen, Eugenia S. REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE.
ORIGINAL SOURCE:
TITCM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.7
Best Local Similarity 64.1
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dallas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
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APPLICANT: Thorpe, Philip E.
APPLICANT: Thorpe, Philip E.
APPLICANT: King, Steven W.
APPLICANT: Gao, Boning
TITLE OF INVENTION: COMBINED TISSUE FACTOR AND
TITLE OF INVENTION: CHEMOTHERAPEUTIC METHODS AND COMPOSITIONS FOR COAGULATION
TITLE OF INVENTION: AND TUMOR TREATMENT
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11

US-09-003-656-13

US-09-003-656-13

Sequence 13, Application US/09009656

Patent No. 6132730

GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: Thorpe, Philip E.
APPLICANT: Gao, Boning
TITLE OF INVENTION: COMBINED TISSUE FACTOR AND FACTOR VIIA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR COAGULATION AND TUMOR TITLE OF INVENTION: TREATMENT:
NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
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                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,217
FILING DATE: COCCURTENTLY Herewith
CLASSIFICATION OFTE: US/09/009,217
FILING DATE: 27-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-MAR-1997
PRIOR APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-JAN-1997
PRIOR APPLICATION NUMBER: US 60/035,920
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: US 60/035,920
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: UTSD:536
TELEPRATION NUMBER: UTSD:536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.7%; Score 16.6; DB Best Local Similarity 64.1%; Pred. No. 12; Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                  ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
CITY: Houston
CITY: Houston
COUNTRY: USA
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
US-09-009-217-13
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0.7%; Score 16.6; DB 1; Length 1440;
Best Local Similarity 64.1%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 14; Indels 0
                                                                                                                                                                                                                                                        GENERAL INCORNATION:
APPLICANT: Morrissey, James H.
APPLICANT: Comp. Philip
TITLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Trisue Factor in Combination with FVIIa
NUMBER OF SEQUENCES:
ADDRESSE: Richards, Medlock & Andrews
STRET: 1201 Blm Street, Suite 4500
CITY: Dallas
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1761 TCCTTTGGTTTTGCATAGTGTCTCTGGCTTCCTGGATG 1799
              1761 TCCTTTGGTTTTGCATAGTGTCTCTGGCTTCCTGGATG 1799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US

COUNTRY: US

CIP: 75270-2197

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,777
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               se recrerecerrerectrassacires de se recreécies de se
                                                              58 recretecriciscrisserresses recresses recreated by
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REGISTRATION NUMBER: 31,966
REPERENCE/PLOCKET NUMBER: OMF B34290C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882202
ALING DATE: 13-MAY-1992
ATTORNEY,AGENT INFORMATION:
NAME: Hansen, Eugenia S.
                                                                                                                                                                              US-08-321-777-3
; Sequence 3, Application US/08321777
; Patent No. 5504067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
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ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433

RESULT 10 US-09-009-217-13 ; Sequence 13, Application US/09009217

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/product= "Tissue Factor"
/note= "Coding portion of human factor VIII cDNA"
/citation= ([1])
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 12;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 14; DB 1; Length 38;
Pred. No. 8;
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Patent No. 6329176

GENERAL INFORMATION:
APPLICANT: Woldike, Helle
APPLICANT: Woldike, Film
APPLICANT: Wilsen, Lars
ITILE OF INVENTION: Method for the Production of FVII
FILE REPERENCE: 5565.204-US
CURRENT APPLICATION NUMBER: US/09/558,027

CURRENT APPLICATION NUMBER: 60/108,065

PRIOR PILING DATE: 1998-11-12

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 4

LENGTH: 38
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                                                                                                                                                                           NAME: TEUJILO, DOTEEN Y.
REGISTRATION NUMBER: 35,719
REFERENCE DOCKET NUMBER: 0MRF B34290CIPC/PCT
TELEPHONE: 214-939-4600
TELEPAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021615
FILING DATE: 19-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 rcachagichággaaangggg 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 0.7%; (1 Similarity 64.1%; 25; Conservative 0
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Best Local Similarity 77.3%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 36.1433
COTHER INFORMATION: /
OTHER INFORMATION: /
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TISSUE TYPE: Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CHYPOTHETICAL: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-08-849-248-6/c
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US-09-558-027-4
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GENERAL INFORMATION:
APPLICANT: Morrissey, James H.
APPLICANT: Morrissey, James H.
APPLICANT: Tomp, Philip C.
TITLE OF INVENTION: Truncated Tissue Factor and FVIIa or
TITLE OF INVENTION: FVII Activator for Blood Coagulation
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 14; Indels
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CONDITY: US
ZIP: 75270-2197
ZONDITR: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTIN Release #1.0, Version #1.25
CURBINT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04493
PTI.ING DATE: 19930512
CITY: Houston
CUNTRY: USA
ZIP: T7210
COMPUTER READABLE FORM:
MEDTION TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rc-Bease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,656
FILING DATE: CONCULTENTLY Herewith
CLASSIFICATION:
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1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRICRAPELICATION DATA:
APPLICATION NUMBER: US 60/042,427
FILING DATE: 27-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,920
FILING DATE: 22-JAN-1997
APPLICATION NUMBER: US 60/035,920
FILING DATE: DATA:
APPLICATION NUMBER: US 60/035,920
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: 41,071
REJECOMMONICATION INFORMATION:
TELEPHONE: 512/418-3000
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 64.1
Matches 25, Conservative
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CITY: Dallas
STATE: Texas
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US-09-009-656-13
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single
        STRANDEDNESS:
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US-09-558-027-4/c
                                                                                                    US-08-849-248-6
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APPLICANT: Husbyn, Mette
APPLICANT: Husbyn, Mette
APPLICANT: Peter
APPLICANT: Orning, Lars
ITLE OF INVENTION: Factor VII Fragment 82-128 and its use
ITLE OF INVENTION: Pactor VII Fragment 82-128 and its use
ITLE OF INVENTION:
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bacon and Thomas
STRET: 625 Slaters Lane, 4th Floor
CITY: Alexandria
STRET: 425 Slaters Lane, 4th Floor
CITY: Alexandria
STRET: 625 Slaters Lane, 4th Floor
CITY: Alexandria
STRET: 625 Slaters Lane, 4th Floor
CITY: Alexandria
STRET: 626 Slaters Lane, 4th Floor
CITY: Alexandria
STRET: 626 Slaters Lane, 4th Floor
CITY: Alexandria
STRET: 1000 NO ALE
COMPUTER READABLE FORM:
MEDIUM TYPE: 12 PREDIO NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
0.6%; Score 12.8; DB 1; Length 141;
Best Local Similarity 70.8%; Pred. No. 65;
Matches 17; Conservative 0; Mismatches 7; Indels
                                                                      APPLICANT: Husbyn, Mette
APPLICANT: Fischer, Peter
APPLICANT: Fischer, Peter
APPLICANT: Orning, Lars
TITLE OF INVENTION: Factor VII Fragment 82-128 and its use
TITLE OF INVENTION: in blood clotting disorders
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,248
FILING DATE: 27 Aug 1997
INFORMATION PCR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nicleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "recombinant DNA".
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Sequence 6, Application US/08849248
Patent No. 5948759
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Patent No. 5948759
GENERAL INFORMATION:
                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                               DB 1; Length 141;
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Patent No. 6329176

Patent No. 6329176

GRERAL INFORMATION:

APPLICANT: Wolders, Finn

APPLICANT: Wielsen, Lars

TITLE OF INVENTION: Method for the Production of FVII

FILE REFERENCE: 5565.204-US

CURRENT APPLICATION NUMBER: US/09/558,027

CURRENT PILING DATE: 2000-04-25

PRIOR PILING DATE: 1998-11-12

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 4

SEQ ID NO 4

LENGTH NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
FILING DATE:
CLASSIFICATION: 435
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Patent No. 5580560
GENERAL INFORMATION:
APPLICANT: Nicolaisen, Else M.
APPLICANT: Woodbury, Soren E.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: Woolf Finn C.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIA
NUMBER OF SOURNESS: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                         Query Match
0.6%; Score 12.6; Di
Best Local Similarity S5.8%; Pred. No. 73;
Matches 24; Conservative 0; Mismatches
TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "recombinant DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              893 AGGCCATTTGCTTAGAATA 912
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FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 24-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: AGTIS, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129.224-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 cacrecerceaederrecreseae 26
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Patent No. 5905185
GENERAL INFORMATION:
APPLICANT: Garner, Ian
APPLICANT: Temperley, Simon M.
APPLICANT: Foster, Donald C.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Prunkard, Dona B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 21-867-0298
INFORMATION FOR SEQ ID NO: 10 SEQUENCE CHARACTRRISTICS: LENGTH: 27 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.5
Best Local Similarity 100.
Matches 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear;
; MOLECULE TYPE: cDNA
US-08-293-778-16
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US-08-756-506-13/c
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US-08-955-636-8
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STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
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ZIP: 10174-6201
COMPUTER READBAILE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
FILING DATE:
CLASSIFICATION: 435
PROS APPLICATION NUMBER: US/08/104,509
FILING DATE: DX 3235/87
PILING DATE: 25-JUN-1987
PRILING DATE: 25-JUN-1987
PRILING DATE: 35-JUN-1987
PRILING DATE: 35-JUN-1987
PRILING DATE: 35-JUN-1987
PRILING DATE: 35-JUN-1987
PRILING DATE: 30 07/434,149
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US-08233-778-16
105-08233-778-16
106-08233-778-16
106-08233-778-16
107-0823-778-16
107-0823-778-16
107-0823-778-10N:
107-0823-77
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0.5%; Score 11.2; D
Best Local Similarity 81.2%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches
                                                                                                APPLICATION NUMBER: DK 3235/87
FILING DATE: 25-JUN-1987
PRIOR APPLICATION DATA: 25-JUN-1987
APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA: 07/88/00103
FILING DATE: 24-JUN-1988
FILING DATE: 25-JUN-1988
FILING DATE: 25-JUN-198
FILING DATE: 25-JUN-198
APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-JUN-199
ATTONIEV,AGENT INFORMATION:
NAME: AGISTATION NUMBER: 34,086
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129,224-US
TELECOMMUNICATION INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1788 GCTTCCTGGATGTTT 1803
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TELEFA: 212-867-0298
INFORMATION FOR SEQ ID NO: 1-
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Score 11, DB 1; Length 27;
Pred. No. 75;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08955636A
Fatent No. 601782
Fatent Normation:
Fatent Normation:
Fatent Normation:
Fatent Represence: 09231/002001
Fatent Represence: 09231/002001
Fatent Patent Application Number: 1997-10-23
FATENT PATENT NORS: 35
FATENT FATENT NORS: 35
FATENT PATENT NORS: 35
FATENT NORS: 10 NOS: 35
FATENT 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/08756506
Fatent No. 5905185
GENERAL INFORMATION:
APPLICANT: Garner, Ian
APPLICANT: Cottingham, Ian R.
APPLICANT: Temperlay, Simon M.
APPLICANT: Poster, Donald C.
APPLICANT: Prefer, Donald C.
APPLICANT: Prefer, Cindy A.
APPLICANT: Promered, Donald C.
APPLICANT: Specific S.
APPLICANT: STREEF: CORRESPONDENCES 2
CORRESPONDENCES 2
APPLICANT: STREEF: 1201 Eastlake Avenue East
TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC TITLE OF INVENTION: ANIMALS
                                                                                                                                                                                                                                                                                                                                                             CONDITY: USA
CONDITY: USA
CONDITY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BEACHING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PEACHININ Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,506
FLING DATE:
CLASSIPTATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SAWABLAR. 37,438
REFERENCE/OCKET NUMBER: 95-28
TELEFANION NUMBER: 95-28
TELEFANION THOROMATION:
TELEFANION TOWER: 37,438
REFERENCE/OCKET NUMBER: 95-28
TELEFANION TOWER: 37,438
TELEFANION TOWER: 37,438
TELEFANION TOWER: 37,438
TELEFANION TOWER: 35-28
TELEFANION TOWER: 35-28
TELEFANION TOWER: 35-267
TELEFANION TOWER: 30-442-667
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: MUCHOL CANADA
TYPE: MUC
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ZIP: 98102
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,506
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                                                                                                                                                                       ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.5%
Best Local Similarity 57.6%
Matches 19; Conservative
                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: line;
INMEDIATE SOURCE:
CLONE: ZC6337
US-08-756-506-13
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US-08-756-506-13
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RESULT 24 US-08-462-261-7/c

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US-08-462-261-7
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                                                                                         Score 10; DB 1; Length 35; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                   RESULT 23
US-08-463-953-7/c
Sequence 7, Application US/08463953
Fatent No. 5502034
GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: "METHODS FOR PRODUCING THROMBIN NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend
STREET: Twentieth Floor
CITY: San Francisco
CITY: San Francisco
CITY: San Francisco
CINTER: CA
                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.4%; Score 10; DB 1; Length 35; 72.2%; Pred. No. 2e+02;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,953
                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-12-2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-541-5603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                              1402 GCAGTAGTCTGGCCTGAC 1419
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                                                                                         0.4%;
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                                                                                                            Best Local Similarity 72.2
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
Matches 13; Conserv
; IMMEDIATE SOURCE:
; CLONE: ZC1324
US-07-998-972A-7
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                                                                                         Query Match
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Sequence 7, Application US/08462261
Patent No. 5527692
GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN NUMBER OF SEQUENCES:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower,
STREET: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US92-11357-7/c

| Sequence 7, Application PC/TUS9211357
| GENERAL INFORMATION: METHODS POR PRODUCING THROMBIN
| APPLICANT: POSTER, Donald C. | TITLE OF INVENTION: METHODS POR PRODUCING THROMBIN NUMBER OF SEQUENCES: 48
| CORRESPONDENCE ADDRESS: ADDRESSES: Townsend and Townsend STREET: Townsend and Townsend STREET: Townsend the Plaza, Stewart Street Tower, CITY: San Francisco | COUNTRY: USA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
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72.2%; Pred. No. 2e+02;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,972
FILING DATE: 30-DEC-1992
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1402 GCAGTAGTCTGGCCTGAC 1419
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REGISTRATION NUMBER: 31,90
REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GGAGTTGGCTCGCCGGAC
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 72.2
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
CLONE: ZC1324
                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                 COUNTRY:
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25-JUN-1987

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0.4%; Score 9.8; DB 1; Length 27; 66.7%; Pred. No. 1.9e+02; tive 0; Mismatches 7; Indels
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
FILING DATE: 13-NOV-1989
FRICA APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 24-UN-1988
FRICA APPLICATION DATA:
APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-UN-1992
ATTORNEY/AGENT INFORMATION:
NAME: AGISTRATION NUMBER: 34,086
REPERENCE/DOCKET NUMBER: 34,086
REPERENCE/DOCKET NUMBER: 34,086
REPERENCE/DOCKET NUMBER: 122-867-0123
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: ILOCACI acid
TYPE: ILOCACI acid
TYPE: ILOCACI acid
TYPE: TUCLEIC ACID
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 25-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 24-JUN-1988
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
FILING DATE:
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Gaps
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0.4%; Score 9.4; DB 1; Length 35;
Best Local Similarity 90.9%; Pred. No. 2.98+02;
Matches 10; Conservative 0; Mismatches 1; Indels
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Patent No. 5502034
GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower,
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: THE PC COMPAILE
COMPUTER: THE PC COMPAILE
COMPUTER: THE PC COMPAILE
COMPUTER: THE PC COMPAILE
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACHILIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,953
FILING DATE: 314
PRIOR APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
PRIOR APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: PACHE 31.990
REGISTRATION NUMBER: 31,990
REGISTRATION NUMBER: 31,990
REGISTRATION NUMBER: 31,990
REGISTRATION NUMBER: 31,990
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TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                             1789 CTTCCTGGATG 1799
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Best Local Similarity 90.9°
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1789 CTTCCTGGATG 1799
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SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                  21 criccredade 31
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STRANDEDNESS: single
                              ; IMMEDIATE SOURCE:
; CLONE: ZC1324
US-07-998-972A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CA
COUNTRY: US
ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-463-953-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 30
US-08-462-261-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/07998972A; Patent No. 547677; GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN NUMBER OF SEQUENCES:
ADDRESSE: Townsend and Townsend STREET: One Market plaza, Stewart Street Tower, STREET: Twentieth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94105
ZURP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ITAM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRAING SYSTEM: PQ-DOS/MS-DOS
SOFTWARE: 19921230
CLASSIFICATION NATA:
APPLICATION NUMBER: US/07/998,972A
FILING DATE: 19921230
CLASSIFICATION TARA-1992
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-MAR-1992
PRICA APPLICATION NUMBER: US 07/816,281
APPLICATION NUMBER: 31,990
REFERENZ/OPCKET NUMBER: 13952-12-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/898,248
FILING DATE: L2-UN-1992
ATTORNEY/AGENT INFORMATION:
NAME: AGITS, Cheryl H.
REGISTRATION NUMBER: 34.086
REFERENCE/DOCKET NUMBER: 3129.224-US
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0128
INFORMATION FOR SEQ ID NO: 17:
SECURINE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: TYPE: TABLET TABLET TO THE TYPE: TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2087 TCTTCAAGGAC 2097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: cDNA US-08-293-778-17
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US-07-998-972A-7
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259 GCACTACCGCATTCCCTCT 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1789 CTTCCTGGATG 1799
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; CLONE: ZC1324
PCT-US92-11357-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 32
US-08-955-636-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application PC/TUS9211357
SEQUENCE T. REPRESTION:
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
ITILE OF INVENTION: METHODS FOR PRODUCING THROWBIN
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower,
STREET: An Francisco
CITY: San Francisco
Sequence 7, Application US/08462261
Patent No. 5527692
FEDERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN NUMBER OF SEQUENCES:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower,
STREET: ADDRESSES:
CONTY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPTRY: USA

CONTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATE OF COMPATIBLE
COMPUTER: DATE OF COMPATIBLE
COMPUTER: DATE OF COMPATIBLE
COMPUTER: DATE OF COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING PATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: PARMELE, SEEVEN W
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-12-2
TELECHONE: 206-467-9600
TELEPHONE: 206-467-9600
TELEPHONE: 206-467-9600
INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.9°
Matches 10; Conservative
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IMMEDIATE SOURCE:
CLONE: ZC1324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US92-11357-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-462-261-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
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Query Match
0.4%; Score 9.4; DB 1; Length 36;
Best Local Similarity 68.4%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 6; Indels
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ZIP: 94105
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11357
APPLICATION NUMBER: PCT/US92/11357
APPLICATION NUMBER: US 07/860,701
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-MAR-1992
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTONEY/AGENT INFORMATION:
NAME: PARMENER: S1-990
ATTONEY/AGENT INFORMATION:
NAME: PARMENER: S1-990
TELEFAX: 415-543-55043
INFORMATION FOR EAG ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 Dase pairs
INFORMATION FOR EAG ID NO: 7:
LENGTH: 35 Dase pairs
TYPE: UNICLEIC ALID
STRANDEDNESS: Single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/08955636A; Patent No. 6017882; Patent No. 6017882; GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT; TITLE OF INVENTION: POLYPEPTIDES; TITLE OF INVENTION: POLYPEPTIDES; CURRENT APPLICATION NUMBER: US/08/955,636A; CURRENT PILING DATE: 1997-10-23; NUMBER OF SEQ ID NOS: 35; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; LINGTH: 36
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CLASSIFICATION: 435
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Sequence 22, Application US/08293778

Sequence 22, Application US/08293778

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Protein C mutagenic oligonucleotide US-08-955-636-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/293,778
                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Nelestuen, Gary
TITLE OF INVENTION: MOLPIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: MOLPEPTIDES
FILE REFREENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PASLEEQ for Windows Version 3.0
LENGTH: 36
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FILING DATE: 25-UN-1987
FILING DATE: 25-UN-1987
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
FILING DATE: 24-UN-1988
FILING DATE: 24-UN-1988
FILING DATE: 12-UN-1988
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-UN-1992
APPLICATION NUMBER: 34,086
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
US-08-955-636-10/c
; Sequence 10, Application US/08955636A
; Patent No. 6017882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 GCACTACCGCATTCCCTCT 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 34
US-08-293-778-22/c
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ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc. STREET: 405 Lexington Avenue, 62nd Floor CITY: New York
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                                                                                                                                                                                                                                                                                                                             Query Match 0.4%; Score 9.2; DB 1; Length 26; Best Local Similarity 78.6%; Pred. No. 2.9e+02; Matches 11; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
COUNTRY: United States of America
2TP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATING
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Nicolaisen, Else M.
APPLICANT: Nicolaisen, Else M.
APPLICANT: Wiberg, Finn C.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: DK 3235/87
FILING DATE: 25-JUN-1987
RION APPLICATION DATE: 3-JUN-1987
APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 24-JUN-1988
PRIOR APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION: NAME: APFLS, Cherryl H.

REGISTRATION NUMBER: 34,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3129.224-US
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APPLICATION NUMBER: US/08/104,509
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Sequence 20, Application US/08293778
. Patent No. 5580560
                                                                                             | INFORMATION FOR SECULD NO: 22: SEQUENCE CHARATERISTICS: LENGTH: 26 base pairs | TYPE: mucleic acid | STRANDEDNESS: single | TOPOLOGY: linear | MOLECULE TYPE: cDNA | US-08-293-778-22
REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 20:
SEGUIENCE CHARACTERISTICS:
LENGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                       1920 GTCTCTGAGGTTCC 1933
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                                                                            212-867-0298
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US-08-293-778-22; Sequence 22, Application US/08293778; Sequence 22, Application US/08293778; Patent No. 5590560

GENERAL INFORMATION:
APPLICANT: Wiberg, Finn C.
APPLICANT: Wiberg, Finn C.
APPLICANT: Wiberg, Finn C.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: Wobliry, Richard
TITLE OF INVENTION: Wobliry, Richard
TITLE OF INVENTION: Wobliry, Richard
STREET: ADDRESSE: 26
CORRESPONDENCE ADDRESS:
STREET: ADDRESSE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
CITY: New York
STATE: New York
                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.4%; Score 8.8; DB 1; Length 42; Best Local Similarity 52.8%; Pred. No. 3.8e+02; Matches 19; Conservative 0; Mismatches 17; Indels
                                                                                                                                                                Length 27;
                                                                                                                                                             0.4%; Score 9.2; DB 1; Length 27 78.6%; Pred. No. 2.9e+02; Ative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Protein C mutagenic oligonucleotide
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COUNTRY: United States of America
2TP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ratentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 36
US-08-955-636-8/C
19-955-636-8/A
Patent No. 6017882
| General No. 6017882
| General No. 6017882
| General No. 6017882
| TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
| TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
| TITLE OF INVENTION: POLYPEPPIDES
| TITLE OF INVENTION: POLYPEPPIDES
| CURRENT APPLICATION NUMBER: US/08/955,636A
| CURRENT FILING DATE: 1997-10-23
| NUMBER OF SEQ ID NOS: 35
| SOFTWARE: FRSELSEQ FOR Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 TTCTTGAAGCCTCTGCTGGCAATACTTCTGGGGCTG 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                         240 CITCIGGGCCAGGG 253
                                                                                                                                                                                                                                                                                                                           2 crecrédacerede 15
                                                                                                                                                                                          Best Local Similarity 78.6%
Matches 11; Conservative
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                       7 MOLECULE 111
US-08-293-778-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÚS-08-955-636-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 8
LENGIH: 42
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                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                            à
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REFERENCE/DOCKET NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129.224-US
TELESCOMMUNICATION INFORMATION:
TELEFRAM: 212-867-0298
FORMATION FOR SECTIONS

TELEFAX: 212-867-0298 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

APPLICATION NUMBER: US/00/104,509
FILING DATE: 25-JUN-1987
FILING DATE: 25-JUN-1987
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
FILING DATE: 24-JUN-1988
FILING DATE: 24-JUN-1988
FILING DATE: 24-JUN-1988
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAMB: AGILS, Cheryl H.
REGISTRATION NUMBER: 34,086

APPLICATION NUMBER: US/08/104,509

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ASSULT 38

KESULT 38

                                                                                                                                                                                                                                                                                                           0.4%; Score 8.6; DB 1; Length 26; 73.3%; Pred. No. 4.2e+02; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
APPLICATION NUMBER: DK 3235/87
FILING DATE: 25-UUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 GAAAGGTGGGGGTCT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 dgaaggregaagaer 26
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 73.33
Matches 11, Conservative
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: CDNA US-08-293-778-22
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0
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0.4%; Score 8.6; DB 1; Length 27;
Best Local Similarity 60.9%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.4%; Score 8.4; DB 1; Length 36; 66.7%; Pred. No. 4.5e+02; tive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Protein C mutagenic oligonucleotide US-08-955-636-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 40

US-08-955-636-10

Sequence 10, Application US/08955636A

Patent No. 6017882

GENERAL INFORMATION:
APPLICANT: Nelseatuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT;
FILLE REFERENCE: 09531/00201

CURRENT APPLICATION HUMBER: US/08/955,636A

UNUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER: OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 24-UN-1988
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-UN-1992
ATTORNEY/AGENT INFORMATION:
NAME: AGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129.224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
TELEFRAX: 212-867-0123
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                509 AGGGTGCTGACAAGAAGGTACAG 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 Aggecerregececcagerecae s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/08955636A
Patent No. 6017882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158 TACTTCTGGGGCTGCTGC 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 TCCTAGAGGAGCTGCGGC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.74
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 39
US-08-955-636-9/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-293-778-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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; SOFTWARE: PastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; PEATORE:
; OTHER PROPRATION: Protein C mutagenic oligonucleotide
US-08-955-636-10
  Query Match
  Best Local Similarity 66.7%; Pred. No. 4.5e+02;
  Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps

QY 158 TACTTCTGGGGCTGCTGC 175

Db 2 TCCTAGAGGAGCTGCGC 19
Search completed: August 9, 2004, 16:52:04
JOb time: 12 secs
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GenCore version 5.1.6  Copyright (c) 1993 - 2004 Compugen Ltd.  cleic search, using sw model  August 9, 2004, 16:54:36; Search time 31 Seconds
GenCore version  Copyright (c) 1993 - 2004  OM nucleic - nucleic search, using sw model  Run on: August 9, 2004, 16:54:36;

Kun on:

August 9, 2004, 18:31:59 (without alignments)
3.697 Million cell updates/sec
Title:
Perfect score: 2279
Sequence:
1 gatcactccttagtgaaag.....ttgtaattctaggtgctgat 2279
Scoring table: IDENTITY NUC

Scoring table: IDENTITY\_NUC Gapop 10.0 , Gapext 0.5

Searched: 61 seqs, 25143 residues Total number of hits satisfying chosen parameters:

122

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 250 summaries

Database : rnpbdb:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CITAMARDID

	Description	÷	Sequence 7, Appli	7	equence 7,	7	7	1	7,	7	_	E	7	6	n N	n N	9		7	7,	ŗ,	7,	7,	۲,	r.	Ľ,		ď	equence 4,	equence 13	equence 9, App	equence 8429,	equence 9623	23323,	Sequence 9623, Ap	
SUMMARIES %	Ē		ă	-10-411-026-		US-10-411-049-7	-10-410-930	10-410-997	10-411-012	$\ddot{a}$	-10-410-913	0-375-741-1	-10-617-619	0-617-619-9	3-382-248-3	8-35	US-09-918-995-8429	0-411-037	0-411-026	10-410-962-	$\stackrel{\circ}{}$	10-410-930-	10-410-997-	10-411-012	10-287-994	10-410-913	-10-617-6	39-782-587B-	-09-782-587B-	3-375-741-	US-10-617-619-9	9-318-992-8	-10-029-38	-386-233	0-029-386-9	
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	4 4 4	115	1332	1332	1332	1332	1332	1332	1332	1332	1332	1440	2040	2106	1361	1361	483	1332	1332	1332	1332	1332	1332	1332	1332	1332	2040	1338	1357	1440	2106	483	555	222	555	
	Query Match Length	ממככוו									6.0			•			•	0.7		0.7							0.7								9.0	
	3	2 1	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6	σ,		17	17	17	17	17	17	17	17	17	17	17		ဖ	w	w	v	4	4		
	Result	- P									ט		-	-			15	9	17	89	6	20	21	22	23.1	42	25		0 27		600	30			3 6	

uence 22, uence 22, uence 22, uence 22, uence 22, uence 10, uence 10, uence 10, uence 10, uence 10, uence 2, ue	fuence 8, fuence 6, fuence 7, fuence 2, fuence 2, fuence 2, fuence 2, fuence 22 fuence 22 fuence 10 fuence 10 fuence 11 fuence 10	quence 10 quence 10 quence 10 quence 10 quence 15 quence 15 quence 15 quence 16	duence 8 gardineros 8 gardineros 8 gardineros 8 gardineros 9 gardinero	Sequence 8, Appliance 9, Appliance 9, Appliance 9, Appliance 9, Appliance 9, Appliance 9, Appliance 10, Appliance	equence 2
650 1 US-10-272 660 1 US-10-273 1 US-10-27	54 1 US-10-349-858-8 32 1 US-10-349-858-8 38 1 US-10-281-727-7 38 1 US-10-398-422A-20 38 1 US-10-398-422A-20 60 1 US-10-273-321-22 60 1 US-10-273-321-22 60 1 US-10-273-321-07 60 1 US-10-273-321-07 60 1 US-10-273-321-07 60 1 US-10-273-321-07 60 1 US-10-273-321-107	1 US-10-27 1 US-10-27 1 US-10-27 1 US-10-27 1 US-09-95 1 US-10-29 1 US-10-29 1 US-10-29 1 US-09-95	1 08-10-22 1 08-1	32 1 US-10-281-727-7 36 1 US-09-951-121A-9 36 1 US-09-951-121A-9 36 1 US-10-255-032-8 36 1 US-10-255-032-8 36 1 US-10-295-682-9 38 1 US-10-296-682-9 38 1 US-10-296-428-2 38 1 US-10-296-428-2 35 1 US-10-109-498-5 50 1 US-10-109-498-5 51 US-10-109-498-5 52 1 US-10-109-498-5 53 1 US-10-109-498-5 54 US-10-109-498-5 55 1 US-10-109-498-5 56 1 US-10-273-28-23 60 1 US-10-273-328-23 51 US-10-273-28-23 52 1 US-10-109-498-5 53 1 US-10-273-28-23 54 US-10-273-228-23	6-60-SD 1 1
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GENERAL INFORMATION:
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: APPLICANT: APER TO BE TECHNOLOGIES, Inc.
APPLICANT: APPLICANT: APER TO BE TECHNOLOGIES, SHAWN
APPLICANT: APER TO BE TECHNOLOGIES
INTERPORT TO BE TECHNOLOGIES
ITILE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE TILE OF INVENTION: PROTEIN REMODELING METHODS
FILE REPERENCE: 040653-01-2653
CURRENT APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-25
PRIOR PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR 
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APPLICANT: Bayer, Robert
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: GRANULCCTTE COLONY STIMULATING FACTOR: REMODELING AND
FILLE OF INVENTION: GRANULCCTTE COLONY STIMULATING FACTOR: REMODELING AND
FILLE REPERENCE: 040853-01-5054
CURRENT FILLING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILLING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR PELLING DATE: 2001-10-10
PRIOR PILLING DATE: 2002-06-07
PRIOR FILLING DATE: 2002-06-07
PRIOR PELLING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR PLILING DATE: 2002-06-17
PRIOR PLILING DATE: 2002-06-17
PRIOR PLILING DATE: 2002-06-25
PRIOR PLILING DATE: 2002-06-25
PRIOR PLILING DATE: 2002-06-17
PRIOR PLILING DATE: 2002-06-25
PRIOR PLILING DATE: 2002-06-25
PRIOR PLILING DATE: 2002-06-25
PRIOR PLILING DATE: 2002-06-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Indels
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0.9%; Score 20.6; Di
Best Local Similarity 59.3%; Pred. No. 2.3;
Matches 35; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Neose Technologies, Inc. APPLICANT: DeFrees, Shawn APPLICANT: Zopf, David APPLICANT: Bayer, Robert APPLICANT: Hakes, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 7, Application US/10410962
Publication No. US20040077836Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1332
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-410-962-7/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Neose Technologies, inc.
APPLICANT: Neose Technologies, inc.
APPLICANT: Neose Technologies, inc.
APPLICANT: Defrees, Shawn
APPLICANT: Sopf. David
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
ITILE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONUGATION OF ALPHA
ITILE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONUGATION OF ALPHA
ITILE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONUGATION OF ALPHA
ITILE OF INVENTION: GALACTOSIDASE A: REMODELING AND GLYCOCONUGATION OF ALPHA
ITILE OF INVENTION: GALACTOSIDASE A: REMODELING AND GLYCOCONUGATION OF ALPHA
ITILE OF INVENTION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR PLILNG DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   440 TICAATIGICTITIAICIGICGAGACTIGCITIGITTIGAAATAIGIATICAATTITGG 498
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               Sequence 3, As Sequence 2, As Sequence 2, As Sequence 3, As Sequence 14, As Sequence 14, As Sequence 14, As Sequence 15, As Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4,
Sequence 2,
Sequence 3,
Sequence 2,
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US-09-951-121A-3
US-10-29-682-3
US-10-29-682-3
US-10-281-727-3
US-09-95-121A-15
US-09-95-121A-15
US-09-95-121A-15
US-10-29-682-14
US-10-29-682-15
US-10-29-682-15
US-10-29-682-15
US-10-29-682-15
US-10-29-682-15
US-10-29-682-15
US-10-29-803-810-8
US-10-29-330-9
US-10-017-122-4
US-00-951-121A-2
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JS-10-295-682-2
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Publication No. US20040043446Al
GENERAL INFORMATION:
               TYPE: DNA
CORGANISM: Homo sapiens
US-10-411-037-7
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Best Local Similarity
Matches 35; Conserv
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US-10-411-026-7/c ; Sequence 7, Application US/10411026

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APPLICANT: Harks, Lowing
APPLICANT: Chen, X
APPLICANT: Chen, X
APPLICANT: Chen, X
APPLICANT: BOWE, Caryn
TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
TITLE OF INVENTION: BETA
FILE REFERENCE: 040853-01-5056
CURRENY PELLING DATE: 2001-10-10
FRIOR APPLICATION NUMBER: US 60/328,523
FRIOR APPLICATION NUMBER: US 60/328,523
FRIOR APPLICATION NUMBER: US 60/344,692
FRIOR APPLICATION NUMBER: US 60/344,692
FRIOR FILING DATE: 2001-10-19
FRIOR FILING DATE: 2002-06-25
FRIOR FILING DATE: 2002-06-25
FRIOR PELLING DATE: 2002-06-16
FRIOR APPLICATION NUMBER: US 60/440,249
FRIOR APPLICATION NUMBER: US 60/407,527
FRIOR FILING DATE: 2002-08-16
FRIOR APPLICATION NUMBER: US 60/407,527
FRIOR FILING DATE: 2002-08-18
FRIOR FILING DATE: 2002-08-18
FRIOR FILING DATE: 2002-08-18
FRIOR FILING DATE: 2002-08-18
FRIOR FILING DATE: 2002-08-16
FRIOR APPLICATION NUMBER: US 60/407,527
FRIOR FILING DATE: 2002-08-16
FRIOR FI
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Publication No. US20040126838A1
GENERAL INFORMATION:
                                                           Bayer, Robert
Hakes, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens US-10-410-930-7
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Sequence 7, Application US/10411049
Publication No US20040082026A1
GENERAL INFORMATION
APPLICANT: Neces Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Caryn
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Bobert
APPLICANT: Bayer, Bobert
APPLICANT: Bayer, David
APPLICANTON NUMBER: US 60/328, 523
PRIOR PLICATION NUMBER: US 60/394, 692
PRIOR APPLICATION NUMBER: US 60/391, 77
PRIOR PLICATION NUMBER: US 60/391, 77
PRIOR APPLICATION NUMBER: US 60/404, 249
PRIOR PLICATION NUMBER: US 60/404, 249
PRIOR PLICATION NUMBER: US 60/407, 527
PRIOR APPLICATION NUMBER: US 60/407, 527
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0.9%; Score 20.6; DB 1; Length 1332;
Best Local Similarity 59.3%; Pred. No. 2.3;
Matches 35; Conservative 0; Mismatches 24; Indels 0; Gaps
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Publication No. US20040115168A1
GENERAL INFORMATION:
                                                     NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
PRIOR FILING DATE: 2002-08-28
                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-410-962-7
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ORGANISM: Homo sapiens
US-10-411-049-7
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                                                                                                                                           SEQ ID NO 7
LENGTH: 1332
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GENERAL INFORMATION:

APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn.

APPLICANT: DeFrees, Shawn.

APPLICANT: DeFrees, Shawn.

APPLICANT: Defrees, David

APPLICANT: Bayer. Robert

APPLICANT: Hakes, David

APPLICANT: Hakes, David

APPLICANT: Hakes, David

APPLICANT: Howe, Caryn

TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCCCONJUGATION OF TITLE OF INVENTION: FSH

FILE REFERENCE: 040853-01-5059

CURRENT APPLICANTON NUMBER: US 60/328,523

FILE REFERENCE: 2001-10-19

PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR PILING DATE: 2001-10-19

PRIOR APPLICATION NUMBER: US 60/394,777

PRIOR APPLICATION NUMBER: US 60/391,777

PRIOR APPLICATION NUMBER: US 60/391,777
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APPLICANT: Neose Technologies, Inc. APPLICANT: DeFrees, Shawn

10664775-4.rnpb

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### PFILICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Bayer, Robert

#### APPLICANT: Hakes, David

### APPLICANT: Hakes, David

### APPLICANT: Hakes, David

### APPLICANT: Hakes, David

### APPLICANT: Bowe, Caryn

### TITLE OF INVENTION: GLYCOCONJUGATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE TITLE OF INVENTION: METHODS

### FILIE OF INVENTION: MUMBER: US/10/410,913

### CURRENT APPLICATION NUMBER: US 60/344,692

### PRIOR PILING DATE: 2001-10-19

### PRIOR FILING DATE: 2001-10-19

### PRIOR FILING DATE: 2002-06-25

### PRIOR PEPLICATION NUMBER: US 60/391,777

### PRIOR PEPLICATION NUMBER: US 60/396,594

### PRIOR PELING DATE: 2002-06-25

### PRIOR PELING DATE: 2002-06-25

### PRIOR PELING DATE: 2002-06-25

### PRIOR FILING DATE: 2002-06-25

### PRIOR FILING DATE: 2002-06-25

### PRIOR PELING DATE: 2002-06-25

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                                                                                                        APPLICANT: Chen, Xi

TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
FILE REPREENCE: 040853-01-5052-00
CURRENT APPLICATION NUMBER: US, 60/320, 994
CURRENT FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: US, 60/320, 523
PRIOR FILING DATE: 2001-10-10
PRIOR PLICATION NUMBER: US, 60/344, 692
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-00-07
PRIOR FILING DATE: 2002-06-07
PRIOR PLING DATE: 2002-06-07
PRIOR PLING DATE: 2002-06-16
PRIOR PLING DATE: 2002-06-17
PRIOR PLING DATE: 2002-06-16
PRIOR PLING DATE: 2002-06-16
PRIOR PLING DATE: 2002-06-16
PRIOR PLING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VANDER: US 60/407,527
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VANDER: US 60/407,527
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VARIENCE: ATTENTION NUMBER: US 60/407,527
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VARIENCE: ATTENTION NUMBER: US 60/407,527
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VARIENCE: ATTENTION NUMBER: US 60/407,527
PRIOR PLING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VARIENCE: ATTENTION NUMBER: US 60/407,527
PRIOR PLING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VARIENCE: ATTENTION NUMBER: US 60/407,527
PRIOR PLING DATE: 2002-08-28
SOFTWARE: PATENTIN VARIENCE: ATTENTION NUMBER: US 60/407,527
PRIOR PLING DATE: 2002-08-28
SOFTWARE: PATENTIN VARIENCE: ATTENTION NUMBER: US 60/407,527
PRIOR PLING DATE: ATTENTION NUMBER: US 60/407,527
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
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Publication No. US20040142856A1
GENERAL INFORMATION:
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1 Similarity 59.3%;
35; Conservative
                                      Bowe, Caryn
Hakes, David
Chen, Xi
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; ORGANISM: Homo sapiens
US-10-287-994-7
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Best Local Similarity
Matches 35; Conserva
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APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Caryn
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
FILE REFERENCE: 040853-01-5051
CURRENT FILING DATE: 2001-010
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/324,692
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
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Pred. No. 2.3;
0; Mismatches 24; Indels 0
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0.9%; Score 20.6; DB 1; Length 1332;
Best Local Similarity 59.3%; Pred. No. 2.3;
Matches 35; Conservative 0; Mismatches 24; Indels 0
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SOFTWARE: Patentin version 3.2
SEQ ID NO 7
LENGTH: 1332
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 59.3%;
Matches 35; Conservative
                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
US-10-410-997-7
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; ORGANISM: Homo sapiens
US-10-411-012-7
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US-10-411-012-7/c
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Sequence 7, Application US/10287994
Publication No. US20040137557A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert

-10-287-994-7/c

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440 TTCAATTGTCTTTTATCTGTCGAGACTTGCTTTTGTAAATATGTATTCAATTTTGG 498
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Publication No. US20040058347A1

GENERAL INFORMATION:

APPLICANT: Alsobrook, et al.

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

FILE REFERENCE: 2140-2568C

CURRENT APPLICATION NUMBER: US/10/382,248

PRIOR FILING DATE: 2003-03-22

PRIOR FILING DATE: 2002-03-26

PRIOR FILING DATE: 2002-03-66

PRIOR FILING DATE: 2002-03-66

PRIOR APPLICATION NUMBER: 60/366,928

PRIOR APPLICATION NUMBER: 60/366,928

PRIOR APPLICATION NUMBER: 60/366,477

PRIOR APPLICATION NUMBER: 60/365,477

PRIOR APPLICATION NUMBER: 60/365,477

PRIOR APPLICATION NUMBER: 60/365,477

PRIOR SEQUENCE: 2002-03-06

NUMBER OF SEQ ID NOS: 82

NUMBER OF SEQ ID NOS: 82

SOFTWARE: CURAS@qList version 0.1
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                                                                                                                                                                                                                                                                                                                                                   Gaps
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| Publication No. US20040110929A1
| GENERAL INFORMATION Soren E
| APPLICANT: Bjorn, Soren E
| APPLICANT: Nicolaisen, Else M
| APPLICANT: Nicolaisen, Else M
| APPLICANT: Nicolaisen, Anker S
| TITLE OF INVENTION: TF Binding Compound
| FILE REFERENCE: 4645.200-US
| CURRENT APPLICATION NUMBER: US/10/617,619
| CURRENT APPLICATION NUMBER: US/002-07-11
| PRIOR FILING DATE: 2003-07-11
| PRIOR FILING DATE: 2003-07-12
| PRIOR FILING DATE: 2003-07-13
| PRIOR FILING DATE: 2002-07-12
| PRIOR FILING DATE: 2002-07-13
| NUMBER OF SEQ ID NOS: 13
| SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                      Query Match

0.9%; Score 20.6; DB 1; Length 2040;
Best Local Similarity 59.3%; Pred. No. 3.2;
Matches 35; Conservative 0; Mismatches 24; Indels 0.
                                                                                                           , OTHER INFORMATION: Synthetic US-10-617-619-12
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TYPE: DNA
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial
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APPLICANT: King, Steven W
APPLICANT: King, Steven W
APPLICANT: King, Steven W
TITLE OF INVENTION: TISSUB FACTOR METHODS AND COMPOSITIONS FOR COAGULATION AND TUMOR
TITLE OF INVENTION: TREATMENT
TITLE OF INVENTION: UNMBER: 105/10/375,741
CURRENT FILING DATE: 1997-00-5-18
PRIOR FILING DATE: 1997-01-27
PRIOR FILING DATE: 1997-01-27
PRIOR APPLICATION NUMBER: 60/035,920
PRIOR FILING DATE: 1997-01-27
PRIOR APPLICATION NUMBER: 60/035,920
PRIOR PRILING DATE: 1997-01-27
PRIOR PILING DATE: 1997-01-22
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US-10-12/c
US-10-617-619-12/c
Sequence 12, Application US/10617619
Fublication No. US20040110929A1
GENERAL INFORMATION:
APPLICANT: Bionny
APPLICANT: Micolaisen, Else M
APPLICANT: Uorgensen, Anker S
TILLE OF INVENTION: TF Binding Compound
FILE REPRENCE: 645: 200-uS
CURRENT FILING DATE: 2003-07-11
FRIOR APPLICATION NUMBER: US/10/617,619
FRIOR APPLICATION NUMBER: US 60/404,568
FRIOR FILING DATE: 2002-07-12
FRIOR APPLICATION NUMBER: US 60/404,568
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
LENGTH: 2040
                                                                                                                                                                       Query Match

0.9%; Score 20.6; DB 1; Length 1332;
Best Local Similarity 59.3%; Pred No. 2.3;
Matches 35; Conservative 0; Mismatches 24; Indels 0;
Matches 35; Conservative 0;
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CORGANISM: Homo sapiens
US-10-375-741-13
TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-375-741-13/c
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                                                                               US-10-410-913-7
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                                                                                                                                                                                                                                        Gaps
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| Sequence 35, Application US/10382248|
| Publication No. 120040058347A1|
| GEMERAL INFORMATION:
| APPLICAMI: Alsobrook, et al. |
| TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME |
| TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME |
| TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME |
| TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME |
| TITLE OF INVENTION: NOVEL PROTEINS 2003-03-05 |
| PRIOR APPLICATION NUMBER: 60/366,928 |
| PRIOR FILING DATE: 2002-03-06 |
| PRIOR FILING DATE: 2002-03-06 |
| PRIOR FILING DATE: 2002-03-06 |
| PRIOR PRILING DATE: 2002-03-06 |
| PRIOR PILING DATE: 2002-03-06 |
| PRIOR PILING DATE: 2002-03-06 |
| NUMBER OF SEQ ID NOS: 82 |
| NUMBER OF SEQ ID NOS: 82 |
| SOFTWARE: CuraSequist version 0.1
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0.8%; Score 17.2; DB 1; Length 1361;
Best Local Similarity 51.3%; Pred. No. 26;
Matches 40; Conservative 0; Mismatches 38; Indels 0;
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Sequence 8429, Application US/09918995
Sublication No. US2003007362341
GENERAL INFORMATION:
APPLICANT: Hyeg, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL VARIOUS CONA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
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; LOCATION: (45)..(1301)
US-10-382-248-35
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ORGANISM: Homo sapiens
                                                ) NAME/KEY: CDS
; LOCATION: (45)..(1301)
US-10-382-248-35
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US-09-918-995-8429
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APPLICANT: CHEL, AI
APPLICANT: CHEL, AI
TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
TITLE OF INVENTION: GALACTOSIDASE A
FILE REPRENCE: O40853-01-5082
CURRENT FILING DATE: 2003-04-09
FRIOR PELICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2002-06-05
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-05
PRIOR FILING DATE: 2002-06-05
PRIOR FILING DATE: 2002-06-05
PRIOR FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-05
PRIOR FILING DATE: 2002-06-05
PRIOR FILING DATE: 2002-06-05
PRIOR FILING DATE: 2002-06-05
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-08-16
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

0.7%; Score 17; DB 1; Length 483;
Best Local Similarity 59.2%; Pred. No. 19;
Matches 29; Conservative 0; Mismatches 20; Indels
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8429
LENGTH: 483
                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
; LOCATION: (1)...(483)
; CHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
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Zopf, David
Bayer, Robert
Hakes, David
Chen, Xi
Bowe, Caryn
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, ORGANISM: Homo sapiens
US-10-411-037-7
                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.7%; Score 17; DB 1; Length 1332; Best Local Similarity 59.2%; Pred. No. 28; Matches 29; Conservative 0; Mismatches 20; Indels
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PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR PELING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR PILING DATE: 2002-06-17
PRIOR PILING DATE: 2002-07-17
PRIOR PILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-18
SOFTWARE: PATCHTON NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-18
SOFTWARE: PATCHTIN VERSION 3.2
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CURRENT APPLICATION NUMBER: US/10/411,049
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin version 3.2
SEQ ID NO 7
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Publication No. US20040115168A1
SENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
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Publication No. US20040082026A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-10-410-962-7
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CRGANISM: Homo sapiens
US-10-411-049-7
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                            PRUBLICANT: NEOSE TECHNOLOGIES, INC.
APPLICANT: NEOSE TECHNOLOGIES, INC.
APPLICANT: DEFESS, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Chan, Xi
TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
FILE REFERENCE: 040853-04-09
FILE REFERENCE: 040853-04-09
FRIOR APPLICATION NUMBER: US 60/328,523
FRIOR APPLICATION NUMBER: US 60/328,523
FRIOR APPLICATION NUMBER: US 60/381,292
FRIOR PILING DATE: 2001-10-19
FRIOR APPLICATION NUMBER: US 60/394,692
FRIOR PILING DATE: 2002-06-07
FRIOR APPLICATION NUMBER: US 60/396,594
FRIOR APPLICATION NUMBER: US 60/407,249
FRIOR APPLICATION NUMBER: US 60/407,227
FRIOR APPLICATION NUMBER: US 60/407,227
FRIOR APPLICATION NUMBER: US 60/407,227
FRIOR FILING DATE: 2002-08-16
FRIOR FILING DATE: 2002-08-16
FRIOR FILING DATE: 2002-08-16
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APPLICANT: Neose Technologies, Inc.
APPLICANT: Copf, David
APPLICANT: Rayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
                 Publication No. US20040063911A1
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: GLYCOPECYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE TITLE OF INVENTION: GLYCOPECYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE TITLE OF INVENTION: METHODS

FILE REFERENCE: 040853-01-5051

CURRENT APPLICATION NUMBER: US 10/411,012

CURRENT FILING DATE: 2003-04-09

FRIOR APPLICATION NUMBER: US 60/324,692

FRIOR APPLICATION NUMBER: US 60/344,692

FRIOR FILING DATE: 2001-10-19

FRIOR FILING DATE: 2001-10-19

FRIOR FILING DATE: 2002-06-07

FRIOR FILING DATE: 2002-06-17

FRIOR FILING DATE: 2002-06-17

FRIOR APPLICATION NUMBER: US 60/396,594

FRIOR APPLICATION NUMBER: US 60/404,249

FRIOR FILING DATE: 2002-08-16

FRIOR FILING DATE: 2002-08-18

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Pred. No. 28;
0; Mismatches 20; Indels
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/10411012
Publication No. US20040132640A1
GENERAL INFORMATION:
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
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Publication No. US20040137557A1
GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 75
SOFWARE: Patentin version 3.2
SEQ ID NO 7
LENCTH: 1332
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Best Local Similarity 59.2%;
Matches 29; Conservative
                                                                                                                                                                                                         TYPE: DNA; ORGANISM: Homo sapiens
US-10-410-997-7
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US-10-411-012-7
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 29; Conserv
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US-10-287-994-7
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APPLICANT: Derres, Snawn
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Bovid
APPLICANT: Bayer, Caryn
APPLICANT: Bowe, Caryn
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF TITLE OF INVENTION: FOH CARS 10.5059
CURRENT APPLICATION NUMBER: US/10/410,997
CURRENT APPLICATION NUMBER: US 60/328,523
FRIOR APPLICATION NUMBER: US 60/328,523
FRIOR PELICATION NUMBER: US 60/344,692
FRIOR FILING DATE: 2002-10-19
FRIOR APPLICATION NUMBER: US 60/391,777
FRIOR APPLICATION NUMBER: US 60/391,777
FRIOR FILING DATE: 2002-06-05
FRIOR FILING DATE: 2002-06-05
FRIOR FILING DATE: 2002-06-07
FRIOR FILING DATE: 2002-07-17
FRIOR APPLICATION NUMBER: US 60/396,594
FRIOR FILING DATE: 2002-07-17
FRIOR APPLICATION NUMBER: US 60/404,249
                                                                                                                                                              APPLICANT: Chen, XI
APPLICANT: Chen, XI
APPLICANT: Chen, XI
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
FILE REFERENCE: 040853-01-5056
CURRENT APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2002-06-07
PRIOR PLICATION NUMBER: US 60/391,777
PRIOR FLILING DATE: 2002-06-07
PRIOR PLICATION NUMBER: US 60/391,777
PRIOR PLICATION NUMBER: US 60/391,777
PRIOR PLILING DATE: 2002-06-16
PRIOR PLILING DATE: 2002-06-16
PRIOR PLILING DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-16
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Pred. No. 28;
0; Mismatches
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FILING DATE: 2002-08-16
APPLICATION NUMBER: US 60/407,527
FILING DATE: 2002-08-28
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Publication No. US20040126838A1
GENERAL INFORMATION:
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Best Local Similarity 59.2%;
Matches 29; Conservative
                                                                                            Robert
                                                                                                                                             David
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; ORGANISM: Homo sapiens
US-10-410-930-7
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US-10-410-997-7
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US-10-617-619-12

US-10-617-619-12

Sequence 12, Application US/10617619

Publication No. US20040110929A1

GENERAL INFORMATION:
APPLICANT: Bjoon Soren

APPLICANT: Nicolaisen, Else M
APPLICANT: Nicolaisen, Anker S

TITLE OF INVENTION: TP Binding Compound
FILE REPERBNCE: 6455.200-US

CURRENT APPLICATION NUMBER: US/10/617,619

CURRENT APPLICATION NUMBER: Danish Application No. PA 2002 01099

PRIOR FILING DATE: 2002-07-11

PRIOR FILING DATE: 2002-07-12

PRIOR FILING DATE: 2002-07-13

SOFTWARE: Patentin version 3.2

SEQ ID NO.12

LENGTH: 2040

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LENGTH: 2040
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0.7%; Score 17; DB 1; Length 2040;
Best Local Similarity 59.2%; Pred. No. 24;
Matches 29; Conservative 0; Mismatches 20; Indels
                                                                                                                                                                                                0.7%; Score 17; DB 1; Length 1332;
59.2%; Pred. No. 28;
tive 0; Mismatches 20; Indels
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; Sequence 2, Application US/09782587B
; Publication No. US20030096338A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PEDERSEN, ANDERS H.
APPLICANT: ANDERSON, KIW V.
APPLICANT: ANDERSON, KIW V.
TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
CURRENT APPLICANTON NUMBER: US/09/782,587B
CURRENT APPLICANION NUMBER: BA 2000 00218
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-12
PRIOR PILING DATE: 2000-02-13
PRIOR PILING DATE: 2000-02-13
PRIOR FILING DATE: 2000-02-13
PRIOR FILING DATE: 2000-02-13
PRIOR FILING DATE: 2000-02-13
PRIOR FILING DATE: 2000-02-13
PRIOR PILING DATE: 2000-02-13
SOFTWARE: PALENTING DATE: 2000-02-13
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Best Local Similarity 59.23
Matches 29; Conservative
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                                                TYPE: DNA
CAGANISM: Homo sapiens
US-10-410-913-7
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US-09-782-587B-2/c
             LENGTH: 1332
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APPLICANT: Bayer, Robert
APPLICANT: Bowe, Caryn
APPLICANT: Bowe, Caryn
APPLICANT: Chen, Xi
TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
FILE REFERENCE: 040853-01-505-00
CURRENT APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR PLING DATE: 2001-10-10
PRIOR PLING DATE: 2001-10-10
PRIOR PLING DATE: 2001-10-19
PRIOR PLING DATE: 2002-06-07
PRIOR PLING DATE: 2002-06-07
PRIOR PLING DATE: 2002-06-07
PRIOR PLING DATE: 2002-06-25
PRIOR PLING DATE: 2002-06-25
PRIOR PLING DATE: 2002-06-25
PRIOR PLING DATE: 2002-06-26
PRIOR PLING DATE: 2002-06-26
PRIOR PLING DATE: 2002-08-16
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0.7%; Score 17; DB 1; Length 1332;
Best Local Similarity 59.2%; Pred. No. 28;
Matches 29; Conservative 0; Mismatches 20; Indels
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TYPE: DNA
ORGANISM: Homo sapiens
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US-10-617-619-9
IS-10-617-619-9
Sequence 9, Application US/10617619
Sequence 9, Application US/10617619
Sequence 9, Application US/10617619
Sequence 9, Application No. US20040110929A1
SEPERAL INFORMATION:
APPLICANT: Bjorn, Soren E
APPLICANT: Nicolaisen, Else M
APPLICANT: Organisen, Anker S
ITLE OP INVENTION: TE Binding Compound
FILE REFERENCE: 6455.200-US
CURRENT FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01099
PRIOR FILING DATE: 2002-07-12
PRIOR FILING DATE: 2002-08-19
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
SEQ ID NO 9
LANDTH 2106
TVENT APPLICATION NUMBER OF SEQ ID NOS: 13
SEQ ID NO 9
LANDTH 2106
TVENT APPLICATION NUMBER OF SEQ ID NOS: 13
SEQ ID NO 9
LEAGTH: 2106
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US-09-918-995-8429/C
Sequence 8429, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT HYSEQ, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
NUMBER OF SEQ ID NOS: 38054
SEQ ID NOS: 8429
LENGTH: 483
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0; Mismatches 14; Indels
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Pred. No. 31;
0; Mismatches
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Pred. No. 24
        PRIOR APPLICATION NUMBER: 60/035,920
PRIOR FILING DATE: 1997-01-22
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 1440
                                                                                                                                                                                                                                                                                                                                                                                                  0.7%;
ilarity 64.1%;
Conservative
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Best Local Similarity 64.1%;
Matches 25; Conservative
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                                                                                                                                                                                                                                       TYPE: DNA; ORGANISM: Homo sapiens
US-10-375-741-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 25; Conservé
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23
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US-10-375-741-13
Sequence 13, Application US/10375741
Sequence 13, Application US/10375741
Sequence 13, Application US/10375741
Sequence 13, Application No. US20030232753A1
GENERAL IRPORMATION:
APPLICANT: King, Steven W
APPLICANT: King, Steven W
APPLICANT: Gao, Boning
TITLE OF INVENTION: TISSUE FACTOR METHODS AND COMPOSITIONS FOR COAGULATION AND TUMOR
FILE REFERENCE: 4001.001999
CURRENT FILING DATE: 2000-05-18
FRICR RAPLICATION NUMBER: 09/573, 835
PRIOR FILING DATE: 1998-01-20
PRIOR FILING DATE: 1998-01-20
PRIOR FILING DATE: 1998-01-27
PRIOR FILING DATE: 1997-01-27
PRIOR FILING DATE: 1997-01-27
PRIOR FILING DATE: 1997-01-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
                                                                                                                                                                                               ch 0.7%; Score 16.6; DB 1; Length 1338; Il Similarity 64.1%; Pred. No. 32; 25; Conservative 0; Mismatches 14; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09782587B
Publication No US20030096338A1
GENERAL INRORMATION:
APPLICANT: PEDERSEN, ANDERS H.
APPLICANT: ANDERSON, KIM V.
APPLICANT: BORNARS, CLAUS
TITLE OF INVENTION: PACTOR VII OR VIIA-LIKE MOLECULES
TITLE OF INVENTION: PACTOR VII OR VIIA-LIKE MOLECULES
GURRENT APPLICATION NUMBER: US/09/782,587B
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: PA 2000 00218
FRIOR APPLICATION NUMBER: 60/184,036
FRIOR APPLICATION NUMBER: 60/241,916
FRIOR APPLICATION NUMBER: 60/241,916
FRIOR APPLICATION NUMBER: 60/241,916
FRIOR APPLICATION NUMBER: 2000-02-22
FRIOR APPLICATION NUMBER: 2000-02-22
FRIOR APPLICATION NUMBER: 2000-02-22
FRIOR APPLICATION NUMBER: 2000-02-22
FRIOR APPLICATION NUMBER: 2000-02-22
FRIOR APPLICATION NUMBER: 2000-02-22
FRIOR APPLICATION NUMBER: 2000-02-22
FRIOR APPLICATION NUMBER: 2000-02-22
FRIOR FILING DATE: 2000-02-22
FRIOR APPLICATION NUMBER: 2000-02-22
FRIOR APPLICATION NUMBER: 2000-02-22
FRIOR APPLICATION NUMBER: 2000-02-22
                                                                                                                                                                                                                                                                                                                                                 1228 GGCCTGGAATTATTTATTATTCATATTTCTTGAATGTG 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1228 GGCCTGGAATTATTATTATTCATATTTTCTTGAATGTG 1266
                                                                                                                                                                                                                                                                                                                                                                                                                           567 GCCCrGGGTTTGCTAGCGTTCCGCTTTTCTAGAATGGG 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               542
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Best Local Similarity 64.1%; Pred. No. 32;
Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
                                    ) NAME/KEY: CDS
; LOCATION: (115)..(1332)
US-09-782-587B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 27
US-09-782-587B-4/c
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LENGTH: 1357
                                                                                                                                                                                       Query Match
Best Local S
Matches 25
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FEATURE:
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10664//5-4.rnpb
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Sequence 9623, Application US/10029386
; Sequence 9623, Application US/10029386
; Sequence 9623, Application US/10029386
; Candra No. US20030194704A1
; Candra No. US20030194704A1
; Candra No. US20030194704A1
; APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GITTLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GITTLE OF INVENTION: MUMBER OF SEQ ID NOS: 34288
; CURRENT FILLING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARES Annowax Sequence Listing Engine vers: 1.1
; SEQ ID NO 9633
; LENGTH: 555
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Publication No. US20030180748A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: GENETIC MARKERS
TITLE OF INVENTION: GENETIC MARKERS
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OCHARIAM. Homo sapiens
FEATURE:
CTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN BONE WARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BONE WARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXTHUMAN HIT: PORTOR, SWALUE 5.00e-76
US-10-029-386-9623
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                                                                                                       OTHER INFORMATION: MAP TO CHRI3.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: NT HIT: gil4783796, EVALUE 1.00e-122
OTHER INFORMATION: EST HUMAN HIT: P08709, EVALUE 3.00e-26
US-10-029-386-23323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.6%; Score 14.6; DB 1; 1
Best Local Similarity 54.7%; Pred. No. 69;
Matches 29; Conservative 0; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
0.6%; Score 14.6; DB
Best Local Similarity 54.7%; Pred. No. 79;
Matches 29; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1905 CTGTCAGTGAGGCTTGTCT
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 34
US-10-272-665-22/c
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Sequence 23323, Application US/10029386
Sequence 23323, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR OTHER REPRESENT HUMAN GENOME-BENOME: AEOMICA-X-C
TITLE OF INVENTION: MANBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 23323
LENGTH: 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5023, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Penn, David R.
APPLICANT: Hanzel, APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, APPLICANT: Hanzel, David R.
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APPLICANT: Hanzel, APPLICANT: Hanzel, David R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415 AGGACTGGAGCTGGTCCTTGCAGGAGCCCCCATTCTGGCATGGACTTGAGGCACACTG 358
                                                                                                                                                                                                                                                                                                                              Gaps
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEART, EVALUE 5.00e-76
US-10-029-386-9623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 14.8; DB 1; Length 555; 56.0%; Pred. No. 75; tive 0; Mismatches 22; Indels
                                                                                                                                                                                                                                            Length 483;
                                                                                                                                                                                                                                                                                                                          26; Indels
                                                                                                                                                                                                                                            0.7%; Score 16.4; DB 1;
55.2%; Pred. No. 30;
tive 0; Mismatches 26;
                                                                                      LOCATION: (1)...(483)
CTHER INFORMATION: n = A,T,C or G
US-09-918-995-8429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 56.0
Matches 28; Conservative
                                                                                                                                                                                                                                        Query Match
Best Local Similarity 55.2
Matches 32, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                   NAME/KEY: misc_feature
LOCATION: (1)...(483)
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US-10-029-386-9623
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## APPLICANT: Braun et al.

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POIL

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POIL

TITLE OF INVENTION: MERCENS

FILE REPRENCE: 24736-2033C

CURRENT APPLICATION NUMBER: US/10/272,756

CURRENT APPLICATION NUMBER: US/687,483

PRIOR APPLICATION NUMBER: 09/687,483

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR PRIOR PRILING DATE: 2000-07-10

PRIOR PRILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 00/127,251

PRIOR PRILING DATE: 2000-07-10

PRIOR PRILING DATE: 2000-07-10

PRIOR PRILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 118

SEQ ID NO 22

LENGTH: 60

TYPE: DNA

ORGANISM: Homo Sapien
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J GENERAL INVORVATION.

J TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POIL

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING POIL

TITLE OF INVENTION: GENERAL MARKERS

FILE REFERENCE: 24736-2033D

CURRENT APPLICATION NUMBER: US/10/273,228

CURRENT FILING DATE: 2000-07-10

PRIOR PELING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 60/159,176

PRIOR PELING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 118

SOFTWARRE: FastSEQ for Windows Version 4.0

SEQ ID NO 22
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0.6%; Score 14.2; DB 1;
Best Local Similarity 62.9%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 13;
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il Similarity 62.9%; Pred. No. 35;
22; Conservative 0; Mismatches
                                                   Sequence 22, Application US/10272756
Publication No. US20030190644A1
GENERAL INFORMATION;
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Publication No. US20030207297A1
GENERAL INFORMATION:
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ORGANISM: Homo Sapien
FEATURE:
OTHER INFORMATION: Probe
US-10-273-228-22
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Best Local Similarity
Matches 22; Conserva
                           JS-10-272-756-22/c
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### APPLICANT: Braun et al.
### APPLICANT: Braun et al.
#### TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
#### TITLE OF INVENTION: GENERATING MARKERS
### TITLE OF INVENTION: GENERATING MARKERS
### CURRENT PILING DATE: 2012-10-15
### CURRENT PILING DATE: 2000-07-10
### PRIOR PILING DATE: 2000-07-10
### PRIOR PILING DATE: 2000-07-10
### PRIOR PILING DATE: 1999-10-13
### PRIOR FILING DATE: 1999-10-13
### PRIOR FILING DATE: 2000-07-10
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### PRIOR PI
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FILE REFERENCE: 24736-2033E
CURRENT APPLICATION NUMBER: US/10/272,665
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 09/687,483
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR FILING DATE: 2000-07-10
PRIOR PLING DATE: 2000-07-10
PRIOR PLING DATE: 2000-07-13
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: FASTSEQ FOR Windows Version 4.0
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0.6%; Score 14.2; D:
Best Local Similarity 62.9%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches
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; Sequence 22, Application US/10273321
; Publication No. US/0030180749A1
; GENERAL INFORMATION:
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Best Local Similarity 62.9
Matches 22; Conservative
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ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
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LENGTH: 60
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US-10-272-756-107/c

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US-10-273-228-107/c
; SQUELICATION WOUNDERFORM US/10273228
; Publication No. US20030207297A1
; GENERAL INFORMATION:
; APPLICANT: Braun et al.
; TITLE OF INVENTION: GENERATING DATABASES AND DATABASES POR IDENTIFYING POI TITLE OF INVENTION: GENERATING DATABASES AND DATABASES POR IDENTIFYING POI TITLE OF INVENTION: GENERAT MARKERS; US/10/273,228
; TITLE OF INVENTION: GENERAL SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE S
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         Length 100;
Query Match 0.6%; Score 14.2; DB 1; Length 1
Best Local Similarity 62.9%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 13; Indels
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CRGANISM: Homo sapien
US-10-272-756-107
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; Sequence 107, Application Wo. US20030180748A1
; Sequence 107, Application No. US20030180748A1
; GENERAL INFORMATION:
    APPLICAMY: Braun et al.
; TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING FOR ITLE OF INVENTION: GENETIC MARKERS
; TITLE OF INVENTION: GENETIC MARKERS
; CURRENT APPLICATION NUMBER: 09/687,483
; PRIOR APPLICATION NUMBER: 60/217,658
; PRIOR APPLICATION NUMBER: 60/217,658
; PRIOR PRILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/217,251
; PRIOR APPLICATION NUMBER: 09/663,968
; PRIOR FILING DATE: 2000-09-19
; PRIOR FILING DATE: 2000-09-19
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FESTSEQ for Windows Version 4.0
; SEQ ID NO 107
; LENGTH: 100
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Sequence 10.7, Application US/10273321

Sequence 10.7, Application US/10273321

GENERAL INFORMATION:

APPLICANT: Braun et al.

TITLE OF INVENTION: GENETIC MARKERS

FILE REFERENCE: 24736-2038

CURRENT APPLICATION NUMBER: US/10/273,321

CURRENT FILING DATE: 2002-10-15

PRIOR APPLICATION NUMBER: 09/687,483

PRIOR APPLICATION NUMBER: 09/217,658

PRIOR PILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR PLING DATE: 2000-07-10

PRIOR PLING DATE: 2000-09-19

NUMBER: FastSEQ for Windows Version 4.0

SEQ ID NO 107

LENGTH: 100

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Best Local Similarity 62.9
Matches 22, Conservative
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CORGANISM: Homo sapien
US-10-272-665-107
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; ORGANISM: Homo sapien
US-10-273-321-107
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### ITILE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POI
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Sequence 106, Application US/10273228

Publication No. US20030207297A1

Sequence 106, Application US/10273228

Publication No. US20030207297A1

APPLICATION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING POINTED OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING POINTED OF INVENTION: METHODS FOR GENERATING DATE: 2002-10-15

CURRENT APPLICATION NUMBER: 09/687,483

PRIOR PILING DATE: 2000-07-10

PRIOR PELLOR TO NUMBER: 60/217,658

PRIOR PELLOR APPLICATION NUMBER: 60/159,176

PRIOR PELLOR APPLICATION NUMBER: 60/159,176

PRIOR APPLICATION NUMBER: 60/159,176

PRIOR PILING DATE: 1999-10-13

PRIOR PILING DATE: 2000-07-10

PRIOR PILING DATE: 00/1007-10

PRIOR PILING DATE: 10/10-13

PRIOR PILING DATE: 10/10-13

PRIOR FILING DATE: 2000-07-10

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PRIOR FILING DATE: 2000-07-10
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Pred. No. 53;
0; Mismatches
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Pred. No. 53;
0; Mismatches
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Publication No. US20030190644A1
GENERAL INFORMATION:
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Best Local Similarity 62.9%;
Matches 22; Conservative (
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 62.9%;
Matches 22; Conservative
    ; SEQ ID NO 106
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-273-321-106
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US-10-272-756-106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ## Sequence 106, Application US/10272665
### Publication No. US20030180748A1
### GENERAL INFORMATION:
### APPLICANT: Braun et al.
### TITLE OF INVENTION: GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
### TITLE OF INVENTION: GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
### TITLE OF INVENTION: GENERATING DATABASES FOR IDENTIFYING PC
### TITLE OF INVENTION: GENERATING DATABASES FOR IDENTIFYING PC
### TITLE OF INVENTION: GENERATING DATABASES FOR IDENTIFYING PC
### TITLE OF INVENTION UNMBER: US/10/272,665
### CURRENT FILING DATE: 2002-10-15
### PRIOR PILING DATE: 2000-07-10
### PRIOR FILING DATE: 1999-10-13
### PRIOR FILING DATE: 1999-10-13
### PRIOR FILING DATE: 2000-07-10
### PRIOR FILING DATE: 2000-07-10
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Publication No. US20030180749A1

GENERAL INFORMATION:

TILE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC

TILLE OF INVENTION: GENETIC MARKERS

TILLE OF INVENTION: GENETIC MARKERS

FILE REPERRENCE: 24736-2033B

CURRENT APPLICATION NUMBER: US/10/273,321

CURRENT APPLICATION NUMBER: 09/687,483

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 2000-07-10

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Pred. No. 53;
0; Mismatches 13; Indels
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Pred. No. 53;
0; Mismatches 13; Indels
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Best Local Similarity 62.9%;
Matches 22; Conservative
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; ORGANISM: Homo sapien
US-10-273-228-107
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ORGANISM: Homo sapien
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Best Local Similarity
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US-10-272-665-106/c
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US-10-273-321-106/c
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Matches 19; Conservative 0; Mismatches
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O.6%; Score 14.2; DB 1; Length 1
Best Local Similarity. 62.9%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 13; Indels
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Sequence 4, Application US/09782587B

Sequence 4, Application US/09782587B

Publication No. US20330096338A1

GENERAL INFORMATION:

APPLICANT: PADERSEN, ANDERS H.

APPLICANT: BORNAES, CLAUS

TITLE OF INVENTION: FATOR VI OR VIIA-LIKE MOLECULES

TITLE OF INVENTION: FATOR VI OR VIIA-LIKE MOLECULES

CURRENT PELLING DATE: 2002-03-26

PRIOR APPLICATION NUMBER: PA 2000 00218

PRIOR PILING DATE: 2000-02-11

PRIOR PILING DATE: 2000-02-13

PRIOR PILING DATE: 2000-02-21

PRIOR PILING DATE: 2000-02-22

PRIOR PLING DATE: 2000-02-22
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PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SECTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 106
LENGTH: 100
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Best Local Similarity 70.4
Matches 19; Conservative
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) LOCATION: (115)..(1332)
US-09-782-587B-2
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                                                                                                                                                                                                  TYPE: DNA
CORGANISM: Homo sapien
US-10-273-228-106
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Sequence 23323, Application US/10029386

Publication No. UG20030194704A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HANZEL, DAVID K.
APPLICANT: HOWEN G.
APPLICANT: APPLICATION UNDER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARES Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 23323
LENGTH: 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 49
US-10-349-858-8/c
US-10-349-858-8/c
Squence 8, Application US/10349858;
Publication No. US20030220247A1
GENERAL INFORMATION:
APPLICANT: HIGH, KATHERINE A.
APPLICANT: CAMIRE, RODNEY M.
APPLICANT: CAMIRE, RODNEY M.
APPLICANT: STAFFORD, DETER J.
APPLICANT: STAFFORD, DARREL W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
PRIOR FILING DATE: 2000-10-18

NUMBER OF SEQ ID NOS: 19

S OSFWARE: Patentin Ver. 2.1

S SEQ ID NO 4

LENGTH: 1357

TYPE: DNA

OTHER INFORMATION: Description of Artificial Sequence: Expression

PEATURE:
OTHER INFORMATION: Cassette for expression of FVII in mammalian cells
US-09-782-587B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: DNA
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN BUNG, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN BUNG, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN BUNG MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EST HUMAN HIT: ALS31727.1, EVALUE 3.00e-26
CHER INFORMATION: SWISSPROT HIT: PO8709, EVALUE 3.00e-37
US-10-029-386-23323
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0.5%; Score 12; DB 1; Length 222;
Best Local Similarity 58.3%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 15; Indels
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Gaps

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GENERAL INFORMATION:

APPLICANT: Nicolaisen, Else Marie
APPLICANT: Nicolaisen, Lars Soegaard
TITLE OF INVERTION: Method for the Production of Vitamin K-Dependent Proteins
TITLE OF INVERTION: Method for the Production of Vitamin K-Dependent Proteins
FILE OF INVERTION: MURBER: US/10/398,422A
CURRENT FELING DATE: 2003-09-02
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: Danish application PA 2001 00430
PRIOR APPLICATION NUMBER: Danish application PA 2001 00751
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-05-14
PRIOR FILING DATE: 2001-05-14
PRIOR FILING DATE: 2001-05-14
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
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PRIOR DATE: 2001-03-16
PRIOR DATE: 2001-03
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                                                                                                                                                                                                                                                                                                          FEATURE:

CTHER INFORMATION: DNA primer for preparation of S314E-FVII US-10-281-727-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 11.6; DB 1;
Pred. No. 1.8e+02;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 TAATATATTTTCTTGAAGCCTCTGCTGGC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 rahahcecriricciesakeascreceec 38
                   PRIOR FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 60/335,383
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/10398422A Publication No. US20040058413A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1999 TICCACTITCAGGICCTG 2016
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Best Local Similarity 77.8%;
Matches 14; Conservative
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Best Local Similarity
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ORGANISM: Artificial
                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 52
US-10-398-422A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 53
US-09-969-357-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

0.5%; Score 11.8; DB 1; Length 54;
Best Local Similarity 69.6%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 11.6; DB 1; Length 32;
Pred. No. 1.8e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: DNA primer for preparation of $314E-FVII
US-10-281-727-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-281-727-6/c
; Sequence 6, Application US/10281727
; Publication No. US20030130191A1
; GENERAL INFORMATION:
    APPLICANT: Persson, Egon
    APPLICANT: Olsen, Ole Hvilsted
    TITLE OF INVENTION: Human Coagulation Factor VII
; TITLE OF INVENTION: Polypeptides
    FILE REFERENCE: 6410.200-US
    CURRENT APPLICATION NUMBER: US/10/281,727
    CURRENT FILING DATE: 2002-10-28
    PRIOR APPLICATION NUMBER: PA 2001 01627
    PRIOR FILING DATE: 2001-11-02
    PRIOR FILING DATE: 2001-11-15
    NUMBER OF SEQ ID NOS: 7
    SOFTWARE: FastSEQ for Windows Version 4.0
    COARDANT APPLICATION NUMBER: OF SEQ ID NOS: 7
    SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20030130191A1
GENERAL INFORMATION:
APPLICANT: Person, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII
FILLE REFERENCE: 6410.200-US
TITLE OF INVENTION: FACTORS
FILE REFERENCE: 018743-0301425
CURRENT APPLICATION NUMBER: US/10/349,858
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 09/526,947
PRIOR PILING DATE: 2000-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 54
TYPE: DNA
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CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: PA 2001 01627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1925 TGAGGTTCCTGTTGGGTTCTTAA 1947
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Best Local Similarity 77.8%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-10-349-858-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 51
US-10-281-727-7
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LENGTH: 32
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Gaps

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US-1U-2/2-065-22, Application US/10272665

j Sequence 22, Application US/10272665

j Bequence 22, Application No. US20030180748A1

j GENERAL INFORMATION:
    TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POIL
    TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING POIL
    TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING POIL
    TITLE OF INVENTION: GENETIC MARKERS
    FILE REFERENCE: 24736-2633E
    CURRENT APPLICATION NUMBER: US/10/272,665
    CURRENT FILING DATE: 2000-07-10
    PRIOR FILING DATE: 2000-07-10
    PRIOR FILING DATE: 1999-10-13
    PRIOR FILING DATE: 2000-07-10
    PRIOR PELICATION NUMBER: 60/119/176
    PRIOR APPLICATION NUMBER: 60/119/176
    PRIOR APPLICATION NUMBER: 60/119/176
    PRIOR APPLICATION NUMBER: 09/663,968
    PRIOR PILING DATE: 2000-09-19
    NUMBER OF SEQ ID NOS: 118
    SOFTWARE: FastSEQ for Windows Version 4.0
    LENGTH: 60
    LENGTH: 60

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APPLICANT: Braun et al.

ITILE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POI

TITLE OF INVENTION: GENETIC MARKERS

TITLE OF INVENTION: GENETIC MARKERS

FILE REFERENCE: 24736-20338

CURRENT APPLICATION NUMBER: US/10/273,321

CURRENT APPLICATION NUMBER: 09/687,483

PRIOR FILING DATE: 2000-07-10

PRIOR PILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 60/17,658

PRIOR PILING DATE: 1999-10-13

PRIOR PILING DATE: 1999-10-13

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-99-19

WOWHER OF SEQ ID NOS: 118

SEQ ID NO 22
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publication No. US20030180749A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 56.8<sup>†</sup>
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-273-321-22
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APPLICANT: Pingel, Hans K
APPLICANT: Klausen, Niels K
TITLE OF INVENTION: Factor VII Glycoforms
FILE REFERENCE: 6207-510-05
CURRENT FILING DATE: 2002-10-02
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: US/09/969,357
CURRENT FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2001-02-14
PRIOR PAPLICATION NUMBER: Danish Application No. PA 2001 00751
PRIOR FILING DATE: 2001-05-14
PRIOR FILING DATE: 2001-05-14
PRIOR FILING DATE: 2001-05-14
PRIOR FILING DATE: 2001-05-16
PRIOR FILING DATE: 2001-01-10
PRIOR FILING DATE: 2001-01-10
PRIOR FILING DATE: 2001-01-10
PRIOR FILING DATE: 2001-01-10
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.2
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; Sequence 2, Application US/10254394
; Publication No. US20030096366A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL THOROMATION:
TITLE OF INVENTION: Method for Production of Rec
TITLE OF INVENTION: Proteins in Eukaryote Cells
FILE REFERENCE: 6480-500-US
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US/10/254,394
CURRENT FILING DATE: 2001-10-02
PRIOR PILING DATE: 2001-10-02
PRIOR PILING DATE: 2001-10-02
PRIOR FILING DATE: 2001-10-02
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
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ORGANISM: Artificial Sequence
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Best Local Similarity 62.1
Matches 18; Conservative
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Novo Nordisk Pharmaceuticals, Inc.

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RESULT 59

US-10-272-665-107

US-10-272-665-107

Sequence 107, Application US/10272665

Publication No. US2003180748A1

Sequence 107, Application No. US2003180748A1

APPLICANT Braun et al.

TITLE OF INVENTION: BRETHIC MARKERS

TITLE OF INVENTION: GENETIC MARKERS

TITLE OF INVENTION: GENETIC MARKERS

FILE REFERENCE: 24736-2033E

CURRENT FILING DATE: 2002-10-15

PRIOR PLICATION NUMBER: 60/217,668

PRIOR PLICATION NUMBER: 60/159,176

PRIOR PLICATION NUMBER: 60/159,176

PRIOR PLICATION NUMBER: 60/217,251

PRIOR PLICATION NUMBER: 09/663,968

PRIOR PLICATION NUMBER: 09/663,968

PRIOR FILING DATE: 2000-07-10

PRIOR PLICATION NUMBER: 09/663,968

PRIOR FILING DATE: 2000-07-10

PRIOR
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Sequence 107, Application US/10273321
Publication No. 102:
GENERAL INFORMATION:
TITLE OF INVENTION: BETHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POILTIFLE OF INVENTION: BETHODS FOR GENERATING DATABASES FOR IDENTIFYING POILTIFLE OF INVENTION: MUMBER: US/10/273,321
CURRENT APPLICATION NUMBER: 10/20-10-15
PRIOR PILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 09/687,483
PRIOR PADLICATION NUMBER: 60/217,658
PRIOR PADLICATION NUMBER: 60/217,658
PRIOR FILING DATE: 2000-07-10
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                  NUMBER OF SEQ ID NOS: 118
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 60
                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Probe US-10-273-228-22
                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo Sapien
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CORGANISM: Homo sapien
US-10-272-665-107
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Best Local Similarity
Matches 21, Conserv
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Publication No. US20030190644A1

GENERAL INFORMATION:

APPLICANT: Braun et al.

TITLE OF INVENTION: GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: GENERAL WARKERS

FILE REFERENCE: 24736-2033C

CURRENT APPLICATION NUMBER: US/10/272,756

CURRENT FILING DATE: 2000-10-15

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 118

SUFFICE FRIENCE FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEEVER FREEFVER FREEF
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Publication No. US2003020729741

GENERAL INCRAMATION:

GENERAL INCRAMATION:

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: GENERAL INCRAMENCE:

TITLE OF INVENTION: GENERATION PRINTER: 24736-20330

CURRENT FILING DATE: 2002-10-15

PRIOR APPLICATION NUMBER: 09/697,483

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 60/217,658

PRIOR FILING DATE: 2000-07-10

PRIOR PELING DATE: 1999-10-13

PRIOR FILING DATE: 2000-07-10

PRIOR PELING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 60/159,16

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 09/663,968
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Pred. No. 3.1e+02;
0; Mismatches 16; Indels
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Pred. No. 3.1e+02;
0; Mismatches 16; Indels
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1 Similarity 56.8%;
21; Conservative
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Best Local Similarity 56.8%;
Matches 21; Conservative
OTHER INFORMATION: Probe
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ORGANISM: Homo Sapien
                                                                                                                           Query Match
Best Local Similarity
Matches 21; Conserva
             ; OTHER INFORM
US-10-273-321-22
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SOFTWARE: FAST
SEQ ID NO 22
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US-10-273-228-22
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Mon Aug 9 1/:4/:28 2004
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Sequence 106, Application US/10272665

Sequence 106, Application US/10272665

Publication NO. US20030180748A1

GENERAL INFORMATION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POI TITLE OF INVENTION: GENETIC MARKERS

TITLE OF INVENTION: GENETIC MARKERS

TITLE OF INVENTION: GENETIC MARKERS

TITLE OF INVENTION: GENETIC MARKERS

FILE REPERBENCE: 24736-2033E

CURRENT FILING DATE: 2002-10-15

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 1299-10-13

PRIOR APPLICATION NUMBER: 60/129,176

PRIOR FILING DATE: 2000-07-10

PRIOR PILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 60/17,251

PRIOR PILING DATE: 2000-07-10

PRIOR SPLING DATE: 2000-07-10

PRIOR SPLING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 118

SOFTWARE: FastSEQ for Windows Version 4.0

TEMPORED: 100 106

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Publication No. US20030180749A1

GENERAL INFORMATION:
APPLICANT: Braun et al.
ITILE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POI TITLE OF INVENTION: GENETIC MARKERS
FILE REFERENCE: 24736-20338

CURRENT APPLICATION NUMBER: US/10/273,321
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0.5%; Score 11.4; DB 1; Length 100;
Best Local Similarity 56.8%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 16; Indels
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Pred. No. 3.6e+02;
0; Mismatches 16; Indels
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              PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/159,176
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: FASTSEQ for Windows Version 4.0
SSOTUNO 107
LENGTH: 100
APPLICATION NUMBER: 60/217,658
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Best Local Similarity 56.8%;
Matches 21; Conservative (
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CORGANISM: Homo sapien
US-10-272-665-106
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, ORGANISM: Homo sapien
US-10-273-228-107
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US-10-272-665-106
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; Sequence 107, Application US/10272756
; Publication No. US20030190644A1
; GENERAL INFORMATION:
    APPLICANT: Brain et al.
    TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
; TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
; TITLE OF INVENTION: MEMBER: US/10/272,756
; CURRENT PILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,658
; PRIOR FILING DATE: 2000-07-10
; PRIOR PILING DATE: 2000-07-10
; PRIOR FILING DATE: 2000-09-19
; NUMBER: 09/663,968
; NUMBER: EastSEQ for Windows Version 4.0
; SEQ ID NO 107
: LEMCTH: 100
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Sequence 107, Application US/1027328
Sequence 107, Application US/1027328
Subjection No. US20030207297A1
GENERAL INFORMATION:
APPLICANT: Braun et al.
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING FILE REFERENCE: 24736-2033D
CURRENT APPLICATION NUMBER: US/10/273,228
CURRENT FILING DATE: 2002-10-15
PRIOR FILING DATE: 2000-07-10
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                                                                                                                                                                                                                                                                                                                                                                       0.5%; Score 11.4; DB 1; Length 100; 56.8%; Pred. No. 3.6e+02; tive 0; Mismatches 16; Indels
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     PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR PILING DATE: 2000-07-10
PRIOR PELING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR PELING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 100
TYPE: DNA
TYPE: DNA
ORGANISM: Homo sapien
US-10-273-321-107
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Best Local Similarity 56.8<sup>3</sup>
Matches 21, Conservative
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CORGANISM: Homo sapien
US-10-272-756-107
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US-10-272-756-107
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Sequence 14, Application US/09951121A
Publication No. US20030104978A1
GENERAL INFORMATION:
APPLICANT: Persson, Egon
APPLICANT: Olsen, Ole Hvisted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: PA 2000
CURRENT FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 33
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Sequence 15, Application US/09951121A

PUBLICATION No. US20030104978A1

GENERAL INFORMATION, Bgon

APPLICANT: Person, Bgon

APPLICANT: Olsen, Ole Hvilsted

TITLE OF INVENTION: Human Coagulation Factor VII Variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2162 CAGGGCCTATTGTAATAGGGTTTTTAGCAGGGACATAT 2198
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Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 8;
                  FILE REPERENCE: 24736-2033D
CURRENT APPLICATION NUMBER: US/10/273,228
CURRENT PILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 09/687,483
PRIOR PILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/127,658
PRIOR FILING DATE: 2000-07-10
PRIOR PRILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-07-10
PRIOR PILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PESCESO for Windows Version 4.0
SEQ ID NO 106
LENGTH: 100
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ORGANISM: Artificial Sequence
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US-10-273-228-106
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Matches
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US-10-272-756-106

Sequence 106, Application US/10272756

Publication No. US20030190644A1

GENERAL INFORMATION:
APPLICANT: Braun et al.

TILLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: GENETIC MARKERS.
TITLE OF INVENTION: GENETIC MARKERS.

TITLE OF INVENTION: GENETIC MARKERS.

CURRENT APPLICATION NUMBER: US/10/272,756

CURRENT PILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR PELICATION NUMBER: 60/117,658

PRIOR PELICATION NUMBER: 60/117,658

PRIOR PELICATION NUMBER: 60/117,251

PRIOR PILING DATE: 1999-10-13

PRIOR PILING DATE: 2000-07-10

PRIOR PELICATION NUMBER: 60/159,176

PRIOR PELICATION NUMBER: 09/663,968

PRIOR PELICATION NUMBER: 09/0-07-10

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Publication No. US20030207297A1
GENERAL INFORMATION:
APPLICANT: Braun et al.
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
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56.8%; Pred. No. 3.6e+02;
cive 0; Mismatches 16; Indels
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CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 09/687,483
PRIOR PILING DATE: 2000-07-10
PRIOR PLING DATE: 2000-07-10
PRIOR PLING DATE: 2000-07-10
PRIOR PLING DATE: 1090-10-13
PRIOR PLING DATE: 2000-07-10
PRIOR PELING DATE: 2000-07-10
PRIOR PLING DATE: 2000-07-10
PRIOR PLING DATE: 2000-07-10
PRIOR PLING DATE: 2000-07-10
PRIOR FLING DATE: 2000-09-19
PRIOR FLING DATE: 2000-09-19
PRIOR FLING DATE: 2000-09-19
PRIOR PLING DATE: 2000-09-19
SOFTWARE: PSECSEQ for Windows Version 4.0
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Best Local Similarity 56.8
Matches 21, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapien
US-10-273-321-106
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; ORGANISM: Homo sapien
US-10-272-756-106
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Best Local Similarity
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US-10-273-228-106
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FILE REFERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/09/951,121A
CURRENT FILING DATE: 2001-09-13
FRIOR APPLICATION NUMBER: PA 2000 01361
FRIOR FILING DATE: 2000-09-13
FRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 33

. PRIOR APPLICATION NUMBER: 60/236,455

; PRIOR FILING DATE: 2000-09-29	; SOFTWARE: FastSEQ for Windows Version 4.0	; SEQ ID NO 15	; LENGTH: 33	; TYPE: DNA	, ORGANISM: Artificial Sequence	FEATURE	; OTHER INFORMATION: Synthetic	US-10-295-682-15		Query Match 0.5%; Score 11.2; DB 1; Dength 33;		Matches 16; Conservative 0; Mismatches 8; Indels 0; Caps		Oy 1401 IGCAGIAGICIGGCCIGACAICIG 1424	7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		
CURRENT APPLICATION NUMBER: US/09/951,121A	CORRENT FILLING WILL: 2001-09-11	PRIOR FILING DATE: 2000-09-13	PRIOR APPLICATION NUMBER: 60/236,455	PRIOR FILING DATE: 2000-09-29	NUMBER OF SEQ ID NOS: 17	SOFTWARE: FastSEQ for Windows Version 4.0	SEO ID NO 15	LENGTH: 33	TYPE: DNA	, ORGANISM: Artificial Sequence	FEATURE:	; OTHER INFORMATION: Synthetic	JS-09-951-121A-15		Query Match 0.5%; Score 11.2; DB 1; Length 33;	Best Local Simitarity 65.78; Fred. NO. 2.55472; Matches 16; Conservative 0; Mismatches 8; Indels 0; Gaps 0;	

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Squence 8, Application US/09951121A
1/3-09-921-13. Application US/09951121A
1/3-09-921-13. Application No. US20030104978A1
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RESULT 69
Us.10.295.682-14/c
is.210.295.682-14, Application US/10295682
Sequence 14, Application US/10295682
Sequence 14, Application US/10295682
Sether of US.20030100740A1
SERELAL INFORMATION:
APPLICANT: Olsen, Ole Hvilsted
ITTLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REPERSINGE: 6224.200-US
CURRENT FILING DATE: 2000-13
CURRENT PILING DATE: 2000-11-15
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LIBROTH: 33

TYPE: DNA ORGANISM: Artificial Sequence

), OTHER INFORMATION: Synthetic US-09-951-121A-8

0 0.5%; Score 10.6; DB 1; Length 36; 76.5%; Pred. No. 4.2e+02; Indels 0; Mismatches Query Match
Best Local Similarity 76.5
Matches 13; Conservative

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RESULT 72 US-09-951-121A-9

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Query Match 0.5%; Score 11.2; DB 1; Length 33; Best Local Similarity 66.7%; Pred. No. 2.5e+02; Matches 16; Conservative 0; Mismatches 8; Indels

TYPE: DNA ORGANISM: Artificial Sequence

), OTHER INFORMATION: Synthetic US-10-295-682-14

FEATURE:

1401 TGCAGTAGTCTGGCCTGACATCTG 1424

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RESULT 70 US-10-295-682-15

Sequence 9, Application US/09951121A

Sequence 9, Application US/09951121A

Publication No. US20030104978A1

GENERAL INFORMATION:
APPLICANT: Bersson, Egon
TITLE OF INVENTION: Human Coagulation Factor VII Variants
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 624.200.0US
CURRENT APPLICATION NUMBER: US/09/951,121A
CURRENT FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: PA 2000 01361
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PASTESQ for Windows Version 4.0

Sequence 15, Application US/10295682
Publication No. US20030100740A1
GENERAL INFORMATION:
APPLICANT: Person, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REPERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US.10/295,682
CURRENT APPLICATION NUMBER: PA 2000 01361
PRIOR PILING DATE: 2000-09-13

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                                                                                                                                                                                                                     Sequence 8, Application US/10295682

Publication No. US20030100740A1

GENERAL INFORMATION:
APPLICANT: Persson, Egon
TITLE OF INVENTION: Human Coagulation Factor VII Variants
TITLE OF INVENTION NUMBER: US/10/295,682

CURRENT FILING DATE: 2002-11-15
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-13

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APPLICANT: Olsen, Ole Hvilsted
TITLE Or INVENTION: Human Coagulation Factor VII Variants
FILE REPRENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: PA 2000 01361
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows, Version 4.0
SEQ ID NO 9
LENGTH: 36
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0.5%; Score 10.6; DB 1;
Best Local Similarity 76.5%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 4;
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Publication No. US20030100740A1
GENERAL INFORMATION:
   2002 CACTITCAGGICCIGAA 2018
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                                                                        4 CACGTTGAGGACCTGGA 20
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ORGANISM: Artificial Sequence
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, OTHER INFORMATION: DNA primer for preparation of E296V/M298Q-FVII
US-10-255-032-8
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OGGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DNA primer for preparation of E296V/M298Q-FVII
US-10-255-032-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/10255032
| Sequence 8, Application US/10255032
| Publication No. US20030100075A1
| General Information:
| APPLICANT: No. US20030100075A10 No. US20030100075A1disk A/S
| TILLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
| TILLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
| CURRENT APPLICATION WHEBER: US/10/255,032
| CURRENT FILING DATE: 2002-09-24
| PRIOR PILING DATE: 2002-09-24
| NUMBER OF SEQ ID NOS: 9
| SOFTWARE: PATENTIN VERSION 3.1
| SEQ ID NO 8
| LENGTH: 36
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0.5%; Score 10.6; DB 1; Length 36;
Best Local Similarity 76.5%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 4; Indels
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TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
FILE REFERENCE: 6357-W0
CURRENT APPLICATION NUMBER: US/10/255,032
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: DK PA 2001 01413
PRIOR PILING DATE: 2001-09-27
WUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
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Pred. No. 4.2e+02;
0; Mismatches 4;
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Pred. No. 4.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                         2002 CACTITCAGGICCTGAA 2018
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                                TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 76.5%;
Matches 13; Conservative
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Best Local Similarity 76.5%;
Matches 13; Conservative
                                                                                                                                  ; OTHER INFORMATION: Synthetic US-09-951-121A-9
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LENGTH: 36
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LENGTH: 36
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US-10-273-321-23/C
Sequence 23, Application US/10273321
Sequence 23, Application US/10273321
Sequence 23, Application William US/10273321
Sequence 23, Application William US/10273321
Sequence 23, Application William US/10273431
Sequence 23, Applicant William US/10273431
SEQUENCE 24736-2038
STILLE OF INVENTION: GENETIC MARKERS
FILE REPERENCE: 24736-2038
CURRENT APPLICATION NUMBER: 09/687, 483
SETOR PILING DATE: 2000-07-10
SPRIOR PILING DATE: 2000-07-10
SPRIOR PILING DATE: 2000-07-10
SPRIOR FILING DATE: 2000-07-10
SPRIOR APPLICATION NUMBER: 60/129,176
SPRIOR FILING DATE: 2000-07-10
SPRIOR APPLICATION NUMBER: 60/217,251
SPRIOR FILING DATE: 2000-07-10
SPRIOR APPLICATION NUMBER: 09/663,968
SPRIOR FILING DATE: 2000-07-10
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FILE REPERBNCE: 24736-2033E
CURRENT APPLICATION WUMBER: US/10/272,665
CURRENT PILING DATE: 2002-10-15
PRIOR PELING DATE: 2000-07-10
PRIOR PILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/159,176
PRIOR FILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-07-10
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 2000-07-10
PRIOR PLING DATE: 2000-07-10
PRIOR PLING DATE: 2000-07-10
PRIOR PLING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
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CORGANISM: Homo sapien
US-10-272-665-23
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0.5%; Score 10.6; DB 1; Length 42;
Best Local Similarity 64.0%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.5%; Score 10.6; DB 1; Length 42; Best Local Similarity 64.0%; Pred. No. 4.5e+02; Matches 16; Conservative 0; Mismatches 9; Indels
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US-10-298-330-8

Sequence 8, Application US/10298330

Publication No. US20030100506A1

GENERAL INFORMATION:
TITLE OF INVENTION: Modified Vitamin K-Dependent

TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 0953-1127001

CURRENT APPLICATION NUMBER: US/10/298,330

CURRENT FILING DATE: 2000-11-18

PRIOR APPLICATION NUMBER: 09/497,591

PRIOR FILING DATE: 2000-02-03

PRIOR FILING DATE: 1990-04-29

PRIOR FILING DATE: 1990-04-29

PRIOR FILING DATE: 1990-04-29

PRIOR FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 27

SOFUTARE: FRAESEQ for Windows Version 4.0

SEQ ID NO 8
        US-09-803-810-8
) Sequence 8, Application US/08803810
) Publication No. US20010018414A1
) GENERAL INFORMATION:
) APPLICANT: Nelsestuen, Gary L.
) TILLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT;
) TILLE REFERENCE: 09531/002001
) CURRENT APPLICATION NUMBER: US/09/803,810
) CURRENT APPLICATION NUMBER: 05/01-03-12
) NUMBER OF SEQ ID NOS: 18
) SOFTWARE: PastSEQ for Windows Version 3.0
) SEQ ID NO 8

LENGTH: 42
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ORGANISM: Artificial Sequence
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ઠ d 42 reacciarecerciaciaciacia de reacciona de deserto de contra de c RESULT 81 US-10-272-756-23/c ; Sequence 23, Application US/10272756 ; Publication No. US20030190644A1

RESULT 79
-10-272-665-23/c
| Sequence 23, Application US/10272665
| Publication No. US20030180748A1
| GENERAL INFORMATION:
| APPLICANT: Braun et al.
| TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PG

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: DNA primer for preparation of S314E/K316H-FVII US-10-281-727-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: DNA primer for preparation of S314E/K316H-FVII US-10-281-727-3
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(WS-10-281-727-3)

(Sequence 3, Application US/10281727

(Publication No. US20030130191A1

(GENERAL INPORMATION:

APPLICANT: Derseon, Egon

TITLE OF INVENTION: Human Cacqulation Factor VII

TITLE OF INVENTION: POLYSEPTIGES

(URRENT APPLICATION NUMBER: US/10/281,727

CURRENT APPLICATION NUMBER: PA 2001 01627

(FRIOR FILING DATE: 2001-11-02

PRIOR FILING DATE: 2001-11-02

(SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LEGGTH: 36
                 JOS-10-281-72-72

JOS-10-281-72-72

Publication No. US20030130191A1

GENERAL INFORMATION:

APPLICANT: Person, Egon

APPLICANT: Olsen, Ole Hvilsted

TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 6410.200-US

CURRENT APPLICATION: NUMBER: US/10/281,727

CURRENT APPLICATION: NUMBER: BA.2001 01627

PRIOR APPLICATION NUMBER: PA.2001 01627

PRIOR FILING DATE: 2001-11-02

PRIOR FILING DATE: 2001-11-15

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO.
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0.5%; Score 10.4; DB 1;
Best Local Similarity 60.7%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 11;
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0.5%; Score 10.4; DB 1;
Best Local Similarity 60.7%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 11;
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ORGANISM: Unknown
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ORGANISM: Unknown
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US-10-281-727-6
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GENERAL INFORMATION:

APPLICANT: Braun et al.

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POTTILE OF INVENTION: GENERATING DATABASES AND DATABASES FOR IDENTIFYING POTTILE OF INVENTION: GENERAL CANAGEMENT OF A CURRENT FILLING DATE: 2012-10-15

CURRENT PELLING DATE: 2022-10-15

PRIOR FILLING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 60/217,658

PRIOR FILLING DATE: 2000-07-10

PRIOR FILLING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 118

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 23

LENGTH: 60
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## Sequence 23, Application US/10273228

## Publication No. US2003020729741

## Sequence 23, Application No. US2003020729741

## SEQ INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PORTILE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PORTILE OF INVENTION: GENERAL WARKERS

## TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PORTILE OF INVENTION OF SEQ. 10-15

## PRIOR REPRINGE 24736-20330

## CURRENT APPLICATION NUMBER: 09/687, 483

## PRIOR PLING DATE: 2000-07-10

## PRIOR PLING DATE: 1999-10-13

## PRIOR PLING DATE: 1999-10-13

## PRIOR PLING DATE: 2000-07-10

## PRIOR PLING DATE: 2000-07-10

## PRIOR PLING DATE: 2000-09-19

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ORGANISM: Homo sapien
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US-10-273-228-23
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US-10-273-228-23/c
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Query Match
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US-10-281-727-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; CTHER INFORMATION: DNA primer for preparation of S314E-FVII US-10-281-727-6
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US-10-281-727-7/c
| Sequence 7, Application US/10281727 |
| Sequence 7, Application US/10281727 |
| Sequence 7, Application US/10281727 |
| Publication No. US20030130191A1 |
| GENERAL INFORMATION: Application Factor VII |
| TITLE OF INVENTION: Human Coagulation Factor VII |
| TITLE OF INVENTION: Polypeptides |
| TITLE OF INVENTION: Polypeptides |
| FILE REPRENCE: 6410.200-US |
| CURRENT APPLICATION NUMBER: US/10/281,727 |
| CURRENT FILING DATE: 2002-10-28 |
| PRIOR FILING DATE: 2001-11-02 |
| PRIOR FILING DATE: 2001-11-15 |
| NUMBER OF SEQ ID NOS: 7 |
| SEQ ID NO S: 7 |
| LENGTH: 32 |
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APPLICANT: Person, Egon
APPLICANT: Person, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 6410.200-US
CURRENT APPLICATION NUMBER: US/10/281,727
CURRENT APPLICATION NUMBER: PA 2001 01627
PRIOR FILING DATE: 2001-11-02
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 32
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; Sequence 8, Application US/09951121A
; Publication No. US20030104978A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; APPLICANT: Olsen, Ole Hvilsted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 GAAAGGTGGGGGTCT 30
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ORGANISM: Unknown
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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Sequence 9, Application US/09951121A

Publication No. US20030104978A1

GENERAL INFORMATION:

APPLICANT: Persson, Egon

APPLICANT: Olsen, Ole Hvilsted

TITLE OF INVENTION: Human Coagulation Factor VII Variants

FILE REFERENCE: 6224_200-US

CURRENT APPLICATION NUMBER: US/09/951,121A

CURRENT FILING DATE: 2001-09-13

PRIOR PILING DATE: 2000-09-13

PRIOR PILING DATE: 2000-09-29

NUMBER: OF SEQ ID NOS: 17

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9

LENGTH: 36
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Sequence 8, Application US/10255332

Sequence 8, Application US/10255332

Publication No. US2030100075A1

GENERAL INFORMATION:

APPLICANT: No. US2030100075A10 No. US20030100075A1disk A/S

TILE REPRENCE: 6357-WO

CURRENT APPLICATION NUMBER: US/10/255,032

CURRENT FILE SO02-09-24

PRIOR APPLICATION NUMBER: DS PA 2001 01413

PRIOR FILING DATE: 2001-09-27
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TITLE OF INVENTION: Human Coagulation Factor VII Variants; FILE REFERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/09/951,121A
CURRENT APPLICATION NUMBER: PA 2000 01361
PRIOR APPLICATION NUMBER: PA 2000 01361
PRIOR APPLICATION NUMBER: 06/236,455
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 8
LIENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.4%; Score 10.2; DB 1; Length 36; Best Local Similarity 80.0%; Pred. No. 5.5e+02; Matches 12; Conservative 0; Mismatches 3; Indels
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Synthetic US-09-951-121A-9
                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
, OTHER INFORMATION: Synthetic
US-09-951-121A-8
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RESULT 93
US-10-398-422A-20/C
is Sequence 2.0. Application US/10398422A
Fubblication No. US20040058413A1
GENERAL INFORMATION:
APPLICANT: Nicolarisen, Else Marie
APPLICANT: Nicolarisen, Lars Socgaard
TITLE OF INVENTION: Method for the Production of Vitamin K-Dependent Proteins
TITLE OF INVENTION: Method for the Production of Vitamin K-Dependent Proteins
FILE REFERENCE: 2010-20-02
FRICH PRINCE DATE: 2003-09-02
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: Danish application PA 2001 00430
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: Danish application PA 2001 00751
PRIOR APPLICATION NUMBER: Danish application PA 2001 00751
PRIOR PLING DATE: 2001-05-14
PRIOR PLING DATE: 2001-05-14
PRIOR FILING DATE: 2001-05-14
PRIOR FILING DATE: 2001-02-6
PRIOR FILING DATE: 2001-02-6
PRIOR FILING DATE: 2001-02-6
PRIOR FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Oserson, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REPERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: PA 2000
PRIOR APPLICATION NUMBER: PA 2000
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR APPLICATION NUMBER: 60/236,455
NUMBER OF SEQ ID NOS: 17
SOFTWARE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SEQ ID NO S: 27
LENGTH: 36
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                                                                                  Query Match

0.4%; Score 10.2; DB 1;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 12; Conservative 0; Mismatches 3;
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Pred. No. 5.5e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/10295682; Publication No. US20030100740A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                2135 CCTTGTGCTTCAGCT 2149
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Best Local Similarity 80.0%;
Matches 12; Conservative
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, OTHER INFORMATION: Synthetic US-10-295-682-9
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7. OTHER INFORMATION: DNA primer for preparation of E296V/M298Q-FVII

(S-10-255-032-8
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US-10-255-032-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/10255032;
Publication No. US20030100075A1
| Publication No. US20030100075A1
| Publication No. US20030100075A16
| APPLICANT: No. US20030100075A16 No. US20030100075A1disk A/S
| TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
| FILE REFERENCE: 6357-W0
| CURRENT APPLICATION WUMBER: US/10/255,032
| CURRENT FILING DATE: 2002-09-24
| PRIOR FILING DATE: 2001-09-27
| NUMBER OF SEQ ID NOS: 9
| SOFTWARE: Patentin version 3.1
| ENGTH: 36
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| Publication No. US20030100740A1 |
| GERERAL INFORMATION: |
| APPLICANT: Persson, Egon |
| APPLICANT: Persson, Egon |
| TITLE OF INVENTION: Human Coagulation Factor VII Variants |
| FILE REPERENCE: 6224.200-US |
| CURRENT APPLICATION NUMBER: US/10/295,682 |
| CURRENT PILING DATE: 2002-11-15 |
| PRIOR PILING DATE: 2002-09-13 |
| PRIOR FILING DATE: 2000-09-13 |
| PRIOR FILING DATE: 2000-09-29 |
| NUMBER OF SEQ ID NOS: 17 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO SEQ ID NOS: 17 |
| CORRESSON OF SEQ ID NOS: 17 |
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NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
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Best Local Similarity 80.0°
Matches 12; Conservative
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US-10-255-032-9/c
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                                                                                                                        LENGTH: 36
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PRIOR PAPPLICATION NUMBER: PCT/DK01/00632
PRIOR PILING DATE: 2001-10-02
PRIOR PILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: PCT/DK01/00634
PRIOR APPLICATION NUMBER: PCT/DK01/00634
PRIOR APPLICATION NUMBER: PA 2002 00460
PRIOR PILING DATE: 2002-03-26
PRIOR FILING DATE: 2002-10-04
NUMBER: PRIOR FILING DATE: 2002-10-04
NUMBER: PRIOR PILING DATE: 2002-10-04
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ORGANISM: Artificial Sequence
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US-10-109-498-6
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Sequence 2, Application US/09969357

Publication No. US20020137673A1

GENERAL INFORMATION:

APPLICANT: Novo Nordisk Pharmaceuticals, Inc.

APPLICANT: Pingel, Hans K

APPLICANT: Riausen, Niels K

APPLICANT: Riausen, Niels K

TITLE OF INVENTION NUMBER: US/09/969,357

CURRENT APPLICATION NUMBER: Danish Application No. PA 2000 01456

PRIOR FILING DATE: 2002-10-02

PRIOR FILING DATE: 2000-10-02

PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00262

PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00430

PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00751

PRIOR PILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-05-14

PRIOR FILING DATE: 2001-05-14

PRIOR FILING DATE: 2001-05-14

PRIOR PILING DATE: 2001-05-14

PRIOR PILING DATE: 2001-05-14

PRIOR PILING DATE: 2001-05-14

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

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Publication No. US2003009636A1

GENERAL INFORMATION:
APPLICANT: Kundsen, Ida Molgaard

TITLE OF INVENTION: Method for Production of Recombinant
FITLE OF INVENTION: Proteins in Eukaryote Cells
FILE REFERENCE: 6480.500-US
CURRENT APPLICATION NUMBER: US/10/254,394
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                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: synthetic US-10-398-422A-20
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                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial
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                                                                                                                                 SEQ ID NO 20
LENGTH: 38
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SOFTWARE: PatentIn version 3.2

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US-10-109-498-5/c

Sequence 5, Application US/10109498

Publication No. US20030044908A1

GENERAL INFORMATION:
TITLE OF INVENTION: Coaqulation Factor VII Derivatives

FILE REFERENCE: 6286.200-US

CURRENT FILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: 60/281,261

PRIOR APPLICATION NUMBER: PA 2001 00477

PRIOR PILING DATE: 2001-03-22

NUMBER OF SEQ ID NOS: 20

SEQ ID NO 5:

SEQ ID NO 5:

LENGTH: 35
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                                                Indels
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Publication No. US20030044908A1
GENERAL INFORMATION:
APPLICANT: Person, Egon
TITLE OF INVENTION:
COURENT APPLICATION WHOBE: US/10/109,498
CURRENT APPLICATION NUMBER: US/10/109,498
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 60/281,261
PRIOR FILING DATE: 2001-04-03
Score 10.2; DB 1;
Pred. No. 5.6e+02;
0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
0.4%; Score 10; DB 1; 1
Best Local Similarity 55.9%; Pred. No. 6.2e+02;
Matches 19; Conservative 0; Mismatches 15
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                                                                                           141 GAAGCCTCTGCTGGCAATACTTCTGGGGCTG 171
                                                                                                                                           34 deaderecreadaaaacerrrradedeed 4
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; OTHER INFORMATION: Nucleotide Primer US-10-109-498-5
Query Match
Best Local Similarity 58.1%;
Matches 18; Conservative
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Sequence 23, Application US/10273321
; Sequence 23, Application US/10273321
; Publication No. US2030180749A1
; GENERAL INPORMATION:
; TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POIL
; TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING POIL
; TITLE OF INVENTION: GENETIC MARKERS
; FILE REFERENCE: 24736-2733.321
; FRICA RAPLICATION NUMBER: 05/687,483
; FRICA RAPLICATION NUMBER: 06/217,658
; FRICA RAPLICATION NUMBER: 06/217,658
; FRICA RAPLICATION NUMBER: 06/159,16
; FRICA RAPLICATION NUMBER: 06/159,176
; FRICA RAPLICATION NUMBER: 06/159,176
; FRICA RAPLICATION NUMBER: 09/663,968
; PRIOR FILING DATE: 1999-10-13
; PRIOR FILING DATE: 2000-07-10
; PRIOR FILING DATE: 2000-07-10
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FASESEQ FOR Windows Version 4.0
; SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/10272756
Publication No. US20030190644A1
Publication No. US20030190644A1
APPLICANT: Braun et al.
TITLE OF INVENTION: METHODS FOR GENETIC MARKERS
FILE REPERRNCE: 24736-2033C
CURRENT APPLICATION NUMBER: US/10/272,756
CURRENT FILLNO BATE: 2002-10-15
PRIOR PILING BATE: 2000-07-10
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0.4%; Score 9.8; DB 1; Length 60;
Best Local Similarity 66.7%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 7; Indels
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        ; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/217,251
; PRIOR FILING DATE: 2000-07-10
; PRIOR FILING DATE: 2000-09-19
; RIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        669 CCCACTATCTGTGTGAGGT 689
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COGANISM: Homo sapien
US-10-272-665-23
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US-10-273-321-23
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| Deblication No. US20302247A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: The Children's Hospital of Philadelphia
| APPLICANT: The Children's Hospital of Philadelphia
| APPLICANT: The Children's Hospital of Philadelphia
| APPLICANT: TARSON, DETER J. APPLICANT: LARSON, DETER J. APPLICANT: LARSON, DARREL W. APPLICANT: LARSON, DARREL W. APPLICANT: LARSON, DARREL W. APPLICANT: CANTER, TOWNENTION: ENGRANGE SACONSINANT VITAMIN K-DEPENDENT CURRENT FILING DATE: 2003-01-25
| FILE REFERENCE: 018743-0301425
| CURRENT FILING DATE: 2003-01-65
| PRIOR FILING DATE: 2000-03-16
| PRIOR FILING DATE: 2000-03-16
| PRIOR FILING DATE: 1999-03-16
| NUMBER OF SEQ ID NOS: 22
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 8
| LENTH: S4
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Publication No. US20030180748A1

Publication No. US20030180748A1

GENERAL INFORMATION:
APPLICANT Braun et al.
TITLE OF INVENTION: GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
TITLE OF INVENTION: GENERATING DATABASES FOR IDENTIFYING PC
TITLE OF INVENTION: 24736-2033E
CURRENT APPLICATION NUMBER: US/10/272,665
CURRENT PILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR PLING DATE: 2000-07-10
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Best Local Similarity 84.6%; Pred. No. 7.3e+02;
Matches 11; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           679 GIGIGIGAGGICAAIAIGIGAITITAGCIGIAGC 712
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PRIOR APPLICATION NUMBER: PA 2001 00477
PRIOR FILING DATE: 2001-03-22
NUMBER OF SEC ID NOS: 20
SECTWARE: FastSEQ for Windows Version 4.0
LENGTH: 35
                                                                                                                                                                                                                                            ; OTHER INFORMATION: Nucleotide Primer US-10-109-498-6
                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 AGAGACTICATAA 129
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ORGANISM: Homo sapiens
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                                                                                                                                                                              TYPE: DNA
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| Sequence 4, Application US/10017122
| Publication No. US20030087244A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: MCCARTHY, Jeanette
| TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
| FILE REPERENCE: MN. -007
| CURRENT APPLICATION NUMBER: US/10/017,122
| CURRENT FILING DATE: 2001-12-14
| PRIOR PLING DATE: 2001-10-09
| RIOR PLING DATE: 2001-10-09
| NUMBER OF SEQ ID NOS: 4
| SOFTWARE: Patentin Ver: 2.0
| SEQ ID NO 4
| TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                     Length 35;
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICATION Regulation Factor VII Derivatives

FILE REFERENCE: 6286.200-US

CURRENT FILING DATE: 2002-03-22

PRIOR FILING DATE: 2002-03-22

PRIOR FILING DATE: 2001-03-03

PRIOR FILING DATE: 2001-03-22

PRIOR FILING DATE: 2001-03-22

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6

LENGTH 35
                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                                                                                                                                                                                     Query Match 0.4%; Score 9.4; DB 1; Best Local Similarity 68.4%; Pred. No. 8.8e+02; Matches 13; Conservative 0; Mismatches 6
PRIOR APPLICATION NUMBER: 60/281,261
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: PA 2001 00477
PRIOR FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
S SEQ ID NO 5
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Nucleotide Primer US-10-109-498-6
                                                                                                                                                                                                                                                      , OTHER INFORMATION: Mucleotide Primer US-10-109-498-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1599 TGCACTGTGGGGAGTTTCT 1617
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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Best Local Similarity 68.4%
Matches 13; Conservative
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US-10-017-122-4
                                                                                                                                                                                                      TYPE: DNA
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| Sequence 23, Application US/1027328
| Publication No. US20000207297A1
| GENERAL INFORMATION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC TITLE OF INVENTION: METHODS FOR GENERATING DATABASES POR IDENTIFYING PC TITLE OF INVENTION: MUMBER: US/10/273,228
| TITLE OF INVENTION: MUMBER: US/10/273,228
| CURRENT FILING DATE: 2000-07-10
| PRIOR PILING DATE: 2000-07-10
| PRIOR FILING DATE: 2000-07-10
| PRIOR FILING DATE: 1999-10-13
| PRIOR FILING DATE: 1999-10-13
| PRIOR FILING DATE: 2000-09-19
| NUMBER OF SEQ ID NOS: 118
| SOFTWARE: FASTESE FOR Windows Version 4.0
| SEQ ID NO 23
| LENGTH: 60
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 60;
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0.4%; Score 9.8; DB 1; Length 60
Best Local Similarity 66.7%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 7; Indels
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Publication No. US20030044908A1
GENERAL INFORMATION:
APPLICAMT: Persson, Egon
TITLE OF INVENTION: Coagulation Factor VII Derivatives
FILE REFERENCE: 6.286.200-US
CURRENT APPLICATION NUMBER: US/10/109,498
CURRENT FILING DATE: 2002-03-22
                 PRIOR APPLICATION NUMBER: 60/217,658
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-07-10
PRIOR PRIOR DATE: 2000-07-10
PRIOR PRIOR DATE: 2000-07-10
PRIOR PRIOR DATE: 2000-09-19
NUMBER: OF SEQ ID NOS: 118
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                669 CCCACTATCTGTGTGAGGT 689
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                     TYPE: DNA
COGANISM: Homo sapien
US-10-272-756-23
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US-10-109-498-5
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Sequence 2, Application US/10295682

Sequence 2, Application US/10295682

Publication No. US20030100740A1

GENERAL INFORMATION:
APPLICANT: Olsen, Ole Hvilsted

TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REPERENCE: 624-200-US

CURRENT APPLICATION NUMBER: US/10/295,682

CURRENT PILING DATE: 2002-11-15

PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-29

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FeatsEQ for Windows Version 4.0

SEQ ID NO 2: LENGTON: US APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION
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APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVANION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224.200-1.15
FULRENT APPLICATION NUMBER: US/10/295,682
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
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SPRIOR FILING DATE: 2000-09-13
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                       Matches 14; Conservative
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Sequence 2, Application US/09951121A
Publication No. US20030104978A1
GENERAL INPORMATION:
APPLICANT: Person. Egon
TITLE OF INVENTYON: Human Coagulation Factor VII Variants
FILE REPRENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/09/951,121A
CURRENT FILING DATE: 2001-09-13
PRIOR PELING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/226,455
PRIOR APPLICATION NUMBER: 60/226,455
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO : SEQ ID NO : LENGTH: 34
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US-09-51-121A-3/C
156quence 3, Application US/09951121A
56quence 3, Application US/09951121A
56quence 3, Application US-00951121A
56MEAL INFORMATION:
66MEAL INFORMATION:
76MEAL INFORMATION:
77HIE OF INVENTION: Human Coagulation Factor VII Variants
FILE REPRENCE: 6224.200-9-13
77HIE OF INVENTION NUMBER: US/09/951,121A
77HIE OF INVENTION NUMBER: US/09/951,121A
77HIE OF INVENTION NUMBER: 00/09-13
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77HIE APPLICATION NUMBER: 00/236,455
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; ORGANISM: Homo sapiens
US-10-017-122-4
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Best Local Similarity
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US-09-951-121A-2
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NESOUR INCOMENTATION:

Sequence 15, Application US/09951121A

Sequence 15, Application US/09951121A

Sequence 15, Application US/09951121A

Publication No. US20030104978A1

GENERAL INFORMATION:

APPLICANT: OS. Sequence 1600.

TILE REFERENCE: 6224.200-US

TILE REFERENCE: 6224.200-US

CURRENT APPLICATION NUMBER: US/09/951,121A

CURRENT FILING DATE: 2001-09-13

PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-29

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15

LENGTH: 33
                                                                                                             APPLICANT: Person, Egon
APPLICANT: Person, Egon
APPLICANT: Olsen, Ole Hvilsted
APPLICANT: Olsen, Ole Hvilsted
APPLICANT: Olsen, Ole Hvilsted
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REPERENCE: 6224.200-08
CURRENT APPLICATION NUMBER: EA. 2001-09-13
FRIOR PILING DATE: 2001-09-13
FRIOR PILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 33
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Sequence 14, Application US/09951121A Publication No. US20030104978A1 GENERAL INFORMATION:
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US-10-281-727-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
, OTHER INFORMATION: DNA primer for preparation of S314E/K316H-FVII
US-10-281-727-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
0.4%; Score 9.2; DB 1; Length 36;
Best Local Similarity 78.6%; Pred. No. 9.7e+02;
Matches 11; Conservative 0; Mismatches 3; Indels
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; Sequence 3, Application US/10281727
; Publication No. US20030130191A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; APPLICANT: Persson, Cle Hvilsted
; TITLE OF INVENTION: Human Coagulation Factor VII
; TITLE OF INVENTION: Polypeptides
; TITLE OF INVENTION: HUMAN COAGULATION Factor VII
; TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII
; TITLE OF INVENTION: DATE: 2002-10-28
; PRIOR PILING DATE: 2001-11-02
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 7
; SSEQ ID NO S: 7
; SSEQ ID NO S: 7
; LENGTH: 36
                                                                                                                 Sequence 2, Application US/10281727

Publication No. US20030130191A1

GENERAL INFORMATION:
APPLICANT: Persson, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Polypeptides
FILE REPERENCE: 6410.200-US
CURRENT APPLICATION NUMBER: US/10/281,727
CURRENT PILING DATE: 2002-10-28
PRIOR FILING DATE: 2001-11-02
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 7
SEQ ID NOS: 7
ILENGE PRICE PRICES OF THE PRICE 
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ORGANISM: Unknown
FEATURE:
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ORGANISM: Unknown
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                                                                                                                                                                                                                                               193 TCCTAGGGTGAGGGTTACCACTGCT 217
                                                                                                                                                                                                                                                                                               30 racredaridecedecaagacrecr 6
                                                                                                                                                                                                                                                                                                                                                                      RESULT 114
US-10-295-682-14
; Sequence 14, Application US/10295682
; Publication No. US20030100740A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
TYPE: DNA ORGANISM: Artificial Sequence
                                            FEATURE:

OTHER INFORMATION: Synthetic

US-09-951-121A-15
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968 TGGATGCAGCAGTA 981

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RESULT 112

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Gaps
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TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
FILE REPERENCE: MIL-007
CURRENT APPLICATION NUMBER: US/10/017,122
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/327,487
PRIOR FILING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
LENOTH: 31
TYPE: DNA
CRGANISM: Homo sapiens
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                                                                                                                                                                  TYPE: DNA
CRGANISM: Artificial Sequence
PEATURE:
COMPATION: Protein C mutagenic oligonucleotide
US-09-803-810-8
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Publication No. US2030100506A1

GENERAL INFORMATION:

APPLICANT: Nelsestuen, Gary L.

TITLE OF INVENTION: Modified Vitamin K-Dependent
TITLE OF INVENTION: Polypeptides
FILE REPERENCE: 09531-12701

CURRENT PELLOATION NUMBER: US/10/298,330

CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/497,591
PRIOR PILING DATE: 2000-02-03

PRIOR PILING DATE: 1999-04-29

PRIOR FILING DATE: 1999-04-29

PRIOR FILING DATE: 1999-04-29

PRIOR FILING DATE: 1999-04-29

PRIOR FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 42
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0.4%; Score 8.8; DB 1;
Best Local Similarity 52.8%; Pred. No. 1.1e+03;
Best Local Similarity 52.0% immatches 17.
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                NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 42
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Publication No. US20030087244A1
GENERAL INFORMATION:
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, OTHER INFORMATION: Primer
US-10-298-330-8
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US-10-017-122-4/c
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US-10-295-682-15/c
US-10-295-682-15/c
Sequence 15, Application US/10295682
Publication No. US20030100740A1
GENERAL INFORMATION:
APPLICANT: Person, Egon
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REPRENCE: 6224-200-US
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT FILING DATE: 2000-11-15
PRIOR PAPLICATION NUMBER: 60/216,455
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/236,455
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 3.3
## APPLICANT: Olsen, Ole Hvilsted
### TITLE OF INVENTION: Human Coagulation Factor VII Variants
### FILE REPERENCE: 6224.200-08
### CURRENT APPLICATION NUMBER: US/10/295,682
### CURRENT FILING DATE: 2002-11-15
### PRIOR APPLICATION NUMBER: PA 2000 01361
### PRIOR APPLICATION NUMBER: 60/236,455
### PRIOR PILING DATE: 2000-09-13
### PRIOR FILING DATE: 2000-09-29
### NUMBER OF SEQ ID NOS: 17
### SOFTWARE: FastSEQ for Windows Version 4.0
### SEQ ID NO 14
### ILENGTH: 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 33;
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Pred. No. 1.1e+03;
0; Mismatches 10
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Publication No. US20010018414A1
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary L.
TITLE OF INVENTION: WODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
TITLE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/99/803,810
CURRENT FILING DATE: 2001-03-12
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60.0%; Pred. No. 1.1e+0
tive 0; Mismatches
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ORGANISM: Artificial Sequence
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Best Local Similarity 60.0%;
Matches 15; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity 60.05
Matches 15; Conservative
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US-09-803-810-8/c
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Sequence 3, Application US/10295682;
Publication No. US20030100740A1
GENERAL INFORMATION:
APPLICANT: Person, Egon
IITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT PILING DATE: 2002-11-15
PRIOR PILING DATE: 2000-09-13
PRIOR PILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 34
                                                                                                                                              APPLICANT PERSON 100 105/10295682

Sequence 2, Application US/10295682

Publication No. US20030100740A1

GENERAL INFORMATION:
APPLICANT: Person, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: PA 2000 01361
PRIOR PILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FARISEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 7.8; DB 1; Length 34
Pred. No. 1.4e+03;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Synthetic US-10-295-682-2
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Publication No. US20030104978A1

GENERAL INFORMATION:
APPLICANT: Person, Egon
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REPERENCE: 6224.200-US
CURRENT FILING DATE: 2001-09-13

PRIOR PILICATION NUMBER: US/09/951,121A

PRIOR PLING DATE: 2000-09-13

PRIOR PLING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-13

SEQ ID NOS: 17

SSOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 34
                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09951121A
| Publication No. US20030104978A1
| GENERAL INPORMATION:
| APPLICANT: Persson. Egon
| APPLICANT: Olsen, Ole Hvilsted
| TITLE OF INVENTION: Human Coagulation Factor VII Variants
| FILE REPERENCE: 6224.200-US
| CURRENT APPLICATION NUMBER: US/09/951,121A
| CURRENT FILING DATE: 2000-09-13
| PRIOR APPLICATION NUMBER: PA 2000
| PRIOR APPLICATION NUMBER: 60/236,455
| PRIOR FILING DATE: 2000-09-29
| NUMBER OF SEQ ID NOS: 17
| SOFTWARE: PastSEQ for Windows Version 4.0
| SEQ ID NO 2
| LENGTH: 34
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0.3%; Score 7.8; DB 1; Length 34;
Best Local Similarity 81.8%; Pred. No. 1.46+03;
Matches 9; Conservative 0; Mismatches 2; Indels
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Pred. No. 1.4e+03;
0; Mismatches 2; Indels
                                       Query Match 0.4%; Score 8.2; DB 1; Length 31; Best Local Similarity 61.9%; Pred. No. 1.46+03; Matches 13; Conservative 0; Mismatches 8; Indels
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Best Local Similarity 81.8%;
Matches 9; Conservative
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; OTHER INFORMATION: Synthetic
US-09-951-121A-3
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; OTHER INFORMATION: Synthetic
US-09-951-121A-2
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Search completed: August 9, 2004, 16:55:08 Job time: 32 secs

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Hi, M.B., Gruber, C., Jessee, J. and Polayes, D.

On Feb 13, 2001 this sequence version replaced gi:12795220.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France
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ACCESSION: AI116939
ACCESSION: AU099140
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ACCESSION: AU099140
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3.139 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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AL531727
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Maximum Match 100%
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length: 2000000000
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Perfect score:
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TITLE
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

1 (Dases 1 to 645)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7252.f F
more information about this cluster, see
therp://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-cS0DM003AE01QPl&cluster=7252.f. Contac
Feng Liang Email: fliang@lifetech.com/URL:
http://fulllength.invitrogen.com/InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DM003AE01QPl.
Location/Qualifiers
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llarity 59.3%; Pred. No. 0.31;
Conservative 0; Mismatches 24; Indels 0;
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Contact: Marra M/Muse EST Project
Washlu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Loui
Tel: 314 286 1800
Fax: 314 286 1800
Email: mouseest@watson.wustl.edu
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Seq primer: custom primer used
High quality sequence stop: 483.
Location/Qualifiers
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/clone="IMAGE:1481822"
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/strain="C57BL"
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               /dev_stage=adult"

/dev_stage=adult"

/lab host="DH10B"

/clone_lib="Sugano mouse liver mlia"

/clone_lib="Sugano mouse liver; pkE18S-FL3; Site_1: DraIII

/cAcTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA

was primed with an oligo dIT) primer represented constituted to a DraIII adaptor (TGTTGGCCTATGTG), digested

and cloned into distinct DraIII sites of the pWE18S-FL3;

vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should

be used to isolate the cDNA insert. Size selection was

performed to exclude fragments <1.5kb. Library

constructed by Dr. Sumio Sugano (University of Tokyo

Institute of Medical Science). Custom primers for

sequencing: 5' end primer CTTTGGTCTAAAAAGTGGG and 3' end

primer CGACCTGCAGCACCAG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. (W.B., Gruber, C. 1201)

1. (W.B., Gruber, C. 1201)

1. (Indered to Contact and normalization)

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2. (Indered to Contact and (1201)

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/clone_lib="Homo sapiens FETAL LIVER"
/clone_lob="Homo sapiens FETAL LIVER"
/note="Organ: liver, Vector: pCMVSPORT 6, 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the pCMVSPORT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
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0.9%; Score 19.8; DB 1; Length 645;
Best Local Similarity 69.2%; Pred. No. 0.87;
Matches 27; Conservative 0; Mismatches 12; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Indels
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/mol_type="mRNA"
/db_xref="taxon.9606"
/clone="CSODMOD3YIO1"
/tissue_type="FETAL LIVER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL531727
AL531727.2 GI:31069559
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TITLE
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AL531727
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ઠે 임 DB 1; Length 1201;

Score 18; DB : Pred. No. 1.1;

0.8%;

Best Local Similarity

Query Match

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AU099140 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HEP20983 similar to Human factor VII serine protease precursor mRNA AU099140
AU099140
BST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a S'-end-enriched cDNA library. Gene 200 (1-2),
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Mus musculus
musculus
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musculus

1 (bases 1 to 609)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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ue37b03.yl Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1482509 5' similar to gb:M13232 COAGULATION FACTOR VII
PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1761 TCCTTTGGTTTTTTGCATAGTGTCTCTGGCTTCCTGGATGTTTTATGCCT 1809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 recretectriciótricéerreagéerecticéeréeratricer
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1677 TCTCAAGGTTAGGAAATTTTTCTTTTTGGTTTTCTTGAAAA 1718
                                    20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.7%; Score 17; DB 1
Best Local Similarity 59.2%; Pred. No. 6.6;
Matches 29; Conservative 0; Mismatches
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="HEP20983"
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
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10664775-4.rst

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Best Local Similarity
Matches 21; Conserv
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COMMENT
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VERSION
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SOURCE
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Eukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi,

Mamala, Eutheria; Rodentia; Sciurognathi, Muridae, Murinae; Mus.

1 (mass 1 to 609)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellerberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                    Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 GGGCTGCTGCCTTTCTCCCTGTCTGATCCTAGGGTTAC-CACTGCTCTCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A1099321 609 bp mRNA linear EST 20-A ue37b03.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1482509 5' similar to gb:M13232 COAGULATION FACTOR VII PRECURSOR (HUWAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.7%; Score 16.3; DB 1; Length 609;
llarity 63.5%; Pred. No. 4.3;
Conservative 0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
      The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                            Seg primer: custom primer used
High quality sequence stop: 289.
Location/Qualifiers
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/clone="IMAGE:1482509"
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Matches 40; Conserv
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 645)
Martan, M. Hillier, Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 02-SEP-1998
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                                                                                                                                                   This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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ue29908.yl Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1481822 5' similar to gb:M13232 COAGULATION FACTOR VII
PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marka M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.6%; Score 14.4; DB 1; Length 609; 65.6%; Pred. No. 7.4; tive 0; Mismatches 11; Indels (
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/mol_type="mRNA"
/strain="C57BL"
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                          MGT:930865
Seq primer: custom primer used
Seq primer: custom primer used
High quality sequence stop: 289.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Email: mouseest@watson.wustl.edu

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Search completed: August
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/lab_host="DH10B"
/lab_host="DH10B"
/lone="lab="Sugano mouse liver mlia"
/lone="lab="Sugano mouse liver; pWE185-FL3; Site_1: DraIII
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/note="lorgan: liver; Vector: liver; livering converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converted converte
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Smil: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 TCTCTGCTTTCTGCTCCAGGTCCAGGACCTCTAGGGACTGCAGTTTTCATAACCCAGGA 109
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1 (bases 1 to 300)

Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.

In silico mapping of the S'-ends of human mRNAs using full-length enriched and S'-end enriched cDNA libraries constructed by
This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:930178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2129 TCCTTGCCTTGTGCTTCAGGTATGTTGCATTCTCAGGGC--CTATTGTAATAGGGTTTTA
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0.6%; Score 13.8; DB 1; Length 645;
Best Local Similarity 56.4%; Pred. No. 7.7;
Matches 44; Conservative 0; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
                                                                                                                                                                                                Seq primer: custom primer used
High quality sequence stop: 483.
Location/Qualifiers
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/clone="IMAGE:1481822"
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Unpublished (2001)
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                                                                                                                                        Query Match
0.6%; Score 13.6; D
Best Local Similarity 61.1%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches
                                               organism="Homo sapiens"
                                                                                                                                                                                                                                                                                       9, 2004, 16:55:39
149-156 (1997).
Location/Qualifiers
1. .300
               FEATURES
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Mon Aug 9 1/:4:11 2004

ACCESSION: AR42570 ACCESSION: BD1212: ACCESSION: AR4652: ACCESSION: AR778747	ACCESSION:M33108 ACCESSION:AX8927	ACCESSION: BD0283: ACCESSION: AXB391 ACCESSION: AF0118 ACCESSION: AF0118	ACCESSION: AF0113 ACCESSION: BC0611. ACCESSION: AX4640	ACCESSION: AY3591 ACCESSION: AX5659 ACCESSION: BC0461	ACCESSION: BD0603 ACCESSION: AR1620	ACCESSION:AR1666 ACCESSION:AF5152	ACCESSION: E63001 ACCESSION: E63001 ACCESSION: E639902	ACCESSION: E62998 ACCESSION: E62999 ACCESSION: E62999 ACCESSION: E611129	ACCESSION: AR1129 ACCESSION: I19358	ACCESSION:119360 ACCESSION:BD1946 ACCESSION:AX5659	ACCESSION: AX9085 ACCESSION: BD0440	ACCESSION: AF3069 ACCESSION: AF3069 ACCESSION: AF3069	ACCESSION: AF3069 ACCESSION: AF3069	ACCESSION: AY1551 ACCESSION: AY1551	ACCESSION: AB0849 ACCESSION: AY0224	ACCESSION: AIO252 ACCESSION: M36551 ACCESSION: M57847	ACCESSION: AR1081 ACCESSION: AX4018	ACCESSION:X64336 ACCESSION:AF0118	ACCESSION: AR2343	ACCESSION: AR2112 ACCESSION: AR2192	ACCESSION: AF5152	ACCESSION: AF0553	ACCESSION: BD0952 ACCESSION: AX8146	ACCESSION:BV0360 ACCESSION:M26235	ACCESSION: U44795 ACCESSION: AF2727	ACCESSION: D21216	ACCESSION: AX7630 ACCESSION: AX7630 ACCESSION: M35672	ACCESSION: AX6755 ACCESSION: AR2192 ACCESSION: AX6755
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## ALIGNMENTS

Qy 1126 TGGAATTATTATTCATATTTTCTTGAATGTGGGTAACATCTTTAGATTGAAGTTTT 1185	Db 108 NYNSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYCYAYTYTY 49  Qy 1186 TCTCCTAGCCTTCTTTAGGTCTGCATTTGAAGATAGATATC 1227  1186 TCTCCTAGCTTCTTTAGGTCTGCATTTGAAGATAGTTTC 1227  Db 48 GYTYAYAYTYAYAYTYAYGYTYAYAYTYTYGYTY 7	2422 bp DNA lin. US 5861374.	AUTHORS BENTHER, K.L., PETEISEN, D. Christian. and Hart, C.E. TITLE Modified Factor VII 19-JAN-1999; FDATURES Location/Qualifiers Source / organism="unknown" //mol_type="unassigned DNA"	Query Match 2.1%; Score 43; DB 1; Length 2422; Best Local Similarity 58.0%; Pred. No. 9.9e-05; Matches 76; Conservative 0; Mismatches 55; Indels 0; Gaps 0; Qy 952 TGTTGAGAATTATCAATGAGCAGTGTTGTGAGATTCTTGTGAATGT 1011	Db 1946	1072 TCTGTCTCTGT 1082
ALIGNMENTS	RESULT 1 AR162089/c LOCUS LOCUS DEFINITION Sequence 17 from patent US 6258558. ACCESSION AR162089 WERSION AR162089.1 GI:16229155	ACTWORDS  ORGANISM  ORGANISM  ORGANISM  ORGANISM  ORGANISM  ORGANISM  ORDASSITION  ORDASSITION  OF SELECTION OF Proteins using RNA-protein fusions  TITLE  Nethod for selection of proteins using RNA-protein fusions  OURNAL  PEATURES  1 . 28  /organism="unknown"  /mol_type="unassigned DNA"	Ouery Match  2.2%; Score 44.7; DB 1; Length 289;  Best Local Similarity 6.8%; Pred. No. 2.8e-05;  Matches 15; Conservative 110; Mismatches 96; Indels 1; Gaps 1;  Qy 1007 AAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	1067 GTGTGTGTGTGTGTGTGTGTGTGTGTGTTCTCTCTCTTTTGATTTTTGGCC 112 168 NYNYSYN	1126 TGGAATTATTTATTATTCATATTTTCTTGAATGTGGGTAACAT 108 NYNYSINYNSYNYNSYNYNYSYNYNYSYNYNYSYNYNYSYN 1186 TCTCCTAGCCTTCTTTAGGTCTGCATTTGAAGATAGATATTC 1286 TCTCCTAGCATTTAGGTCTGCATTTGAAGATAGATATTC 1286 TCTCCTAGCATTTAGGTCTGCATTTGAAGATAGATATTC 1286 TCTCCTAGCATTTAGGTCTGCATTTGAAGATAGATATTC 1286 TCTCCTAGCATTTAGAAGATAGATATTC 1287 TCTCTTAGAAGATAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	AYTYTYGYTYAYAYAYTYAYGYTYAYAYTYGYT  1. from patent US 6281344.  1. GI:16242009  1. GI:16242009  1. Coation/Coation molecules and 1 acid-protein fusion molecules and 1 us 6281344.  1. Coation/Qualifiers  1. Coation/Qualifiers  1. Coation/Qualifiers  1. Coation/Qualifiers  2. 2% Score 44.7; DB 1; Lity 6.8%; Pred. No. 2.8e-05; Servative 110; Mismatches 96; GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG

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Location/Qualifiers

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/organism="unknown"

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1 (bases 1 to 2422)
Hart,C.E., Petersen,L.C., Hedner,U. and Rasmussen,M.E. Modified factor VI
Patent: US 6183743-A 1 05-FEB-2001;
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Thorpe, P.B. and Edgington, T.S.
Methods for the specific coagulation of vasculature
Patent: US 6004555-A 25 21-DEC-1999;
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Berkner,K.L., Petersen,L.Christian., Hart,C.E., Hedner,U. and Bregengaard,C.
Modified factor VII
Patent: US 583382-A 1 10-NOV-1998;
1...2422
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2.1%; Score 43; DB 1; Length 2422;
Best Local Similarity 58.0%; Pred. No. 9.9e-05;
Matches 76; Conservative 0; Mismatches 55; Indels
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Sequence 1 from patent US 5833982.
AR052946
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Sequence 1 from patent US 6168789.
AR122899
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AR052946/c
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AR122899/c
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REFERENCE AUTHORS

PAT 08-SEP-2000

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AUTHORS REFERENCE

952 TGTTGAGAATTATCAATGAGCAGTGTTTGTGGATTCTTGTTATCTTGCACTTGTGAAGTG 1011 

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                     2007 TGIGCATATCTCTAIGTGCGTGTGCATCGGTGTGTTTGCGTATCTCTGTGTGACCATCTG 1948
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Thorpe, P.E. and Edgington, T.S.
Methods and compositions for the specific coagulation of
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Seguence 5592 from Patent W00194629.
AX335083
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Patent: US 6093399-A 25 25-JUL-2000;
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/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
/db xref="taxon:9606"
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Location/Qualifiers
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1. .2462
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                                                               1072 TCTGTGTCTGT 1082
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Matches 76,
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AX335083/c
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Human factor VII serine protease precursor mRNA, complete cds,
clone lambda-HVII2463.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2462;
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| Organism="Homo sapiens"
|mol_type="unassigned DNA"
|db_xxef="texon:9606"
|/note="EMBL/GenBank Accession No. M13232"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.1%; Score 43; DB 1; Length 2462
Best Local Similarity 58.0%; Pred. No. 9.9e-05;
Matches 76; Conservative 0; Mismatches 55; Indels
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factor VII; serine protease; serum glycoprotein.
Home sapiens (human)
Home sapiens
                                                                                                      AX409604 2551 from Patent WO0229103.
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1887 TCCATGTGTGT 1877
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952 IGTTGAGAATTATCAATGAGCAGTGTTTGTGGATTCTTGTTATCTTGCACTTGTGAAGTG 1011

0; Mismatches 55; Indels

76; Conservative

Matches

2007 TGTGCATATCTCTATGTGCGTGTGCATCGGTGTGTTGCGTATCTCTGTGACCATCTG

1072 TCTGTGTCTGT 1082

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                                                                                                                                                                                                                                                                                                unidentified
unclassified.
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(Lasselfied.)
Furederitsuku, E.H., Maaku, J.M., Shiyaaron, J.B., Kiyasuriin, E.B., Maagaretsuto, W.I., Richiyaado, J.U. and Chiyaaruzu, E.G.
DNA ENCODING FACTOR VI.
Patent: JP 1987000283-A 2 06-JAM-1987,
HEMOJIENETEITSUKUSU INC NIPPON SODA CO LTD, NISSAN CHEM IND LTD,
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PR 17-ARP-1985 US 85 724311, 16-DEC-1985 US 85 810002 FUNEDERITSUKU BES 724311, 16-DEC-1985 US 85 810002 FUNEDERITSUKU BAAGUNA, MAAKU JIEI MARII,
EL SHIYAARON JIEI BAZUBII,
PI KIXARNIN ERU BAAKUNAA, MAACARETSUTO WAI INSUREE, PI RICHIYAADO JII UNEUDOBERII, CHIYAARUZU ERU GUREI PC CI2NI5/00,A6IK37/465,CI2NS/00,CI2N9/50,(CI2N9/50,CI2R1:91); CC
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216. .1436
/product='factor VII'
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anti-sense: No;
*source: library:cDNA library;
*source: clone=lambdaVII 2463;
Location/Qualifiers
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2462. .<2480
/note='polyA tail'.
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06-JAN-1987
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hypothetical: No;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / LTAIN 1 ALL LONG WAS QALBILL CLILIGLOGCLAAVEVTQEBAHGVIHRRRRANAFILE
ELREGELEREKCKEGCSFEBAREIFKDAERTKLFWISYSDDOCASSFOONGGSCKD
LQSYICFCLPAFEGNNCETHKDDQLICVNENGGCEGYCSDHTGTKRSCRCHEGYSLLA
DGVSCTPTWEYFCGKTPILERRANASKPQRIVGSKVCPRGECPWQVLLLVNGAQLCGG
TLINTIWVSAAHCFPKIRWRNLIAVLGEHDLSEHDGDEGSRRVAQVIIISSTYVPGT
THNDIALLRLHQPVVTRVPLCLPPRFTFSERTTAPVRFSXVSGWGLIDRGATALE
IMVLANVPRLANTQDCLQSRRVGDSPNITEYMFCAGYSDGSKDSCKGDSGCFHATHYRG
TWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRSEPRPGYLLRAFFFP"
                                                                                                                                                                                                                                                                                                                                                                                      /product="coagulation factor VII"

/protein id="AAA88040.1"

/db xref="G1:182801"

/translation="MVSQALRILCILIGLGGCLAAGGVAKASGGETRDMPWKPGPHRV

/translation="MVSQALRILCILIGLGGCLAAGGVAKASGGETRDMPWKPGPHRV

/translation="MVSQALRILCILIGLGGCLAAGGVAKASGGETRDMPWKPGPHRV

SYSDGDQCASSPCQWGSCKCDGLGSTGCTGTGARGGRDGCTATAGTKRSCRCHEGYSLLAAGGVSCTPTVEYPCGKIPILEKRNASKPQGRIVGGKV

YCSDHTGTKRSCRCHEGYSLLAADGVSCTPTVEYPCGKIPILEKRNASKPQGRIVGGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPKGECPWQVLLLVNGAQLCGGTLINTIWVVSAAHCFDKIKGWRNLIAVLGEHDLSEH
DGDEQSRRYAQVIIBSTYVPGTTNHDIALLRLAQPVVLTDHYVPLCLPERTESERTLA
FVRFSLVSGWGQLLDRGATALELMVLNVPRLMTQDCLQQSRKVGDSPNITEYMFCAGY
SDGSKDSCKGDSGGEHATKRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQKL
MRSEPRPGVLLRAPFP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1] sequenced two alternatively spliced mRNAs that produced shortened signal peptides. One is presented as factor VIIb below. Location/Qualifiers
                                  Original source text: Homo sapiens liver cDNA to mRNA.
Draft entry and sequence in computer-readable form for [1] kindly
provided by F.S.Hagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.1%; Score 43; DB 1; Length 2462; Best Local Similarity 58.0%; Pred. No. 9.9e-05; Matches 76; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                 'note="precursor for factor VIIa and b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36. .215
/note="factor VIIa signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(36. .99,166. .215)
/note="factor VIIb signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216. .671
'product="coagulation factor VII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       772. .1433
product="coagulation factor VII"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(36. .99,166. .1436)
/note="preprofactor VIIb"
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                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/db_xref="GI:182800"
                                                                                                                                                                                                                                                                                                       'product="FVIIa mRNA"
                                                                                                                                                                                                                                                             type="liver"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166. .2462
/note="factor VIIb"
/number=2
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Purederitanku, E.H., Maaku, J.M., Shiyaaron, J.B., Kiyasuriin, E.B., Maagarestuco, W.I., Richiyaado, J.U. and Chiyaaruzu, E.G.
DNA ENCODING FACTOR VII
Patent: JP 1987000283-A 1 06-JAN-1987,
HEMOJIENETEITSUKUSU INC NIPPON SODA CO LTD, NISSAN CHEM IND LTD,
                                                                                                                                                                                                        Unclassified.
Unclassified.
1 (bases 1 to 2483)
1 (bases 1 to 2483)
1 Hagen, F.S., Murray, M.J., Busby, S.J., Berkner, K.L., Insley, M.Y., Woodny, R.G. and Gray, C.L.
Expression of factor VII and IX activities in mammalian cells Patent: EP 0200421-A2 3 10-DEC-1986;
Location/Qualifiers.
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CC *source: library=cDNA library, lambdagt11 cDNA library; CC
*source: clone=lambdaVII 2115, lambdaVII 1923; FH Key
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/product='factor VII peptide' FT
2106. .2111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.1%; Score 43; DB 1; Length 2483; Best Local Similarity 58.0%; Pred. No. 9.9e-05; Matches 76; Conservative 0; Mismatches 55; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="unassigned DNA"
Sequence 3 from Patent EP 0200421.
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hypothetical: No;
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CC topology: Linear
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VERSION
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                                                                                                                                                                                               1695 IGCATATCTCTATGTGCGTGTGCATCGGTGTTTGCGTACTCTGTGTGACCATCTGTGT 1636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unclassified.

1 (bases 1 to 2438)
Hagen, F.S., Murray, M.J., Busby, S.J., Berkner, K.L., Insley, M.Y., Moodbury, R.G. and Gray, C.L.
Expression of factor VII and IX activities in mammalian cells
Patent: BP 0200421-A2 6 10-DEC-1986;
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ch 2.1%; Score 41.6; DB 1; Length 2177; Similarity 57.8%; Pred. No. 0.00023; 74; Conservative 0; Mismatches 54; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
2.1%; Score 41.6; DB 1; Length 2438;
Best Local Similarity 57.8%; Pred. No. 0.00023;
Matches 74; Conservative 0; Mismatches 54; Indels 0;
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Sequence 6 from Patent EP 0200421.
107991.1 GI:589297
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/organism="unknown"
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BC040125.1 GI:25455627
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  Query Match
Best Local Similarity
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                                       Matches
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1129. .<2177.

Location/Qualifiers

exon 3'UTR

댪

source

FEATURES

/organism="unidentified" /mol\_type="genomic RNA" /db\_xref="taxon:32644"

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 84 Row: m Column: 9 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9961350. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 300)
Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.S., Reinhard, C., Giese, K., Randazzo, F., Kennedy, G.C., Pot, D., Nassam, A., Lamson, G., Drananac, R., Crkvenjakvv, R., Dickson, M., Drmanac, S., Labat, I., Leshkowitz, D., Kita, D., Garcia, V., Jones, L.W. and Crain, B.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1504 TTTTTTTTTTTTTTTTTTTTTGAGTGGGATCTCACTTTAATGGAGAGGACGTTATGAC 1445
                                                                                                           Submitted (22-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.systemsbiology.org
conteat: amadangsystemsbiology.org
Anup Madan, Jessica Fahey, Erlehon, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Ean Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Lissue type="Brain, adult, 6 pooled whole brains"
/clone lib="NIH MGC 114"
/lab hSst="DH10B"
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                         Contact: MGC help desk Email.inh.gov logabes, Inc. Bmail. inh.gov logabbs.remail.inh.gov logabes.rement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML) DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1532 GIGITITIGIA I GCTICITIGIA CCTIGALAGGCA I CTITICICA AGG 1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37.4; DB 1; Length 1573; Pred. No. 0.0028; O Mismatches 81; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1444 crecegedearidacritifecerresecaaseceriserritares 1398
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                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="IMAGE:5764698"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BD211952.1 GI:33021722 JP 2002519000-A/94.
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                           (bases 1 to 1573)
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Matches 86; Conservative
                                                                                         Direct Submission
                                                          Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BD211952
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                                                                                      TITLE
JOURNAL
                              REFERENCE
                                                       AUTHORS
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L. (bases 1 to 1443)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaffer, C.F., Bhat, N.K.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaffer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Morze, T., Mang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.,
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Aramson, R.D., Mullahy, S.J., Boasto, P.H., Richards, S.,
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,
Villalon, D.K., Mozny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmitz, J., Myers, R.M.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

N.D. 22288277
OS Homo sapiens (human)
PN 72 202519000-A/94
PP 72 202519000-A/94
PP 28-JAN-1999 JF 2000556580
PF 28-JAN-1999 JF 2000556580
PR 28-JAN-1999 JF 2000565680
PR 28-JAN-1998 US 60/080144,03-APR-1998 US 60/080515 PR 31-APR-1998 US 60/080144,03-APR-1998 US 60/080515 PR 28-OCT-1998 US 60/10534 PR 28-OCT-1998 US 60/10534 PR 28-OCT-1998 US 60/10534 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/10523
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HAGGE:3899480), complete cds.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1403)
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/db_xref="taxon:9606"
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Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1792)

RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

RAUSBERG, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., More, T., Wax, S.I., Wang, J., Hsieh, P.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Carcia, A.M., Gay, L.J., Hullyk, S.W.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whilling, M., Madan, A., Rodrigues, S.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalalsk, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 50 Row: h Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4506114.
Location/Qualifiers
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//organism="Momo sapiens"
//db_xref="temRNA"
//db_xref="temsNa"
//clone="MGC:34565 IMAGE:5188604"
//tissue_type="Colon, Kidney, Stomach, adult, whole pooled"
//clone_lib="NNH" MGC_116"
//lab_host="DH108"
//note="Vector: pCMV-SPORT6"
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Web site: http://www.hgsc.bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sheed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (02-UUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
   VIIIa), mRNA (cDNA clone MGC:34565 IMAGE:5188604), complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.R. Consortium (LINL)
DNA Sequencing Py: Baylor College of Medicine Human Genome
Sequencing Center:
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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Conteat: MGC help desk
Bmail: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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/db_xref="MIM:176860"
                              BC034377
BC034377.1 GI:21707770
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                                                                                                                                Homo sapiens (human)
Homo sapiens
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Conscrtium (LIML)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome.
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site.
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 14 Row: 1 Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21614535. Location/Qualifiers
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CLPDASIHLPPNTHCWISGWGSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQ
GPITEDMLCAGYLEGERDACLGDSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYI
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QQLNRVVGGEDSTDSEWPWIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLF
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                                                                                           Direct Submission
Submitted (29-UTN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186. .902
/note="Tryp_SPC; Region: Trypsin-like serine protease"
/db_xref="CDD:cd00190"
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db_xref="LocusID:64063"
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/tissue_type="Pancreas, epithelioid carcinoma"
/clone_lib="NIH_MGC_70"
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1.4%; Score 28; DB 1; Length 1403;
Best Local Similarity 63.2%; Pred. No. 0.78;
Matches 43; Conservative 0; Mismatches 25; Indels
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                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Taball: cgabbs-rømail.nih.gov
Tissue Procurement: ATCC
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/product="protease, serine, 22"
/protein_id="AAM09726.1"
/db_xref="Clil6307276"
/db_xref="LocusID:64063"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                 (bases 1 to 1403)
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                                                            Strausberg, R.
   2477932
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BC034377/c
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AUTHORS
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PAT 14-JUN-2002
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I (bases I to 1843)

Beckmann, R.J., Schmidt, R.J., Santerre, R.F., Plutzky, J.,
Crabree, G.R. and Long, G.L.

The structure and evolution of a 461 amino acid human protein C precursor and its messenger RNA, based upon the DNA sequence of cloned human liver cDNAs

Nucleic Acids Res. 13 (14), 5233-5247 (1985)
                                                                                                                                                                                                                                                                        Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/hote="unnamed protein product; protein C precursor"
                                                                                                                                                                                                                                                                                                                                    Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G. Gene expression profiles in liver cancer Patent: WO 0229103-A 3673 11-APR-2002; GENE LOGIC INC (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.3%; Score 25.2; DB 1; Length 1843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="EMBL/GenBank Accession No. X02750"
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Location/Qualifiers
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/db_xref="G1:763120"
/db_xref="GOA:P04070"
/db_xref="SWISS-PROT:P04070"
                                                                                                                            AX411026
Sequence 3673 from Patent WO0229103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.4;
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0; Mismatches
1778 rcgrggrrgrgrrrrrakrcrrrr 1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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/organism="Homo sapiens"
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Human liver mRNA for protein C.
X02750
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/db_xref="taxon:9606"
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Homo sapiens (human)
Homo sapiens
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AX411026/c
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HSPROTC/c
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RRGDSPWQVYLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGSYDLRRWEKW
ELDDIKEVFVHPNYSRKSTTONDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAG
QETLVTGWGYHSSREKEARRRTFVLANFIKIPVVPHRECSEVMSNWSENMLCAGILG
DRQDACEGDSGGPWVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                present in a rarge number of membrane-bound and extracellular (mostly animal) proteins. Many of these proteins require calcium for their biological function and calcium-binding sites have been found to be located at the N-terminus of particular EGF-like domains.
                      /codon_start=1 /products for coagulation factors Va /products_protein C (inactivator of coagulation factors Va and VIIIa)"
                                                                               /protein_id="AAH34377.1"
/db_xref="G1:2170771"
/db_xref="LocusID:5624"
/db_xref="LocusID:5624"
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SFLEEDRHSSILRRCITEBIOFDEBAKBIRONDDTLAFWSKHVDGDQCLVLPLEHPCA
SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRC
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/note="GLA; Region: Domain containing Gla
/note="GLA; Region: Domain containing Gla
/gamma-carboxyglutamate) residues"
/db_xref="CDD:smart00069"
353. 451
/note="EGF_CA; Region: Calcium-binding EGF_like domain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        692. .1399
/note="Tryp SPc; Region: Trypsin-like serine protease"
/db_xref="CDD:cd00190"
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1.3%; Score 25.2; DB 1; Length 1843;
Best Local Similarity 55.8%; Pred. No. 4.4;
Matches 48; Conservative 0; Mismatches 38; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 27.2; DB 1; Length 1792; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28; Indels
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0; Mismatches
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/organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AR390799.1 GI:40113146
                                                                                                                                                                                                                                                                                                                DKEAPQKSWAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.4%;
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AR390799/c
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/gene="GAP43"

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Macaca mulatta growth associated protein 43 (GAP43) gene, 3' UTR.
AY083553
AY083553.1 GI:20146915
          SFLEELRHSSLERECIĒBICDFEBAKBIPQNVDDTLAFWSKHVDGDQCIVLPLEHPCA
BLOCGHGTOTOBGIBGODRSGWERPERCQREVSFLNSSLDNGGCTHVCLBEVGRRRC
SCAPGYKLGDDLLGCHPAVKPCGRPWKRMEKKRSHLKRDTBDGEDQVDPRLIDGKNT
RRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKN
BLDDIKEVFYHPNYSKSTTDNOIALHLAQPATLSGTTVSTTVSTLABATARAN
QETLVTKWYHSSKSTTDNOIALHLAQPATLSGTTVSTLABATARABA
QETLVTKWYHSSRSTARARTFVLNFIKIPVVHNECSEVMSNWYGENMLGAGILG
DRQDACEGDSGGPMVASFHGTWFLVGVLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MWQLTSLLLFVATWGISGTPAPLDSVFSSSERAHQVLRIRKRAN
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
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                                                                                                                                                                                                                                                                                                                                       553. .730
hote="activation peptide region (aa 144-169)"
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                                                                                                                                                                                                         note="serine protease region (aa 170-419)"
1759. 1764
                                                                                                                                          98. .196
/note="signal peptide (aa -42 to -10)"
                                                                                                                                                                                                                                                                                                         97. .634
note="EGF-domain II (aa 92-137)"
                                                                                                                                                                                         note="propeptide (aa -9 to -1)"
                                                                                                                                                                                                                                                                        159. .496
'note="EGF-domain I (aa 46-91)"
                                                                                                                                                                                                                                                                                                                                                                                       note="heavy chain (aa 57-419)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Macaca mulatta"
/mol_type="genomic_DNA"
/db_xref="taxon:9544"
<1. . . 251
<1. . . 251
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Macaca mulatta
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AY083553/c
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KOGDSPWQAILLDSKKKLACGGVLIHTSWVLTAAHCVBGTKKLTVRLGBYDLRRRDHW
BLDLDIKEILVHPNYTRSSSDNDIALLRLAQPATLSKTIVPTCLPNNGLAQOELTQAG
GETVTGWGYQSDRIKDGRRNRTFILTFIR.PLVARNRCVSVMKNVVSENMLCAGIIG
NTRDACDGDSGCPMVVFFRGTWFLVGLVSWGEGCGHTNNYGIYTKVGSYLKWIHSYIG
EKGVSLKSQKL"
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PCCCHGTCIDGIGSFSCSCDXGWEGKFCQQELRFQDCRVNNGGCLHYCLEESNGRRCA
CAPGYELADDHMRCKSTVNPPCGKLGRWIEKRRKILKRDTDLEDELEPDPRIVMGTLT
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Mus musculus
Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 1499)
1 (daa, N., Sato, M., Tsujimura, A., Iwase, R. and Hashimoto-Gotch, T.
Isolation and characterization of a mouse protein C cDNA
0. Blochem. 111 (4), 491-495 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-clotting activity, anti-coagulation factor, blood coagulation factor, calcium binding, mouse protein C; phospholipid binding, serine protease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (31-JAN-1992) Masahiro Sato, Hoechst Japan Co., Ltd., Pharma Research Laboratories; 1-3-2 Minamidai, Kawagoe, Saitama 350, Japan (E-mail:rkikuno@ddbj.nig.ac.jp, Tel:0492-43-6149, Fax:0492-41-6475)
                                                                                                                                                                  Gaps
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                                                                                                        1.2%; Score 24.4; DB 1; Length 251; 82.4%; Pred. No. 5.7; cive 0; Mismatches 6; Indels (
/product="growth associated protein 43"<1. .>251
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Baboratory for Molecular Biology
Pharma Research Baboratories
Hoechst Japan Co., Ltd.
1-3-2 Minamida, Kawagoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sub_species="domesticus"
/db_xref="taxon:10090"
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protein_id="BAA01235.1"
|db_xref="G1:220386"
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/strain="BALB/c"
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/codon_start=1
                                                       /gene="GAP43"
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0492-41-6475
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(bases 1 to 1499)
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D10445.1 GI:220385
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716 TCCGTTGACTATCCTTGGATCTGGTTCCAGTTCATCTTCTAAGTCTGTGTCTCGTTTGAG 657
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/strain="FVB/N"
/db_xref="taxon:10090"
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BC013896/c
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/product="anticoagulant protein C"
/product="anticoagulant protein C"
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CAPGYELADDHMRCKSTVMFPCGKLGRWIEKKRKILKRDTDLEDELEPDPRIVNGTLT
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ELDLIKELUYHDYTRSSENDIALLRAQPATLSKTIVYTCLTUNGAGGELAGELTQAGG
ETVYTGWGYGSDRIKOGRRNETEIJFIRIR IPPLVARRSCEVGVKNVVSBNMLGAGIIG
TRDACDGDSGGPNVVFFRGTWFLVGLVSWGEGCGHTNNYGIYTKVGSYLKWIISYIGE
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 1580)
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Submitted (OZ-NOV-2000) Genetics, Washington University, 4444
Forest Park Avenue, St. Louis, MO 63108, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus anticoagulant protein C mRNA, complete cds. AF318182
                                                                                          Score 24; DB 1; Length 1499;
Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.2%; Score 24; DB 1; Length 1580;
46.9%; Pred. No. 8.8;
ive 0; Mismatches 85; Indels
                                                                                                                                 85; Indels
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/product="activation peptide"
644. .1393
                                                                                                                               0; Mismatches
                              644. .1393
/product="serine protease"
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/strain="C57BL"
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                                                                                          1.2%;
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Mammatist succeptary Rocentral Scillinghacilly multimes; must, mammatist succeptary R.D., Peingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagper, L., Shemmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhar, N.K., Distribul, S.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Distribul, S.R., Brownstein, M. Ponaldo, M.F., Casavant, T.L., Scapeton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scapeton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshlyuki, S., Carninolf, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Fullyk, S.M., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Fullyk, S.M., Sanchez, A., Multing, M., Madan, A., Rodrigues, S., Sanchez, A., Whilling, M., Madan, A., Rodrigues, S., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Green, B.D., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M., Schein, J. B., Nores, S.J. and Marra, M.A., Schein, J. B., Worley, W. Sanilus, D.E., Schmerch, A., Schein, J. B., Wolches, S.J. and Marra, M.A., Rodrigues, S., Schmerch, A., Schein, J. B., Wolches, S.J. and Marra, M.A., Schein, J. B., Volches, S.J. and Marra, M.A., Proc. Natl. Acad. Sci. U.S., 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                              HCU13896 1603 bp MRNA linear ROD 03-OCT-2003 Mus musculus protein C, MRNA (CDNA clone MGC:13870 IMAGE:4211329), complete cds.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6679476.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Submitted (07-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Contact: MGC help deek
Email.capbe.remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadanesystemsbiology.org
contact: amadanesystemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurad]
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
1905 GTCCTGAAATGTTTTACTCATTTTCCTCCCAGTATTTACA 1944
                                                                                               656 GATCTTGCGTTTCTTCTATCCACCTCCCCAGTTTCCCA 617
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BD121258.1 GI:23216168
JP 2002010789-A/13335.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                       16; Conservative
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C12N15/00
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PLEENRRGSLERRECMBETCOPERAQE:PRODOCEAPPODGCOS
PCCHGHOTODGIGSFCSCDKGWEGKFCQOELRFODGVNNGGCLHYCLEBSNGRRCA
CAPGYELADDHMRCKSTVNFPCGKLGRWIEKKRKILKRDTDLEDELEPDPRIVNGTLT
KGDSPWQALLLDSKKKLACGGYLIHFSWYLTPRAVDGFKTWTVRTGRSDHW
ELDLDIKEILVHPWYTRRSSSDNDIALLRLAQPATLSKTIVPTCLPNNGLAQELTQAGG
ETVVTGWGYQSDRIKDGRRNRTFILLFIRIPLVARNBCCVEVMKNVVSENMLCAGIIGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175. 357

Jote="GLA; Region: Domain containing Gla
/gamma-carboxyglutamate) residues. A hyaluronan-binding
domain found in proteins associated with the extracellular
matrix, cell adhesion and cell migration...
/db xref="CDD:smart00069"
400. x489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETVVTGWGYQSDRIKDGRRNRTFILTFIRIPLVARNECVEVMKNVVSENMLCAGIIGD
TRDACDGDSGGPMVVFFRGTWFLVGLVSWGEGCGHTNNYGIYTKVGSYLKWIHSYIGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="EGF; Region: EGF-like domain. There is no clear separation between noise and signal. pfam00053 is very similar, but has a instead of conserved cystaines. Includes some cytokine receptors. The EGF domain misses the N-terminus regions of the Ca2+ binding EGF domains. The family is hard to model due to many similar but different sub-types of EGF domains. Pfam certainly misses a number of EGF domains.
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/db_xref="CDD:smart00020"
/clone="MGC:13870 IMAGE:4211329"
lissue type="Liver, normal. 5 month old male mouse."
clone lib="NCI CGAP_Li9"
lab_hes="DH108"
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1.2%; Score 24; DB 1; Length 1603;
Best Local Similarity 46.9%; Pred. No. 8.8;
Matches 75; Conservative 0; Mismatches 85; Indels
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Sequence 17202 from patent US 6639063.
                                                                                              note="Vector: pCMV~SPORT6"
                                                                                                                                                                                                                                                      /codon_start=1
/product="protein C"
/protein_id="AAH13896.1"
/pb_xref="GI:15530230"
/db_xref="GI:15530230"
                                                                                                                                                           /note="synonym: PC"
/db_xref="LocusID:19123"
/db_xref="MGI:97771"
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                                                                                                                                              gene="Proc"
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                                                                                                                                                                                                                                                                                                                    88 CCTAGGGTGAGGGTTACCACTGCTCTCTCTCCTTTCTCTAACACTTCTGGGCCAGGG 147
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JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
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1 (bases 1 to 364)
1 (bases 1 to 364)
1 (bases 1 to 364)
1 (bases 1 to 2001) Johert, S. and Giordano, J.E.
1 EST and Giordano, J.E.
1 Patent: JP 2002010789-A 13335 15-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
                                                                                                                                                                                                                                                                                                                                                         1/21,
C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00, PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 TAGGGGCACTACCGCATTCCCTCTCTTCCAAACACTTCTATTTCTTG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'organism='Homo sapiens (human)'.
                                                                                                                                                                                                            1.2%; Score 23.8; DB 1; Length 364; Similarity 14.7%; Pred. No. 8.5; Conservative 53; Mismatches 40; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 364;
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Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y. EST's and encoded human proteins
Patent: US 6639063-A 17202 28-OCT-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST and encoded human protein
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/mol_type="genomic DNA"
/db xref="taxon:9606"
                                                                                                                              /organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
JP 202210789-A/13335
15-JAN-2000
07-ANG-2000 JP 2000280989
05-AUG-1999 US 60/147499
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                                                                                Location/Qualifiers
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Gaps

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BD126609 868 bp DNA linear PAT 18-SEP-2002 Primer for synthesizing full-length cDNA and use thereof. BD126609
                                                                                                                                                                                                              107 ATTGGAGTTGCAAAGATTCATTGAGGGAGCAAGGAAGGAGGAGCACCTCAGCATTAAGGA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JAN-2002
07-JUL-2000 JP 2000253172
TOSHIO OPP, TETSOO MISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 ATTGGÅAGTTGCAAAGATTCATTGAGGGGAGCAAGGAAGGAGGAGCCTCAGCCTTTAGGA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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DP 2002017375-A/2040.

JP 2002017375-A/2040.

JP 2002017375-A/2040.

JP 2002017375-A/2040.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 868)

Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,

Makamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002017375-A 2040 22-JAN-2002; HELIX RESEARCH INSTITUTE
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                                                                                                                  1.2%; Score 23.8; DB 1; Length 868; 57.3%; Pred. No. 9.3; tive 0; Mismatches 32; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.2%; Score 23.8; DB 1; Length 868; Best Local Similarity 57.3%; Pred. No. 9.3; Matches 43; Conservative 0; Mismatches 32; Indels (
       1. .868
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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PI TETSUJI OTSUKI,HISASHI KOGA
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JP 2002017375-A/2040
                                                                                                                                                                                                                                                                                                        441 GAAATAGICIGIAAA 455
                                                                                                                                                                                                                                                                                                                                                    167 GCTTTCCTTTTÄÄÄ 181
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                                                                                                                                                                 43; Conservative
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                                                                                                                                             Best Local Similarity
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                                                                                                                       Query Match
         source
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DEFINITION
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VERSION
KEYWORDS
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AUTHORS
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         PAT 15-DEC-2003
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JP 202017375-A/91
22-JAN-2002
07-JUL-2000
JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 TGCCCACTGCATCAGGAATCTCCATATCCCCCTCTCTCTGTCCTTCTCTAGTCCCTCT 262
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                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammallai; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 868)
                                                                                                                                                                                                                             Bracco,L., Brinkman,B. and Coignard,F.
Variants of human kallikrein-2 and kallikrein-3 and uses thereof
Patent: WO 03076610-A 23 18-SEP-2003;
Exonhit Therapeutics S.A. (FR)
Location/Qualifiers
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Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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Patent: JP 2002017375-A 91 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 1.2%; Score 23.8; DB 1; Length 394; l Similarity 48.2%; Pred. No. 8.5; 67; Conservative 0; Mismatches 72; Indels (
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         DNA
Sequence 23 from Patent W003076610. AX839180
                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="unassigned DNA" /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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JP 2002017375-A/91.
Homo sapiens (human)
Homo sapiens
                                                                        AX839180.1 GI:39922629
                                                                                                                    Homo sapiens (human)
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Best Local Similarity
                                                                                                                                             Homo sapiens
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VERSION
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BD124660
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                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                  AUTHORS
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AY040345/c LOCUS DEFINITION ACCESSION VERSION VERSION SOURCE SOURCE ORGANISM

JOURNAL MEDLINE PUBMED

REFERENCE AUTHORS

TITLE JOURNAL

FEATURES

CDS

REFERENCE AUTHORS

TITLE

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PAT 18-SEP-2002
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                                                                                                                                                                                                                                                                        217 SSKYMSTCRKSSKKCRYSATYYYSCMMKWKKYCMMSATYSGCMMWRWYCYSCMMSRYSCT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryoff a, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 364)
Edwards, J.B.D.M., Jobert, S. and Giordano, J.B.
Est and encoded human protein
Patent: JP 2002010789-A 13335 15-JAN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
JP 2002010789-A/13335
15-JAN-2002
17-JAN-2002
05-AUG-1999 US 60/147499
JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
                                                                                                                                                                                       614 GITITAȚGAACTIGGGIGACATIGIGITIGGIGCAIAGACATIAAGAATIGCAAIGICCI
                                                                                                                                                                 554 TIGAAGTAGCCCACTATCTGTGTGTGAGGTCAATAJGTGATTTTAGCTGTAGCTGTGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11/21,
C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00,
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                                                                            ch 1.1%; Score 23; DB 1; Length 364; 1 Similarity 10.5%; Pred. No. 14; 14; Conservative 67; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST and encoded human protein
Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA

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    .364
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    /mol_type="genomic DNA"

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EST and encoded human protein.
BD121258
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JP 2002010789-A/13335.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity
Matches 14; Conservat
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PN JP 200
PD 15-JAN
PF 07-AUG
PI JEAN
GIORDANO
PC C12N1/21,
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C12N15/
CC ES
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NSGQKCRSHEVPFGGKVPLLQAGKAADHQVDLRSRIVGGSECPKGHCPWQVLLKYGEK
GFCGGVIYKPWYMITAAHCLEKLKVKEKLRINAGEHBLADSTDGJIQVDQWFTHPAY
VSETAADSDIALLRIRTPIVYSVYAVPVCLPLEBMARFELMVSKHTVSGWGKRSEDGP
TSRLLRELLVPR RRYGGGGPLVTRYNDT
AFLGIVSWGKGCARPGSYGIYTRVSNYLQWIRQTTNTIH"
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Direct Submission
Submitted (14-JUN-2001) Cellular and Structural Biology, University of Texas Health Science Center at San Antonio, 7703 Floyd Curl Drive, San Antonio, TX 78229, USA
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                                                                                                                  Danio rerio (zebrafish)

Danio rerio

Danio rerio

Danio rerio

Danio rerio

Danio rerio

Actinopterygii, Meopterygii, Teleostel; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

Cypriniformes; Cyprinidae; Danio.

Cyprinidae; Danio.

Demonstration of 1671)

Demonstration of the extrinsic coagulation pathway in teleostei: identification of zebrafish coagulation factor VII

Proc. Natl. Acad. Sci. U.S.A. 98 (15), 8768-8773 (2001)
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1.2%; Score 23.6; DB 1; Length 1671;
Best Local Similarity 54.7%; Pred. No. 11;
Matches 47; Conservative 0; Mismatches 39; Indels 0;
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Unclassified.
3 I (bases I to 364)
5 Edwards J. B. LD. M., Jobert. S. and Giordano, J.-Y.
5 Edwards J. B. LD. M., Jobert. S. and encoded human proteins
Location/Qualifiers
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1. .1302
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RESULT 34
AR425705/c
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SOURCE
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q à AUTHORS TITLE JOURNAL FEATURES

REFERENCE

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                                                     AF465274 1329 bp mRNA linear VRT 02-FBB-2003 1Akifugu rubripes coagulation factor VIIb precursor, mRNA, complete
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GRQCIAEVERPCGQLPPPETGPDQTVVGQTRLVGTNHCPKGECPWQVLVQLHGQSHCG
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                                                                                                                                                                                                                                                   Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Buteleostei; Neoteleostei; Acanthomorpha, Acanthomorpha, Acanthomorpha, Acanthomorpha, Acanthomorpha, Acanthomorpha, Acanthomorpha, Tetradontidea, Tetradontidea, Takifugu.

Tetradontoidea, Tetradontidae, Takifugu.

Davidson, C.J., Hirr, R.P., Lal, K., Shell, P., Elgar, G.,
Tuddenham, E.G.D. and McVey, J.H.
Comparative sequence analysis and molecular evolution of blood coagulation genes from Gallus gallus and Fugu rubripes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases I to 1329)
McVey.7.H., Davidson,C.J., Lal,K., Snell,P. and Elgar,G.
Direct Submission
Submitted (04-JAN-2002) Haemostasis Group, MRC Clinical Sciences
Centre, The Faculty of Madicine, Imperial College, Hammersmith
Campus, Du Cane Road, London W12 ONN, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /EC. number="3.4.21.21"
/Eunction="serum prothrombinconversion accelerator"
/function="serum prothrombinconversion accelerator"
/note="vitamin K dependent serine protesse; similar to
Fugu rubripes FVII; synthesized in liver; contains 2
EGF-like domains; member of peptidase family SI/trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 16;
0; Mismatches 10; Indels
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                                                                                                                                                                                                         rubripes (Fugu rubripes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /moi_type="mRNA"
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1. _1329
                                                                                                                                                      AF465274.1 GI:28194019
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Best Local Similarity 74.4%;
Matches 29; Conservative
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                                                     AF465274
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AX774765/c
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RESULT 36
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1 (Dases 1 to 1507)

Messier, T.L., Pittman, D.D., Long, G.L., Kaufman, R.J. and Church, W.R. Cloning and expression in CoS-1 cells of a full-length cDNA encoding human coagulation factor X Gene 99 (2), 291-294 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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o
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                                                                                                                                                                                                                                                                                                                                                                                      Length 1507;
                         Raponi,M.
Methods for assessing and treating leukemia
Parent: WO 03038129-A 81 08-MAY-2003;
Ortho-Clinical Diagnostics, Inc. (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                           1.1%; Score 23; DB 1;
60.3%; Pred. No. 16;
iive 0; Mismatches 25
                                                                                                                                                                                                  organism="Homo sapiens"
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/gene="F10"
/EC_number="3.4.21.6"
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/db_xref="taxon:9606"
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|. .1507
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1. .1507
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/gene="F10"
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/note="putative VECTOR sequence Bacteriophage lambda (J02459); putative"

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C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 TCTCTCTCTCCCTTTCTCTAACACTTCTGGGCCAGGGTAGGGGGCCACTACCGCATTCCCTC 170
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(Dases 1 to 385)

Edwards, J.B.D.M., Dollair, B. and Jordan, J.Y.

Sequence tag and encoded human protein
Patent: JP 2001269182-A 4566 02-0CT-2001;
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Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vartebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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JP 2001269182-A/4566
02-CCT-2001
24-FEB-2000 JP 2000118773
26-FEB-1999 US 60/122487
JARN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
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                                                                          Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y. Expressed sequence tags and encoded human proteins Patent: EP 1033401-A 8650 06-SEP-2000; Genset (FR)
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1. .385
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57.1%; Pred. No. 25;
tive 0; Mismatches 3
                                                                                                                                                                                           Location/Qualifiers
1.385
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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1.1%; Score 22; DB
Best Local Similarity 57.1%; Pred. No. 25;
Matches 40; Conservative 0; Mismatches
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2001269182-A/4566.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 57.1<sup>3</sup>
Matches 40, Conservative
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PC C12N5/10,
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(bases 1 to 193)

Evans, B.A., Yun,Z.X., Close,J.A., Tregear,G.W., Kitamura,N., Nakanishi,S., Callen,D.F., Baker,E., Hyland,V.J., Sutherland,G.R.
                                                                             Gaps
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Location/Qualifiers
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                           1.1%; Score 23; DB 1; Length 1507;
60.3%; Pred. No. 16;
ive 0; Mismatches 25; Indels
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Pred. No. 23;
0; Mismatches 15; Indels
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/note="kallikrein mRNA and introns"
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Biochemistry 27 (9), 3124-3129 (1988)
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/gene="KLK1"
/note="kallikrein intron D"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="19q13.3"
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/note="G00-120-118"
/number=4
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kallikrein; kininogenase.
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Best Local Similarity 67.4%;
Matches 31; Conservative
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Homo sapiens
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                                                       Similarity 60.3
38; Conservative
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PAT 27-AUG-2002

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AF011898 860 bp mRNA linear VRT 09-SEP-1997 AF011898
                                                           YHFCGGSLINSQWVVSAAHCYQTASRISVRIGEHNIFVNEGTEQOIQASKAÎQHPQYN
SWTIDNDIMLIKLSSPATLNQYAQAIALPSSCVNTGVMCTISGWGETQTSIGSPDVLM
CVQAPVLSDTSCRNSYPGDITNNMICLGYLEGGKDSCQGDSGGPVVCNGELQGIVSWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MHGLILALLVGVAAAAPYMYEDHIVGGSECAAHSQPWQVSLNIG
                                                                                               154 AGICTIGICGITGGITGGIGIGIGIGITGITGTCIGGIATGIGATAGIGIAGGGIGGIGAGGTGT 213
                                                                                                                                                                                                                                                                                                                                                                         Petromyzon marinus (sea lamprey)
Petromyzon marinus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Hyperoartia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (01-JUL-1997) Molecular Biotechnology, University of
Washington, Seattle, WA 98195, USA
Location/Qualifiers
                     0; Gaps
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The Molecular Evolution of the Vertebrate Trypsinogens
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Petromyzon marinus trypsinogen Al mRNA, complete cds.
AF011352
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                     Indels
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                     42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mmRNA"
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1. 1860_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Petromyzon marinus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGCALPNYPGVYTKVCNYNAWIAQTIAAN"
                                                                                                                                        0; Mismatches
                                                                                                                                                                            214 rrccedrecadactracccrrrcreric 242
  52.8%; Pred. No. 27;
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/product="trypsin a2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="TRYPA2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="TRYPA2"
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                                                                                                                                                                                                                                                                                                                                     AF011898.1 GI:2367494
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 860)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 860)
Best Local Similarity 52.89
Matches 47; Conservative
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Best Local Similarity 68.28
Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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ACCESSION
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AF011898/c
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AF011352/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274 bp DNA linear VRT 23-JAN-2001
Brachyramphus brevirostris haplotype KMH ribosomal protein 40 gene,
Argorgon
                                                                              PAT 15-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 TCTCTCTCTCCCTTTCTCTAACACTTCTGGGCCAGGGTAGGGGCACTACCGCATTCCCTC 170
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2 (Dasses 1 to 274)
Pacheco, N.M. and Friesen, V.L.
Direct Submission
Submitted (21-SEP-2000) Department of Biology, Queen's University,
Kingston, ON K7L 3NG, Canada
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 TCTCACACTCCCAGCCTCCCACAATCCGAGACTGGATGAGGGGCACCAGGACCAGTGCACC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachyramphus brevirostris
Brachyramphus brevirostris
Eukaryota, Metazoa (Dordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Charadriiformes; Alcidae;
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                         Bracco, L., Brinkman, B. and Coignard, F. Variants of human kallikrein-2 and kallikrein-3 and uses thereof Patent: WO 03076610-A 6 18-SEP-2003; Exonhit Therapeutics S.A. (FR) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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Pacheco, N. M. and Friesen, V. L.
A molecular investigation of hybridization in Brachyramphus
                                                                                                                                                                                                                                       Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1%; Score 21.8; DB 1; Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.1%; Score 22; DB 1; Length 409;
Best Local Similarity 57.1%; Pred. No. 25;
Matches 40; Conservative 0; Mismatches 30; Indels
                                                                                linear
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Sequence 6 from Patent WO03076610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF306920.1 GI:12382292
                                                                                                                                                                            Homo sapiens (human)
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ACCESSION
VERSION
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SOURCE
ORGANISM
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VERSION
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AF306920
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AUTHORS
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AUTHORS
                                      RESULT 42
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VRT 11-JUN-2001
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Gaps

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Hyperoartia,
Petromyzontiformes, Petromyzontidae, Petromyzon.

    (bases 1 to 861)

                                                                                                                                                                 The molecular evolution of the vertebrate trypsinogense
                                         Petromyzon marinus (sea lamprey)
Petromyzon marinus
    GI:2293477
    AF011352.1
                                                                                                                                             Roach, J.C.
                                                           ORGANISM
VERSION
KEYWORDS
                                                                                                                                             AUTHORS
                                                                                                                       REFERENCE
                                                                                                                                                                                    JOURNAL
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Direct Submission Submitted (25-JUN-1997) Molecular Biotechnology, University of Washington, Seattle, WA 98185, USA Location/Qualifiers Unpublished 2 (bases 1 to 861) Roach, J REFERENCE AUTHORS JOURNAL FEATURES

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i. .50
/evidence=not\_experimental /evidence=not\_experimental 51. .746 /product="trypsin Al" mat\_peptide

Gaps ô DB 1; Length 861; 14; Indels 1.1%; Score 21.6; Di 68.2%; Pred. No. 35; tive 0; Mismatches Conservative Local Similarity 30; Query Match Matches

1446 TITIBATATICITICITICITICIATACITITAGIGATIA 1489 860 ritiriririririahahdericacarririahricarra 817 d

ncvel149
Mus musculus coagulation factor VII, mRNA (cDNA clone MGC:74281
MAGE:30305571), complete cds. BC061149.1 GI:38511701 BC061149 RESULT 46 BC061149/c LOCUS ORGANISM ACCESSION VERSION KEYWORDS SOURCE

Mus musculus (house mouse) REFERENCE

Mus musculus ("Ouze mouse)

\*\*Rudarota: Metazoa; Chordata: Craniata: Vertebrata; Buteleostomi; Mus musculus

\*\*Bukaryota: Metazoa; Chordata: Craniata: Vertebrata; Buteleostomi; Mammaliai: Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

\*\*I (Dases 1 to 1869)

\*\*Strausberg, R.D. Feingold, E.A., Grouse, L.H., Derge, J.G., Schuler, G.D., Altschul, S.F., Zeeberg, B., Wagner, L., Schneefer, C.F., Bhat, N.K., Altschul, S.F., Jordan, H., Moore, T., Max, S.I., Mang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Bromstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loqquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Halle, S., Garcia, A.M., Gay, L.J., Hultyk, S.M., Villallon, D.K., Muzny, D.M., Gadergren, B.J., Lu, X., Gibbs, R., Villallon, D.K., Muzny, D.M., Madan, A., Rodrigues, S., Pahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.bgc.stanford.edu
Conteat: (Dickson, Mark mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 53 Row: n Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6753805. Location/Qualifiers Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.W., Sutterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Direct Submission Submitted (03-MOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: D. Michael Brownstein CDNA Library Preparation: Michael Brownstein / Ted Usdin NIH-MGC Project URL: http://mgc.nci.nih.gov (bases 1 to 1869) Strausberg, R. Laboratory 2477932 22388257 MEDLINE PUBMED REFERENCE TITLE JOURNAL AUTHORS JOURNAL REMARK FEATURES TITLE

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ALELMSIEVPRIMTQDCLEHAKHSSNTPKITENMFCAGYMDGTKDACKGDSGGPHATH YHGTWYLTGVVSWGEGCAAIGHIGVYTRVSQYIDWLVRHMDSKLQVGVFRLPLL" misc feature

79. .264 /note="GLA; Region: Domain containing Gla (gamma-carboxyglutamate) residues" /db\_xref="CDD:smart00069" 268. 378 misc\_feature

/note="EGF\_CA; Region: Calcium-binding EGF-like domain, present in a large number of membrane-bound and extracellular (mostly animal) proteins. Many of these

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The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bloinformatics Assessment Genome Res. 13 (10), 2265-2270 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EWPWQVSIQRNGSHFCGGSLIAEQWVLTAAHČFRNTSETSLYQVLLGARQLVQPGPHA
MYRRVRQVESDPLLYQGTASADVALVELEAPVPTHVILDVCLIADPSVTETGWCWV
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EGKKDACKGDSGGPLVCLVGQSWLQAGISWGEGCARQNRPGVYIRVŢAHHNWIHRII
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                                                                                                                                                                                                                                 Direct Submission
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coagulation factor vii derivatives
Patent: WO 02077218-A 2 03-OCT-2002;
NOVO NORDISK A/S (DK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.0%; Pred. w...
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/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6098 bp
Sequence 2 from Patent W002077218.
AX565990
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAQ89464.1"
/db_xref="GI:37183329"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /locus tag="UNQ1884"
36. .908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /locus_tag="UNQ1884"
/note="PRO4327"
                                                                                                                                                                                                                                                                                                                           iocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="MPN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthetic construct
synthetic construct
artificial sequences.
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Best Local Similarity 49.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31; Conservative
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Matches 31; Conserv
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                                                                                                                                                                                                   Clark, H. F
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                                                                                                             JOURNAL
                                                                                                                                              PUBMED
                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                           FEATURES
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                   TITLE
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proteins require calcium for their biological function and calcium-binding sites have been found to be located at the Arberminus of particular EGF-like domains"

(Ab xref="CDD:cd00054" | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302 | 1302
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[ bases 1 to 1129]

Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Barcon, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lawis, L., Liao, D., Mark, M., Robbie, B., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansıra, D., Yil, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAT 16-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E., Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Sherwood, S., Smitth, V., Stewart, T.A., Tumas, D., Watanabe, C.K., Wood, W.L. and Zhang, Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                 589. .1302
/note="Tryp SPc; Region: Trypsin-like serine protease"
/db_xref="CDD:cd00190"
                                                                                                                                                                                                                                                                                                                           Gaps
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Homo sapiens clone DNA99391 MPN (UNQ1884) mRNA, complete cds.
AY359106
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                                                                                                                                                                                                                                                               DB 1; Length 1869;
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1129 bp 1
Sequence 221 from Patent WO0140466.
                                                                                                                                                                                                                                                                  Score 21.6;
Pred, No. 37
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Location/Qualifiers
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Homo sapiens
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AY359106/c
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VERSION
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AUTHORS
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FEATURES

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KEYWORDS

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Gaps

note="Vector: pCMV-SPORT6"

'gene="F10"

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gene
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Klausher, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Alsohul, S.P., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.P., Jordan, H., Moore, T., Wars, S. I., Wang, J., Hsieh, F.,

Diatchenko, L., Marushina, K., Parmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdain, T.B., Toshiyuki, S.,

Carninoi, P., Prange, C.C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Wullahy, S.J., Bosak, S.A., McEwan, P.D.,

McKernan, K.J., Malek, J.S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sancher, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Boutfard, G.G., Blakesley, K.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skallak, U., Saailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.G. and Marra, M.A.,

Generation and initial analysis of more than 15,000 full-length
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogev
CDNA Library Preparation: Life Technologies, Inc.
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HOMO Sapiens coagulation factor X, mRNA (cDNA clone MGC:57588
FMAGE:5723510), complete cds.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9961350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1541)
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                               BC046125.1 GI:28374355
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Homo sapiens
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Strausberg, R.
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/clone="MGC:57588 IMAGE:5723510" /tissue type="Ovary, pooled from 3 adults" /clone\_lib="NIH\_MGC\_125"

/lab host="DH10B"

/organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606"

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/note="GLA; Region: Domain containing Gla (gamma-carboxyglutamate) residues. A hyaluronan-binding domain found in proteins associated with the extracellular matrix, cell adhesion and cell migration" /db xref="CDD:smart00065" 318. .401
                                                                                                                                                                                                                                                                                                                                                                          DFNQTQFERGDNNLTRIVGGQECKDGECPWQALLINEENEGFCGGTILSBFYILTAAH
CLYQAKRFKVRVGDRNTEQEEGGEAVHEVEVVIKHNRFTKETYDFDIAVLRLKTPITF
RMVVAPACLPERDWAESTLMTQKTGIVSGFCRTHEKGRQSTRLKMLEVPYVDRNSCKL
                                                                                                                                                                                                                              /db_xref="locusID:2159"
/translation="MGRPLHLVLLSASLAGLLLLGESLFIRREQANNILARVTRANSF
                                                                                                                                                                                                                                                                                    LEEMKKGHLERECMEETCSYEEAREVFEDSDXTNRFRWKYKDGDOCETSPCONGGKCK
DGLGEYTCTCLEGFEGKNCELFTRKLGSLDNGDCDOFCHEEGNSVVCSCARGYTLADN
GKACIPTGPYPCGKQTLERRKRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGEGCARKGKYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="EGF; Region: EGF-like domain. There is no clear separation between noise and signal. pfam00053 is very similar, but has 8 instead of 6 conserved cysteines. Includes some cytokine receptors. The EGF domain misses the N-terminus regions of the Ca2+ binding EGF domains. The family is hard to model due to many similar but different sub-types of EGF domains. Pfam certainly misses a number of EGF domains.
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1 (base1 to 267)
Jacobs, K., Mccoy, J.M., Lavallie, E.R., Racie, L.A., Merberg, D., Treacy, M., Spaulding, V. and Agostino, M.J.
Pacetce apressed sequence tags (sESTs)
Patent: JP 2001518793-A 724.16-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1533 TGTTTTGTATGCTTCTTGTACCTTGATAGGCATCTCTTTCTCAAGGTTAGGAAATTTT 1590
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KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Tryp_SPc; Region: Trypsin-like serine protease"
|db_xref="CDD:smart00020"
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                                                                                                                                        product="coagulation factor X precursor"
protein id="AAH46125.1"
db_xref="GI:28374356"
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tive 0; Mismatches. 23; Indels
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Secreted expressed sequence tags (SESTs).
BD060364
/note="synonyms: FX, FX, db_xref="LocusID:2159"
/db_xref="MIM:227600"
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10-APR-1997 US 08/83731
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16-0CT-2001
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/codon_start=1
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/organism="unknown"
/mol_type="unassigned DNA"
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Best Local Similarity 56.5%;
Matches 39; Conservative
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                                                                                                                                                                                                                                                                                            243 GATGCATTGACCTCAAACACTCTCTCTAGTATCCCATTTCTGTTGGATTTCTTTTCTCAATC 184
                                      Strandedness:
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Sostak, 7, W., Roberts, R.W. and Liu, R.
Method for selection of proteins using RNA-protein fusions
Patent: US 6258558-A 17 10-JUL-2001;
                   PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC Strai
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                                                                                                                                                                                               1.0%; Score 21; DB 1; Length 267; Similarity 49.5%; Pred. No. 44; Conservative 0; Mismatches 55; Indels
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Szostak, J.W., Roberts, R.W. and Liu, R.
Nucleic acid-protein fusion molecules and libraries
Patent: US 6281344-A 17 28-AUG-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.0%; Score 21; DB 1; Length 289; 17.6%; Pred. No. 44;
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                                                                                Location/Qualifiers.
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AR162089
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                                                                                                                                                 /mol_type="genomic DNA"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                           289 bp
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/organism≈"Zea mays"
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                                                                  Topology: Linear;
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   DAVID MERBERG,
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ASGTLQRLAVPLLPAAQCGNANTTANNFCAGYTEGDHASCRGHDGSPLVTRYGETSFL
TGVVSWGRGCGPPGYYMIYTKVENFLIWMDTVMKTNTEDKSEQIANVSTKN"
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1 (bases 1 to 172)

1 (bases 1 to 172)

2 (comprehensia, R., Day, K. and Jagadeswaran, P. Comprehensive analysis of blood coagulation pathways in teleostei: Evolution of coagulation factor genes and identification of generalis factor vIIi

2 (bases 1 to 1722)

2 (bases 1 to 1722)
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Location/Qualifiers
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Pred. No. 52;
0; Mismatches 30; Indels
Query Match
1.0%; Score 21; DB 1; Length 289;
Best Local Similarity 17.6%; Pred. No. 44;
Matches 12; Conservative 33; Mismatches 23; Indels
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/note="clotting factor"
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I (bases 1 to 1206)
Fukushima, K., Mizuguchi, J., Yuguchi, M., Nakagaki, T. and Iwanaga, S.
Fukushima, K., Mizuguchi, J., Yuguchi, M., Nakagaki, T. and Iwanaga, S.
Fahenocoagulation factor VII modification
Patent: JP 2001061479-A 5 13-MAR-2001,
JURIDICAL FOUNDATION THE CHEMO SERO THERAPEUTIC RESEARCH INSTITUTE
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    /organism="synthetic construct"

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JP 2001061479-A/5
13-MAR-2001
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JP 2001061479-A/6
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artificial sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Analysis of the partial nucleotide sequences and deduced primary structures of the protease domains of mammalian blood coagulation factors VII and X Eur. J. Haematol. 52 (3), 162-168 (1994)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (18-007-1993) Masahiro Murakawa, Harasanshin General
Submitted (18-007-1993) Masahiro Murakawa, Harasanshin General
Hospital, Division of Hematology; 1-8 Taihaku-machi, Hakata-ku,
Fukucka, Fukucka 812, Japan (Tel:092-291-3434, Fax:092-291-3266)
Submitted (18-001-1993) to DDBJ by:
Masahiro Murakawa
Division of Hemotology
Harasanshin General Hospiral
Harasanshin General Hospiral
1-8 Taihaku-machi, Hakata-ku
Fukucka, Fukucka 812
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Murakawa,M., Okamura,T., Kamura,T., Kuroiwa,M., Harada,M. and
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1.0%; Score 20.8; DB 1; Length 48.
Best Local Similarity 57.8%; Pred. No. 53;
Matches 37; Conservative 0; Mismatches 27; Indels
                                 Rat gene for coagulation factors X, partial cds. D21215. D21215.1 GI:415309
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/db_xref="taxon:10116"
                                                                                                                                                                                                                    Rattus norvegicus (Norway rat)
Rattus norvegicus
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artificial sequences.
1 (bases 1 to 1206)
Fukushima, K., Mizuguchi, J., Yuguchi, M., Nakagaki, T. and Iwanaga, S.
Hemocoagulation factor VII modification
Patent: JP 2001061479-A 6 13-MAR-2001,
JURIDICAL FOUNDATION THE CHEMO SERO THERAPEUTIC RESEARCH INSTITUTE
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KENJI FUKUSHIMA, JUN MIZUGUCHI, MASATO YUGUCHI, TOMOHIRO
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1.0%; Score 20.6; DB 1; Length 1206;
Best Local Similarity 59.3%; Pred. No. 64;
Matches 35; Conservative 0; Mismatches 24; Indels 0;
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1.0%; Score 20.6; DB 1; Length 1206;
Best Local Similarity 59.3%; Pred. No. 64;
Matches 35; Conservative 0; Mismatches 24; Indels 0
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/organism='Artificial Sequence'
Location/Qualifiers
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Query Match
Best Local Similarity 59.3%;
Matches 35; Conservative
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Matches 35; Conservative
A61K37/465
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E63000/c
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E62999/c
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CI2NIS/09, AGIK38/43, AGIP7/04, C07K14/755, C12N9/76, C12NI5/00, PC
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Fukushiman,k., Maruguchi,J., Yuguchi,M., Nakagaki,T. and Iwanaga,S.
Hemocoagulation factor VII modification
Patent: JP 2001061479-A 2 13-MAR-2001;
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334 TICAATIGICTITITAICIGICGAGACTIGCTITIGIALAAIAIGIATICAATITIGG 392
                                444 TTTGCTGGCATTTCTTTTTTTTTAGAATAGGTATTTTTTCCACATGGATATTCAACTGTGG 386
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Pred. No. 64
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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C12N15/09, A61K38/43, A61P7/04, C07K14/755, C12N9/76, C12N15/00, PC
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C12N15/09, A61K38/43, A61P7/04, C07K14/755, C12N9/76, C12N15/00, PC
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DP 2001061479-A/3.

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loases 1 to 1221)

Fukushima, K., Mzuguchi, J., Yuguchi, M., Nakagaki, T. and Iwanaga, S.

Hemocoagulation factor VII modification

Patent: JP 2001061479-A 3 13-MAR-2001;

UKIDICAL FOUNDATION THE CHEMO SERO THERAPEUTIC RESEARCH INSTITUTE

SO Artificial Sequence

PN 12-2001061479-A/3

PD 13-MAR-2001
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                                                                                                                                                                                                                                                                                                                          1.0%; Score 20.6; DB 1; Length 1221; 9.3%; Pred. No. 64; ve. 0; Mismatches 24; Indels 0;
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                                                                                  Location/Qualifiers
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Unclassified.

1 (Dasss 1 to 1440)

Thorpe, P.E., King, S.W. and Gao, B.
Combined tissue factor and factor VIIa methods and compositions for coagulation and tumor treatment
Patent: US 6132730-A 13 17-OCT-2000;

Location/Qualifiers
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1.0%; Score 20.6; DB 1; Length 14
Best Local Similarity 59.3%; Pred. No. 65;
Matches 35; Conservative 0; Mismatches 24; Indels
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1 Similaritý 59.3%; Pred. No. 65;
35; Conservative 0; Mismatches
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Location/Qualifiers
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Sequence 3 from patent US 5504064.
119358.1 GI:1599713
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Sequence 3 from patent US 5504067.
119360.
119360.1 GI:1599715
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CIZNI5/09,A6IK38/43,A6IP7/04,C07K14/755,CIZN9/76,CI2N15/00, PC
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                 artificial sequences.

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Thorpe, P.E., King, S.W. and Gao, B.
Combined tissue factor and chemotherapeutic methods and compositions for coagulation and tumor treatment Patent: US 6132729-A 13 17-CCT-2000;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.0%; Score 20.6; DB 1; Length 12 Best Local Similarity .59.3%; Pred. No. 64; Matches 35; Conservative 0; Mismatches 24; Indels
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    organism="synthetic construct"

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Pred. No. 65;
0; Mismatches
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Sequence 13 from patent US 6132729.
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Matches 35, Conservative
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1 (bases 1 to 1440)

Morrissey.d.H. and Comp.P.C.

Treatment of FVII

With an activator of FVII

Patent: US 5504064.A 3 02-APR-1996;

Location/Qualifiers
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Morrissey, J. H. and Comp, P. C.
Treatment of bleeding with modified tissue factor in combination with FVII.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.0%; Score 20.6; DB 1; Length 144
Best Local Similarity 59.3%; Pred. No. 65;
Matches 35; Conservative 0; Mismatches 24; Indels
  linear
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Gaps

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PAT 18-DEC-2003

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334 TTCAATTGTCTTTTATCTGTCGAGACTTGCTTTTGTTTTGAAATATGTATTCAATTTTGG 392
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                                                                                                                                                                                                                                                                                                         Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 TIGCACTGGTFGGAGTTGTGGAGACGCCCTTGAGTCTCAGTACGAGTGTGCGTGAGTGTG 63
                                                                                                                                                                                                                                                                                                                                                     Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y. Expressed sequence tags and encoded human proteins Patent: EP 1033401-A 24371 06-SEP-2000;
Query Match
1.0%; Score 20.6; DB 1; Length 6098;
Best Local Similarity 59.3%; Pred. No. 65;
Matches 35; Conservative 0; Mismatches 24; Indels 0;
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Sequence 24371 from Patent BP1033401.
AX908508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
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JP 2001269182-A/20287.
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Homo sapiens
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                   334 TICAATIGICTITITATCIGICGAGACTIGCTITGTITIGAAATATGTATTCAATTTIGG 392
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                                        659 TTTGCTGGCATTTCTTTTTTTTAGAATAGGTATTTTTCCACATAGGATATTCAACTGTGG 601
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Thorpe, P.E., King, S.W. and Gao, B.
11ssue factor methods and compositions for coagulation and tumor
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BOARD OF RECENTS THE UNIVERSITY OF TEXAS SYSTEM
BOARD OF RECENTS THE UNIVERSITY OF TEXAS SYSTEM
BOARD 14-MAY-2002
BY 14-MAY-2002
BF 20-JAN-1997 US 60/035920,27-JAN-1997 US
PT AR-1997 US 60/045427
BI PHILIP E THORPE, STEVEN W KING, BONING GAO
BOARD 14-MAY-149
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Location/Qualifiers
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/mol type="unassigned DNA"
/mol type="nassigned DNA"
/noFe="taxon:32630"
/noFe="Plasmid DNA pLN174"
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Patent: WO 02077218-A 2 03-OCT-2002;
NOVO NORDISK A/S (DK)
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/organism="unidentified"
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/db_xref="taxon:32644"
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AX565990.1 GI:26001242
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C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
linear PAT 27-AUG-2002
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[Dases I to 223)

Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.

Sequence tag and encoded human protein
Patent: JP 2001269182-A 20287 02-0CT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
JP 2001269182-A/20287
02-CCT-2001
02-EB-2000 UP 2000118773
26-FEB-1999 US 60/122487
JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
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GI:12382285
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Brachyramphus brevirostris
Eukaryota, Metazca, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Charadriiformes, Alcidae,
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Pacheco, N.M. and Friesen, V.L.
A molecular investigation of hybridization in Brachyramphus
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Pred. No. 63;
0; Mismatches 51; Indels
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/mol_type="genomic DNA"
/db xref="raxon:28693"
/haplotype="KWE"
join(<1. -14,264. .>280)
/product="ribosomal protein 40"
/note="coding region not determined"
                                                                                                                                                                                                    26;
                                                                                                                                                    1.0%; Score 20.4; DE
58.1%; Pred. No. 62;
tive 0; Mismatches
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
          Location/Qualifiers
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Best Local Similarity 50.0%;
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/number=5
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Best Local Similarity 58.19
Matches 36; Conservative
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280 bp DNA linear VRT 23-JAN-2001
Brachyramphus brevirostris haplotype KMB ribosomal protein 40 gene,
intron 5 and partial sequence.
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2 (Dases 1 to 280)
2 (Dases 1 to 280)
Pacheco, N. M. and Friesen, V.L.
Direct Submission
Submitted (21-SEP-2000) Department of Biology, Queen's University,
Kingston, ON K7L 3NG, Canada
Location/Qualifiers
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Archosauria; Aves; Neognathae; Charadriiformes; Alcidae;
Brachyramphus brevirostris
Brachyramphus brevirostris
Bukaryota, Metazca, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Charadriiformes, Alcidae,
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Pacheco, N. M. and Friesen, V.L.
A molecular investigation of hybridization in Brachyramphus
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Pacheco, M. and Friesen, V.L.
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Sequence update by submitter
On Feb 7, 2003 this sequence version replaced gi:14279677.
                                                                 Brachyramphus.
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intron 5 and partial sequence.
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Direct Submission
Submitted (21-SEP-2000) Department of Biology, Queen's University,
Xingston, ON K7L 3N6, Canada
Localion/Qualifiers
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Pacheco, N.M. and Friesen, V.L.
A molecular investigation of hybridization in Brachyramphus
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Pacheco,N.M. and Friesen,V.L.
Direct Submission
Submitted (21-SSPP-2000) Department of Biology, Queen's University,
Kingston, ON K7L 3N6, Canada
Location/Qualifiers
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1 (Dases 1 to 2072)

Hu, Z. and Garen, A.

Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer proc. Natl. Acad. Sci. U.S.A. 98 (21), 12180-12185 (2001)
                     Brachyramphus brevirostris
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Charadriiformes, Alcidae,
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Pacheco, N. M. and Friesen, V. L.
A molecular investigation of hybridization in Brachyramphus
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Hu,Z. and Garen,A.
Direct Submission
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Z. and Garen, A.
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Drosophila straubae isolate 5 mastermind (mast) gene, partial cds.
AY155152 GI:28975316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila straubae
Drosophila straubae
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Bukaryota, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophila, mayaguana subcluster.
I (bases 1 to 183)
O'Grady, P.M. II, Durando, C.M., Heed, W.B., Wasserman, M., Etges, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (25-SEP-2002) Invertebrate Zoology, American Museum of
Natural History, Central Park West at 79th Street, New York, NY
10024, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 183)
O'Grady, P.M. II, Durando, C.M., Heed, W.B., Wasserman, M., Etges, W.
and DeSalle, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.0%; Score 20.4; DB 1; Length 2072;
Best Local Similarity 61.1%; Pred. No. 74;
Matches 33; Conservative 0; Mismatches 21; Indels 0; Gaps
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/mol_type="genomic DNA"
/isolate="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'country="Navassa Island"
                                                                                       organism="Homo sapiens"
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clone="12"
                                                                                                                                                                          'db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="mastermind"
<1. .>183
Location/Qualifiers
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                                                                                                                       type="mRNA"
                                                                                                                                                                                                                                                             note="hfVIlasm"
                                                                                                                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="mast"
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/gene="mast"
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                                                  source
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VERSION
KEYWORDS
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FEATURES
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Direct Submission
Submitted (10-APR-2002) Naotaka Hamasaki, Kyushu University
Submitted (10-APR-2002) Naotaka Hamasaki, Kyushu University
3-1-1 maidashi, Higashi-ku Fukuokasi, Fukuoka 812-8582, Japan
(B-mail:hamaaaki@colm.med.kyushu-u.ac.jp, Tel:81-92-642-5770,
Fax:81-92-642-5772)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="LSKQQASQVLVRKRRANSLLEETKQGNLERECIBELCNKEEARE
                                                                                                           PRI 07-JAN-2003
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                                                                                                                                                                                                                                                                                      Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria; Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                               Hamasaki, N., Dong Chon, K., Kinosita, S., Iida, H., Inoue, S., Watanabe, K., Kurihara, M., Wada, Y. and Ono, M. Gene analysis of anticogulation factors in Japanese thrombotic pattents. Genetic background of thrombophilia in Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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1.0%; Score 20.2; DB 1; Length 214;
Best Local Similarity 51.7%; Pred. No. 69;
Matches 46; Conservative 0; Mismatches 43; Indels 0
                                                                                      214 bp DNA linear
Homo sapiens PROS1 gene for Protein S, partial cds,
ABNAR102 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol type="genomic DNA"
/isolate="patient: PS 1"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="BAC54134.1"
/db_xref="GI:27531050"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Protein S"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
51 GTTGCTGTTGCTGTTG 31
                                                                                                                                                                                             AB083386.1 GI:27531049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25. .182
/gene="PROS1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <25. .>182
/gene="PROS1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'replace="g"
                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
2 (bases 1 to 214)
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                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                               AB083386
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                                                                RESULT 77
AB083386/c
                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                   ORGANISM
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
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/codon\_start=3 /product="mastermind" /protein\_id==12805136.1" /db\_xref="G1:28975317" /translation="DikkLQQQQAMQQQQQHHAQQQQQHPNGPKMGVPMGGAGNFA

gene="mast"

0

298 TAAGCIGIGGIGGICAGATAG 318

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Query Match 1.0%; Score 20.2; DB 1; Length 183; Best Local Similarity 53.1%; Pred. No. 68; Matches 43; Conservative 0; Mismatches 38; Indels 0; Gaps

43; Conservative

KQQQQQVVTXXQQQQQ"

임 ò a Ω

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Tao,N., Barbazuk,W.B., Llu,u., ...,...
Direct Submission

Submitted (10-dan-2001) Genomics, Monsanto, 800 North Lindbergh
Blvd., Creve Coeur, MO 63167, USA
Blvd., Creve Genomic sequences generated from the Monsanto
Derived from rice genomic sequences generated from the Monsanto
Rice Genome Sequencing project. Please see
http://www.rice-research.org for more information. The sequence
http://www.rice-research.org for more information. The sequence
data were produced primarily in the laboratories of Dr. Leroy Hood
at the University of Washington in Seattle.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AY023221 227 bp DNA linear PLN 07-FSB-2001 Oryza sativa microsatellite MRGSS46 containing (GCT)X9, closest to avonative G132, genomic sequence.
                                                                                                                                                        Oriza sativa

bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, biliopsida, Poales, Poaceae, Birhartoideae, Oryzee, Oryza.

Birhartoideae, Oryzee, Oryza.

Dases 1 to 227)

Tao, N., Barbazuk, W.B., Liu, J., Wu, K. and Barry, G.F.

Simple sequence repeats from Monsanto rice genomic sequences
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tao,N., Barbark,W.B., Liu,J., Wu,K. and Barry,G.F.
Direct Submission
Submitted (10-JAN-201) Genomics, Monsanto, 800 North Lindbergh
Blvd., Creve Coeur, MO 63167, USA
Blvd., Creve Genomic sequences generated from the Monsanto
Rice Genome Sequencing project. Please see
http://www.rice-research.org for more information. The sequence
data were produced primarily in the laboratories of Dr. Leroy Hood
at the University of Washington in Seattle.
Location/Qualifiers
Oryza sativa microsatellite MRG4798 containing (AGC)X9, closest to marker G132, genomic sequence.
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1 (bases 1 to 227)
Tao,N., Barbauk,W.B., Liu,J., Wu,K. and Barry,G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 TGAAGCCTCTGCTGGCAATACTTCTGGGGCTGCTGCCTTTCTCCCTGTC 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.0%; Score 20.2; DB 1; Length 227;
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/note="microsatellite MRG4798"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.3%; Pred. No. 70;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa"
/mol_type="genomic DNA"
/db_xref="taxon:4530"
1. .227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_type=tandem
/rpt_unit="agc"
                                                                              AY022473.1 GI:12705689
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                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 227)
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                                                                                                                                    Oryza sativa
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Best Local Similarity
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     DEFINITION
                                                                                                                              SOURCE
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AUTHORS
                                                        ACCESSION
                                                                              VERSION
KEYWORDS
                                                                                                                                                                                                                                                             REFERENCE
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Submitted (09-MRY-2002) Naotaka Hamasaki, Kyushu University
Hospital, Department of Clinical chemistry and laboratory medicine;
3-1-1 maidasi, Higasi-ku Fukuokasi, Fukuoka 812-8582, Japan
(E-mail:hamasaki@colm.med.kyushu-u.ac.jp, Tel:81-92-642-5770,
                                                                                                                                                                                                                                                                                         linear PRI 07-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hamasaki, N., Kang, D., Kinoshita, S., Iida, H., Inoue, S., Watanabe, K., Kurihara, M., Wada, Y. and Ono, M. Gene analysis of anticoagulation factors in Japanese thrombotic patients. Genetic background of thrombophilia in Japan
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  184 CTICIATITICITGATITICIAÇÇICATITITAACICAGIAGIGAGITGITIGGIT 243
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                                                     150 CTTCTTCTTTATTGCACAGTTCTTCGATGCATTCTCTTTCAAGATTACCCTGTTTGGTTT 91
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens PROS1 gene for PS22, partial cds.
                                                                                                        244 CCATAAGTTTGTAAGTTTTCTGTTGTTTC 272
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db_xref="GI:27531281"
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/isolate="16"
/db_xref="taxon:9606"
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Best Local Similarity 51.7%;
Matches 46; Conservative (
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2 of 14
Homo sapiens (human)
Homo sapiens
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Biochemistry 29 (34), 7853-7861 (1990)
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1 (bases 1 to 272)
Ploos van Amstel, H.K., Reitsma, P.H., van der Logt, C.P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Original source text; Human DNA.
Draft entry and computer-readable sequence for [Biochemistry 29, 7853-4861 (1990)] kindly submitted
by H.K.Ploos van Amstel, 13-JUL-1990.
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/note="protein S alpha; G00-120-721; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.0%; Score 20.2; DB 1; Length 272; Best Local Similarity 51.7%; Pred. No. 71; Matches 46; Conservative 0; Mismatches 43; Indels (
                                                                                                             Score 20.2; DB 1; Length 227; Pred. No. 70;
                                                                                                                                                                                                                                                                             Homo sapiens protein S alpha (PROS1) gene, exon 2. M36551 J02918
                                                                                                                                                18; Indels
   /mol_type="genomic_DNA"
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1. 727
/note="microsatellite MRG5546"
                                                                                                                                                0; Mismatches
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/mol_type="genomic DNA"
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                                                                  /rpt_type=tandem
/rpt_unit="gct"
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Homo sapiens (human)
Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 352)
Schmidal, D.K., Tatro, A.V., Phelps, L.G., Tomczak, J.A. and Long, G.L. Organization of the human protein S genes
Biochemistry 29 (34), 7845-7852 (1990)
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Best Local Similarity 63.3%; Pred. No. 79;
Matches 31; Conservative 0; Mismatches 18; Indels
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/mol_type="genomic DNA"
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join(W578401:837. .912,135. .181)
                                                                                                                                                                                                                                                                                                                                                                                                           /gene="PS-alpha"
order(M57840.1:913..1014,1..134)
/gene="PROS1"
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Gibbs, C.S., Leung, L.L.K. and Tsiang, M.
Polypeptides and coagulation therapy
Patent: US 6110721-A 1 29-AUG-2000;
                                                                                                                                                                                               Original source text: Human liver DNA. Location/Qualifiers
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Sequence 1 from patent US 6110721.
AR108139
AR108139.1 GI:12823626
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/gene="PROS1"
/note="G00-120-721"
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/dev_stage="ammocoete"
/tissue_lib="anterior intestine"
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/evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Petromyzon marinus (sea lamprey)
Petromyzon marinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
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                                                                                                          49. .147
169. .1431
/product≈"protein C"
1514. .1519
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/gene="TRYPA3"
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2 (bases 1 to 855)
                                                                                                                                                                                         Query Match
Best Local Similarity 68.3%
Matches 28, Conservative
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Best Local Similarity
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Submitted (03-FEB-1992) Okafuji T., Mol Biology Research Lab,
Daiichi Pharmaceutical Co LTD, 16-13 Kitakasai 1-Chome, Edogawa-ku,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear ROD 12-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLEEVRAGSLERECMEETCDFEEAQETFQNVEDTLAFWIKYFDGDQCSTPPLDHQCDS
PCCGHGTCIDGLGGFSCSCDKGWEGRFCQQEMGFQDCRVKNGGCYHYCLEETRGRRCR
                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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On Nov 19, 2003 this sequence version replaced gi:251769.
Location/Qualifiers
                                                                                                                                                                                Mendrick,D., Porter,M.W., Johnson,K.R., Castle,A.L. and
Elashoff,M.R.
Moleculat Loxicology modeling
Patent: WO 0210453-A 1575 07-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                  Score 20.2; DB 1; Length 1543;
Pred. No. 82;
                                                                                                                                                                                                                                                                                                                           /mol_type="unassigned_DNA"
/db_xref="taxon:10116"
/note="EMBL/GenBank_Accession_NO._NM_012803"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 1543)
Makfulji,T., Makawa,K., Nawa,K. and Marumoto,Y.
The CDMA cloning and mRNA expression of rat protein C
Biochim. Biophys. Acta 1131 (3), 329-332 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            814 CATCCTTTACTCTAAGGTGATGTCTATCCATGGTAGGTTG 854
1408 CATCCCTTTCCCCTATGTAGCTGTGGATCCATTTGAGGTAG 1368
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X64336 S40352
X6436 I GI:S6962
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/protein_id="CAAA5617.1"
/db_xref="G1:56963"
                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
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/db_xref="SWISS-PROT:P31394"
Sequence 1575 from Patent W00210453.
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/clone="28000"
                                                                        Rattus norvegicus (Norway rat)
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                  AX401899
AX401899.1 GI:21338079
                                                                                                                                                                                                                                                         Gene Logic, Inc. (US)
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Best Local Similarity 68.3%;
Matches 28; Conservative
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CAPGYELADDHAHCRPTVNFPCGKLWKRIDKKRKNFKRDIDPEDEBLELGPRIVNGTL
TKQGDSPWQAILLDSKKKLACGGVLIHTSWVLTAAHCLESSRKLTVRLGEYDLRRRDP
BEDLDIAFEUVHPPNYRSNSDNDIALBLGOPATLSKTIVPICLPNSGLAQELSQAG
QETVYTGWGYQSDKYKDGRRRRFILTPIR.FILPLAARNDCMQVWRNVVSENMLCAGIIG
DTRDACDGDSGGPMVVFFRGTWFLVGLVSWGEGGGHLNNYGVYTKVGSYLKWIHSYIG
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YHPGGGSELNSQWWVSAAHCYQTASIS.RNIGBHNIFWNSPGTEQQIQASKSIQBPQYN
SWTIDNDIMLIKLSSPATUKSSPATUKYAQA TALPSSCVWTGVWCTISGWGSTQTSQTSGPDVLM
CVQAPVLSDTSCRNSYPGDITNNMICLGYLBGGKDSCQGDSGGPVVCNGELQGIVSWG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
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Submitted (01-UTL-1997) Molecular Biotechnology, University of
Washington, Seatule, WA 98195, USA
Location/Qualifiers
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Petromyzon marinus trypsinogen a3 (TRYPA3) mRNA, complete cds
AF011899
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0; Gaps

DB 1; Length 1166;

/organism="unknown" /wol\_type="genomic DNA"

Location/Qualifiers 1. .1166

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Query Match 1.0%; Score 20; DB 1; Length 1166 Best Local Similarity 58.3%; Pred. No. 91; Andels Matches 35; Conservative 0; Mismatches 25; Indels
   JOURNAL Patent: US 6426199-A 2 30-JUL-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              609 TGCTTGTTTTATGAACTTGGGTGACATTGTGTTTGGTGCATAGACATTAAGAATTGCAAT 668
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855 TITITITITITITITAGITCACATITITATICATITAGITA 812
                                                                                                                                                                                                                                               1 (bases 1 to 1130)
Darrow, A., Qi,U. and Andrade-Grodon,P.
DNA encoding the human serine procease T
Patent: US 6458564-A 8 01-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
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Darrow, A., Qi,J. and Andrade-Grodon,P.
Darrown activation system
Patent: US 6420157-A 8 16-JUL-2002;
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Darrow,A., Qi,J. and Andrade-Grodon,P.
DNA
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Location/Qualifiers
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                                                                                                   Sequence 8 from patent US 6458564. AR234337
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                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
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                                                                                                                                                          AR234337.1 GI:27277021
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ARŽ21273.1 GI:23328188
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                                                                                                                                                                                                                             Unclassified.
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AF515269 1722 bp MRNA linear VRT 15-NOV-2002
Danio rerio coagulation factor VIIi mRNA, complete cds.
AP515269
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                                                                                                                                                                                                                 linear PAT 25-SEP-2002
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609 IGCTIGITTIAIGAACTIGGGIGACATIGIGITIGGGIGCATAGACATIAAGAATIGCAAT 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             609 TGCTTGTTTTATGAACTTGGGTGACATTGTGTTTGGTGCATAGACATTAAGAATTGCAAT 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanumanthalah, R., Z., Day, K. and Jagadeeswaran, P.
Comprehensive analysis of blood coagulation pathways in teleostei:
Evolution of cagulation factor genes and identification of
Estafish factor VIII
Elood Cells Mol. Dis. (2002) In press
2 (bases 1 to 1722)
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1 (bases i to 1722)
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Submitted (24-MAY-2002) Cellular & Structural Biology, University of Texas Health Science Center at San Antonio, 7703 Floyd Curl Drive, San Antonio, 17 78229, USA
Location/Qualifiers
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1.0%; Score 20; DB 1; Length 1169;
Best Local Similarity 58.3%; Pred. No. 91;
Matches 35; Conservative 0; Mismatches 25; Indels
                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 1169)
Darrow, A., Qi, J. and Andrade-Grodon, P.
Zymogen activation system
Patent: US 6420157-A 7 16-JUL-2002;
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                                                                                                                                                                                                   Sequence 7 from patent US 6420157.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
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27._.1358
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                                                                                                                                                                                                                                                                                                    AR219284.1 GI:23320254
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                                                                                                                                                                                                                                                                                                                                                                                                    Unknown.
Unclassified.
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SEREE
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BD095271/c
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KEYWORDS
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                                                                                              /traislation="MTLGAAAVLLCVLTLRSTSAVFLSKDEASALLQRFRRANSGFLE
EMKAGNLERECVEBICDYBEAREVFEDDDRTKQFWLSYSNKEPCLTNPCRNNGTCVYL
ADSYYCLGSECYEGKYCEKGLEETLKCQYNGGCEQFCDGSARRSGSGARSGTAADD
GTSCVSQVDYPCGKIPVQKNTSQNQFGGILGPRGHCPWQVLIDYNGBSVCGGALLEG
PWLITAAHCYHQKDTRELKAYTGEHDLDVLDGSBEPYEVSAVFIHPNYDPETLDSDLA
LIRLRVPVQRSLYAVPICLPTPQLARSELWAARFHTLSGWGTRTAGHNLRREKGLKGP
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Homo sapiens Peutz-Jeghers syndrome protein (LKB1) gene, exon 8.
AF055326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene expression profiling of primary breast carcinomas using arrays of candidate genes
Patent: WO 0246467-A 331 13-JUN-2002;
                                                                                                                                                                                                                       ASGTLQRLAVPLLPAAQCGNANTTANMFCAGYTEGDHASCRGHDGSPLVTRYGETSFL
TGVVSWGRGCGPPGYYMIYTKVENFLIWMDTVMKTNTEDKSEQIANVSTKN"
                                                                                                                                                                                                                                                                                                                                                                                                           1354 Triringrada carrade da renecic de reneditor de renederar de contrador de 1295
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                                                                                                                                                                                                                                                                                                                                                                     858 TITITGGATGCAGTAGGATGGATCTTTTTTTCATATCCATTCTGTTACCCAGTATCT 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 TGTCTTCACGCGTGTCTCTGTGTTTGTGGACTGGATTCACAAGGTCATGAGACTGGGTTA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bertucci, F., Houlgatte, R., Birnbaum, D., Nguyen, C., Viens, P. and
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1.0%; Score 19.8; DB 1; Length 254;
Best Local Similarity 51.7%; Pred. No. 90;
Matches 45; Conservative 0; Mismatches 42; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..254 / note="3' terminal sequence. macrophage stimulating (hepatocyte growth factor-like) (MST1) gene."
                                                                                                                                                                                                                                                                                  1.0%; Score 20; DB 1; Length 1722; ilarity 50.0%; Pred. No. 92; Conservative 0; Mismatches 50; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      918 TITICTAGAGAAATTAAGATCATTGAGTCATTGATGTTGA 957
                 /codon_start=1
Produce="coagulation factor VIIi"
/protein_id="AAN71000.1"
/db_xref="GI:25005099"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/note="primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
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Sequence 331 from Patent WO0246467,
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'note="clotting factor"
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ACCESSION
VERSION
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HSLKB1PJ7/c
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Structural coordinate and NMR chemical shift of protein and undilization thereof.
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Structural coordinate and NVR chemical shift of protein and
utilization thereof.
Patent: WO 0142453-A 3 14-JUN-2001;
BIOMOLECULAR ENGINEERING RESEARCH INSTITUTE, DAISUKE KODA, HIDEKAZU
                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 268) Arizientyte,E., Roth,S., Loukola,A., Hemminki,A., Lothe,R.A., Sternig,A.E., Fossa,S.D., Salovaara,R.E. and Aaltonen,L.A. Somatic mutations in LKB1 are rare in sporadic colorectal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deses 1 to 268)
Avizienyte, E., Roth, S., Loukola, A., Hemminki, A., Bignell, G.R.,
Avizienyte, E., Roth, S., Loukola, A., Hemminki, A.,
Birect Submission
Submitted (25-MAR-1998) Department of Medical Genetics, Haartman
Institute, University of Helsinki, P.O. Box 21 (Haartmaninkatu 3),
Helsinki FIN-70014, Finland
Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 384)
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                                                                                                                                                                                                                                                                                                                                                                                                                   Low frequency of somatic mutations in the LKB1/Peutz-Jeghers syndrome gene in sporadic breast cancer Cancer Res. 58 (7), 1384-1386 (1998)
                                                                                                                                                                                                                                                                                testicular tumors
Cancer Res. (1998) In press
2 (bases 1 to 268)
Bignell, G.R., Barfoot, R., Seal, S., Collins, N., Warren, W. and
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1.0%; Score 19.8; DB 1; Length 268;
Best Local Similarity 60.0%; Pred. No. 90;
Matches 33; Conservative 0; Mismatches 22; Indels C
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01-DEC-2000 WO 2000JP008501
06-DEC-1999 JP 99P 346193
DAISUKE KODA,HIDEKAZU HIROAKI,HIDEKI SUMIMOTO PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
/map="19p13.3"
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WO 0142453-A/3
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/number=8
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Homo sapiens (human)
Homo sapiens
7 of 8
Homo sapiens (human)
Homo sapiens
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 556)
Wade, C.M., Kulbokas, B.J. III, Kirby, A.W., Zody, M.C., Mullikin, J.C., Lander, E.S., Lindblad-Toh, K. and Daly, M.J.
The mosaic structure of variation in the laboratory mouse genome 22354684
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S212P6822PB7.T0 CZECHII/Ei Mus musculus STS genomic, sequence
Structural coordinate and NMR chemical shift of protein and utilization
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0
                                                                                        organism='Homo sapiens (human)'.
                                                                                                                                                                                                             Query Match 1.0%; Score 19.8; DB 1; Length 384; Best Local Similarity 77.4%; Pred. No. 93; Matches 24; Conservative 0; Mismatches 7; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                    1580 TAGGAATTTTTCTTTTTGGTTTTCTTGAA 1610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene encoding serine proteases
Patent: WO 03064641-A 56 07-AUG-2003;
Geneprot, Inc. (CH)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      178 ráddgaacarrrcrrrraadgrrrranggaa 148
                                                                                                                                                                                                                                                                                                                                                                                                              394 bp I Sequence 56 from Patent W003064641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="unassigned DNA"
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1. 394
/note="exon 14"
                                                                                                                      1. .384
/organism="Homo sapiens"
/mol type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .394
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                                                                   .336
                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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Matches 33; Conservative
                                  thereof
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AX814618/c
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mRNA linear MAM 27-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Original source text: Pig liver, cDNA to mRNA.
Draft entry and computer-readable sequence for [1] kindly provided
by G.Sarkar, 18-JUL-1989.
WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 12981/SvImJ, C3H/HeJ, and BALBA/CByJ. The WGS reads were placed uniquely on the MGSCv3 C57BL/6J assembly and SNP detection was carried out by SSAHA-SNP. 225,000 reads were
                                                                                                                        as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J and the train from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.

Location/Qualifiers
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Sarkar, G., Roeberl, D.D. and Sommer, S.S.
Direct sequencing of the activation peptide and the catalytic domain of the factor IX gene in six species
Genomics 6 (1), 133-143 (1990)
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1.0%; occ. ... 77;
Best Local Similarity 69.2%; Pred. No. 97;
Matches 27; Conservative 0; Mismatches 12; Indels
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/map="- 8 22-490 13020709-13020240"
/clone_lib="CZECHII/Ei"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pig factor IX mRNA, partial cds. M26235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
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factor IX.
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Sus scrofa
                                                                                                       annotated
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Contact: Kerstin Lindblad-Toh Whitehead Institute for Biomedical Research, Center for Genome

320 Charles Street, Cambridge, MA 02141, USA

Research

COMMENT

Tel: 617521477 Fax: 6172890903 Email: kersli@genome.wi.mit.edu Primer A: None

Primer B: None STS size: 556 Protocol:

dd δ 원

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Synthetic construct mutated mouse factor VII molecule immunoconjugate mRNA, complete cds.
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ALBLMSIEVPRLMTQDCLEHAKHSSNTPKITENMFCAGGWDGTKDACAGDSGGGPHATH
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Submitted (26-MAY-2000) Molecular Biophysics and Biochemistry, Yale
University, 266 Whitney Ave, New Haven, CT 06520, USA
Location/Qualifiers
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PKSCDKTHTCPPCPAPELLGGESVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
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YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK"
                                                                                                                                                                                                                                                                                                                                      synthetic construct artificial sequences.

1 (Dases 1 to 2078)

1 (Asses 2 to 2078)

1 (Asses 2 to 2078)

1 (Asses 2 to 2078)

2 (Asses 2 to 2078)

3 (Asses 2 to 2078)

4 (Asses 2 to 2078)

5 (Asses 2 to 2078)

6 (Asses 2 to 2078)

7 (Asses 2 to 2078)

8 (Asses 2 to 2078)

8 (Asses 2 to 2078)

8 (Asses 2 to 2078)

8 (Asses 2 to 2078)
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Hu, Z. and Garen, A.

Intratumoral injection of adenoviral vectors encoding tumor-targeted immunoconjugates for cancer immunotherapy Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9221-9225 (2000) 20381364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="mfVIIasm; contains active site mutation"
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1.0%; Score 19.8; DB 1; Length 2078;
Best Local Similarity 69.2%; Pred. No. 1e+02;
Matches 27; Conservative 0; Mismatches 12; Indels 0;
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/transI_table=11
/product="mutated mouse factor VII molecule
581 CTGCTGGAGTTTTTTTTTTTACAACAGGTATTCTCCA 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="synthetic construct"
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Hu, Z. and Garen, A.
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                                                                                                                   RESULT 99
AF272773/c
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      NIFLKFGSGYVSGWGRVFNRGRSATILQYLKVPLVDRATCLRSTKVTIYSNMFCAGFH
EGGKDSCLGDSGGPHVTEVEGTSFLTGIISWGEECAVKGKYGIYTKVSRYVWW"
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QDHLKSYVCFCLLDFEGRNCEKSKNEQLICANENGDCDQYCRDHVGTKRTCSCHEDYT
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LQPDENS CKRYCHER PECAR, PAYCHEN SERORI VGGOVYCPKGEC WQAALKINGLI.
CGAVILLDRAWI VITAAHCPUNI RYWGNI TVVWGEEHDF SEKDGDEGVRRYTTQVIVPDKYI
RGKINHDI DALLKIHRPWYTTDVYVPLOLDERSF SENTLARI RFSRVSGWGLLGGEGATAALELANS IBVRAWINGOCLEHAKHSSNIPKI TENMECAGYNDGTKGACKGDSGGHATH
YHGTWYLTGVVSWGEGCAAI GHIGVYTRVSQYIDWILVRHMDSKLQVGVFRLPLI."
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Mus musculus coagulation factor VII (fVII) mRNA, complete cds.
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2 Cascen, E.D. Iduscogie, E., Carmeliet, P., Collen, D. and Castellino, F.J.
Direct Submission
Submitted (105-787-1966) Elliot D. Rosen, Chemistry, Univ. of Notre Dame, Notre Dame, IN 46556, USA
Location/Qualifiers
                                                                                                                                                                                                      192 TCTTGATTTCTATCTTGGCTCATTTTTAACTCAGTAGTGAGTTGTTTGGTTTCCATAAGT 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1. (bases 1 to 1850)
                                                                                                                                                                                                                                                          156 TTTGGCGTTTTCTCCACCAACAATTCGAATAAAGTCGTCAGATTGGTTGCTTTCAGT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Characterization of a cDNA encoding murine coagulation factor VII Thromb. Haemost. 75 (3), 481-487 (1996)
                                                                                                                                                  0; Gaps
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Castellino, F.J.
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                                                                                        DB 1; Length 813;
                                                                                     Query Match 1.0%; Score 19.8; DB 1; Length 81 Best Local Similarity 49.5%; Pred. No. 99; Matches 51; Conservative 0; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                   252 TIGIAAGITITCIGITGITCIGITGITGITGITATCIAG 294
                                                                                                                                                                                                                                                                                                                                                                       96 GAGGCTATCCAAATTGGTTCAACTTCAGTAGAATTTTCATAG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1766 CIGCCTGAGATTCTCTCTTCTATCTCTTGTATTCTGTCA 1804
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/note="54 A nucleotides"
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1. .1850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          musculus (house mouse)
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Matches 27; Conserv
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coagulation factor IX; serine protease.
Homo sapiens (human)
Homo sapiens
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Nucleic acids encoding proteases
Patent: WO 03040333-A 37 15-MAY-2003;
Decode Genetics EHF. (IS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism≈"Homo sapiens"
/mol_type≈"unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                               609 bp I
Sequence 37 from Patent WO03040393.
AX763043
                                                                                                               1, .596
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/product="coagulation factor X"
/product="coagulation" = BANGAF7.1"
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ACLPEKDWABATLMTQKSGIVSGFGRTHEKGRQSHILKKLEVPYVDRNTCKLSTSFTI
TQNMFCAGYDAKPEDACQGDSGGPHVTRFKDTYFVTGIVSWGESCARKGKVGIYTKVT
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                                                                                                                                                                                                      Analysis of the partial nucleotide sequences and deduced primary structures of the protease domains of mammalian blood coagulation factors VII and \boldsymbol{X}
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rođentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (18-OCT-1993) Masahiro Murakawa, Harasanshin General
Hospital, Division of Hematology, 1-8 Taihaku-machi, Hakata-ku,
Fukuoka, Fukuoka 812, Japan (Tel:092-291-3434, Fax:092-291-3266)
Submitted (18-Oct-1993) to DDBU by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 AATATGATGGGGGTCTTCAGCCTGAGCACGCGATGTCGAAGTCGTAGGTCTCCCTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                    Mesocricetus.
1 (bases 1 to 484)
Murakawa,M., Okamura,T., Kamura,T., Kuroiwa,M., Harada,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xu, J., Lodes, M.J., Secrist, H., Benson, D.R., Meagher, M.J.,
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1.0%; Score 19.6; DB 1; Length 484;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 49; Conservative 0; Mismatches 49; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 AACTIGITOTOTITIAIGACCACGICCACCICAIGIT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'organism="Mesocricetus auratus"
                                                                                                                                                                                                                                                                         Haematol. 52 (3), 162-168 (1994)
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                  D21216.1 GI:415304
coagulation factor X.
Mesocricetus auratus (golden hamster)
Mesocricetus auratus
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/db_xref="taxon:10036"
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Harasanshin General Hospiral
1-8 Taihaku-machi, Hakata-ku
Fukuoka, Fukuoka 812
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Location/Qualifiers
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ACCESSION
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 873)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 GATGTAGCGGGAGAAGGTGATGGGTCTGCTGAGTTGGAGGAGTGCAATGTCGCCCTGG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       621 GAACTTGGGTGACATTGTGTTTTGGTGCATAGACATTAAGAATTGCAATGTCCTCTTGG 678
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Stolk, J.A., King, G.E., Wang, T. and Jiang, Y. Compounds for immunotherapy and diagnosis of colon cancer and methods for their use methods for their use Patent: WO 0.149716-A 931 12-JUL-2001; CORINA CORPORATION (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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1.0%; Score 19.6; DB 1; Length 596;
Best Local Similarity 58.6%; Pred. No. 1.1e+02;
Matches 34; Conservative 0; Mismatches 24; Indels C
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Human coagulation factor IX mRNA, partial cds.
M35672
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1.0%; Score 19.6; DB 1; Length 1142;
Best Local Similarity 58.6%; Pred. No. 1.1e+02;
Matches 34; Conservative 0; Mismatches 24; Indels 0;
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                                                                                                                       linear
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Darrow,A., Qi,J. and Andrade-Grodon,P.
Zymogen activation system
Patent: US 6420157-A 8 16-JUL-2002;
Location/Qualifiers
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Sequence 31 from Patent WO02055704.
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/db_xref="taxon:9606"
                                                                                                                       1142 bp
Sequence 8 from patent US, 6420157.
AR219285
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Best Local Similarity 58.68
Marches 34, Conservative
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                                                                                                                                                                                                                                                                                                                                                         Unclassified.
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                                                        RESULT 105
AR219285/c
                                                                                                                                                          DEFINITION
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                 source text: Human adult liver, cDNA to mRNA. Location/Qualifiers
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Best Local Similarity 58.6%; Pred. No. 1.18+02;
Matches 34; Conservative 0; Mismatches 24; Indels
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Curagen Corporation (US)
Location/Qualifiers
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Matches 37; Conserv
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AX675583/c
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El6187 17 bp DNA linear PAT 28-JUL-1999
Partial sequence of cDNA encoding G protein-coupled receptor.
El6187
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C12N15/09,A61K31/70,A61K31/70,A61K31/70,A61K31/70,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 177)
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PN UP 1988146192-A/11
PD 02-UTW-1998
PF 26-DEC-1996 UP 1996348328
PR 28-DEC-1995 UP 995 343371, 15-MAR-1996 UP 96P 59419, PP 12-AUG-1996 UP 96P 21865, 18-SEP-1996 UP 96P 246573 PI HINDWA KINIJI, HABATAKE YUUGO, KAWAMATA YUJI, HOSOYA MASAKI, PI
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                                  Query Match 1.0%; Score 19.4; DB 1; Length 177; Best Local Similarity 57.4%; Pred. No. 1.18+02; Matches 35; Conservative 0; Mismatches 26; Indels 0
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1.0%; Score 19.4; DB 1; Length 177;
Best Local Similarity 57.4%; Pred. No. 1.1e+02;
Matches 35; Conservative 0; Mismatches 26; Indels 0
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/mol_type="unassigned DNA"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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topology: Linear;
hypothetical: No;
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UP 1998146192-A/11
Homo sapiens (human)
Homo sapiens
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Hinuma, S., Habata, Y., Kawamata, Y., Hosoya, M., Pujii, R., Fukusumi, S.
and Kitada, C.
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Unclassified.
(Dases 1 to 177)
Hinuma, S., Hosoya, M., Fujii, R., Ohtaki, T., Fukusumi, S. and Ohgi, K.
G-procein coupled receptor procein and a DNA encoding the receptor
Patent: US 6114139-A 30 05-SEP-2000,
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                                                                                                                                                                                                                                                                                                                                                                621 GAACTTGGGTGACATTGTGTTTGGTGCATAGACATTAAGAATTGCAATGTCCTCTTGG 678
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1.0%; Score 19.4; DB 1; Length 177;
Best Local Similarity 57.4%; Pred. No. 1.1e+02;
Matches 35; Conservative 0; Mismatches 26; Indels 0; Gaps
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1.0%; Score 19.6; DB 1; Length 1169;
Best Local Similarity 58.6%; Pred. No. 1.1e+02;
Matches 34; Conservative 0; Mismatches 24; Indels 0;
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                                                                                              1 (bases 1 to 1169)
Darrow,A., Qi,J. and Andrade-Grodon,P.
Zymogen activation system
Patent: US 6420157.A 7 16-JUL-2002;
Location/Qualifiers
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Patent: US 6228984-A 25 08-MAY-2001;
Location/Qualifiers
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Sequence 30 from patent US 6114139.
AR109618
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/mol_type≈"unassigned DNA"
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/mol_type="genomic DNA"
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GI:23320254
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/organism="unknown"
/mol_type="mRNA"
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                                                      E27213 177 bp DNA linear PAT 18-JUN-2001 Novel physiologically active substance, process for producing the same and utilization thereof. E27213
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CIZNS/10,C12P21/02,G01N33/53,G01N33/577//C12P21/08,(C1ZN15/09,
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C12N15/09, A01K67/027, A61K38/00, A61K38/00, C07K14/47, C07K16/18,
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Shuji, M. RYO, F. Yuji, K. and Hirokazu, M. Utilization of peptide
Patent: JP 1999071300-A 11 16-MAR-1999;
TAKEDA CHEM IND LTD
ON Unidentified
BN JP 1999071300-A/11
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    .177
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JP 1999009286-A/4
19-JAN-1999
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E28271
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JP 1999071300-A/11.
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PD 16-MAR-1999

PF 22-UUN-1998 JP 1998175007

PR

PR

SHUJI HINUMA, RYO FUJII, YUJI KAWAMATA, HIROKAZU MATSUMOTO PC

A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, PC

A61K38/00,

PC A61K38/00,

PC A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61
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(C12P21/02, C12R1:91), A61K37/02, A61K37/02, A61K37/02, A61K37/02,
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Hinuma, S., Ito, Y. and Fujii, R.
G protein coupled receptor protein production, and use thereof
Patent: US 658810-A 30 25-MAR-2003;
Location/Qualifiers
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1.0%; Score 19.4; DB 1; Length 177;
Best Local Similarity 57.4%; Pred. No. 1.1e+02;
Matches 35; Conservative 0; Mismatches 26; Indels (
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Location/Qualifiers
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Sequence 310 from patent US 6114139.
AR109885
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AR300928
AR300928.1 GI:31688601
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AX839191/c
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Hinuma, S., Habata, Y., Kawamata, Y., Hosoya, M., Fujii, R., Fukusumi, S.
and Kitada, C.
Polypeptida, C.
Polypeptic their production and use
Patent: US 6228984-A 127 08-MAY-2001;
Location/Qualifiers
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4-coumarate coA ligase; 4cl gene.
6-colium multiflorum (Italian ryegrass)
Lolium multiflorum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Poeae; Lolium.
                                           1 (bases 1 to 204)
Hinuma, S., Hosoya, M., Fujii, R., Ohtaki, T., Fukusumi, S. and Ohgi, K.
G-protein coupled receptor protein and a DNA encoding the receptor
Patent: US 6114139-A 310 05-SEP-2000;
Location/Qualifiers
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Sequence 127 from patent US 6228984.
AR150703
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                                                                                                                                1. .204
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                                                                                                                                                                                                 1.0%;
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Best Local Similarity 57.4%
Matches 35; Conservative
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AJ586104
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AJ586104/c
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                                                                      2 (bases 1 to 249)
Bettany, A.U.E.
Direct Submission
Submitted (13-OCT-2003) Bettany A.J.E., Plant, Animal & Microbial
Science, Inst. Grassland & Environmental Research, Plas Gogerddan,
Aberystwyth, Ceredigion SY23 3EB, UNITED KINGDOM
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Variants of human kallikrein-2 and kallikrein-3 and uses thereof
Patent: WO 03076610-A 34 18-8EP-2003;
Exonhit Therapeutics S.A. (FR)
Location/Qualifiers
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Best Local Similarity 60.4%; Pred. No. 1.1e+02;
Matches 32; Conservative 0; Mismatches 21; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="activation of thioester substrates for phenylpropanoid synthesis"
cDNA and genomic clones of Festuca arundinacea and Lolium
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/organism≈"Lolium multiflorum"
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/mol_type="unassigned DNA"
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/BC_number="6.2.1.12"
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AX839191.1 GI:39922640
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                      multiflorum
Unpublished
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Best Local Similarity
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Query Match
Best Local Similarity 55.1$
Matches 38; Conservative
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KEYWORDS
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                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(Dases I to 352)
Schmidel, D.K., Tatro, A.V., Phelps, L.G., Tomczak, J.A. and Long, G.L. Organization of the human protein S genes
Biochemistry 29 (34), 7845-7852 (1990)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Variants of human kallikrein-2 and kallikrein-3 and uses thereof
Patent: WO 03076610-A 23 18-SEP-2003;
Exonhit Therapeutics S.A. (FR)
Location/Qualifiers
                                                                                                                 S protein; anticoagulant cofactor; vitamin K-dependent protein.
2 of 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.0%; Score 19.4; DB 1; Length 352; Best Local Similarity 55.1%; Pred. No. 1.2e+02; Matches 38; Conservative 0; Mismatches 31; Indels
                                                                  linear
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                                                             HUMPS02
Human S protein-alpha (PS-alpha) gene, exon 2.
MS7841 J02917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="PS-alpha"
order(MS7840.1:913. .1014,1. .134)
/gene="PROS1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="liver"
join(M57840.1:837. .912,135. .181)
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                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/note="G00-120-721"
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                                                                                                             GI:190535
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                                                                                                                                                                                                                                                  111 TCTCTCTCTCTCTCTCTAACACTTCTGGGCCAGGGTAGGGGCACTACCGCATTCCCTC 170
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 471)
                                                                                                                                                                                                                                                                                                                                                           111 TCTCGCACTCCCAGCCTCCCACAATCCGAGACAGGATGAGGGGTGCAGCACCAATCCACG 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dog gene for protein C (precursor of vitamin K-dependent serine protease), partial cds (catalytic region).
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protein C; serine protease zymogen; vitamin K-dependent serine protease; blood cogqulation-related.
Canis familiaris (dog)
Canis familiaris
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Best Local Similarity 55.1%; Pred. No. 1.2e+02;
Matches 38; Conservative 0; Mismatches 31; Indels 0; Gaps
                                                                                                                            0; Gaps
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1.0%; Score 19.4; DB 1; Length 394; 55.1%; Pred. No. 1.2e+02; tive 0; Mismatches 31; Indels
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/function="regulation of blood coagulation"
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/product="protein C"
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Matches 32; Conserv
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

I (bases 1 to 829)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schefer (C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Gunaratne, P.H., Richards, S.W.,
Villadon, D.K., Muzny, D.M., Sodergren, E.J., Hulyk, S.W.,
Villadon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
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Mus musculus trypsin 4, mRNA (cDNA clone MGC:74265 IMAGE:30306436),
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                                                                                                                                                                                                                                                                                                                                                           Original source text: Sheep liver, cDNA to mRNA.

Draft entry and computer-readable sequence for [1] kindly provided by G.Sarkar, 18-JUL-1989.

Location/Qualifiers
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                                                                                                                                              Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea
Bovidae, Caprinae, Ovis.
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                                                                                                                                                                                           Sarkar, G. Koeberl, D.D. and Sommer, S.S.
Direct sequencing of the activation peptide and the catalytic domain of the factor IX gene in six species
Genomics 6 (1), 133-143 (1990)
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BC061135.1 GI:38511692
                       GI:165878
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Best Local Similarity 55.1
Matches 38; Conservative
                                                                 Ovis aries (sheep)
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LDAPPLLPQADCEASYPGKTNNMIVYGFLEGGKDSCGQEDSGGPVVCNGQLQGIVSWGY Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 53 Row: o Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6755892. Location/Qualifiers CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Neb site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, ö Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Submitted (03-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, 83. 739 /note="Tryp SPC; Region: Trypsin-like serine protease" /db\_xref="CDD:cd00190" Gaps 1587 ITTTTCTTTTTGGTTTTCTTGAAAIATTTTCCCTGCTTTTGACCTGCCTTC 817 tritritritritritritceaeggaaritcactritaricacaraargactric Length 829; Indels NIH-MGC Project URL: http://mgc.nci.nih.gov /mol\_type="mRNA" /db\_xref="taxon:10090" /clone="MGC:74265 IMAGE:30306436" 1.0%; Score 19.4; DB 1; 0.4%; Pred. No. 1.3e+02; 'note="synonyms: 0910001B19Rik, GCALKDNPGVYTKVCNYVDWIONTIAAN" /tissue type="Liver, mouse" /clone lib="NIH MGC 177" /lab\_host="DH10B" /note="Vector: pDNR-LIB" 0; Mismatches /db\_xref="LocusID:22074"
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PAT 08-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             496 AGCATTICTCTGTTTCGTTTTTTTTGAGATGACCTAACTGTTGGAGAAAAATGGGGT 552
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Thorpe, P.E. and Edgington, T.S.
Methods and compositions for the specific coagulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1126;
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                                                                                                                                                                                                                                                               Unclassified.
1 (bases 1 to 1126)
Thorpe, P.E. and Edgington, T.S.
Methods for the specific coagulation of vasculature Patent: US 6004555-A 27 21-DEC-1999;
                                              linear
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1.0%; Score 19.4; DB 1;
Best Local Similarity 47.9%; Pred. No. 1.3e+02;
Matches 56; Conservative 0; Mismatches 61;
                                              DNA
                                AR095306 1126 bp C Sequence 27 from patent US 6004555. AR095306 AR095306.1 GI:10023064
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Patent: US 6093399-A 27 25-JUL-2000;
Location/Qualifiers
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ARI03990
ARI03990.1 GI:12816698
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PRI 08-NOV-1994

linear

mRNA

1126 bp

HUMFX Human factor X mRNA. K01886 K01886.1 GI:182820

DEFINITION ACCESSION VERSION

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Original source text: Human liver, cDNA to mRNA, clone lambda-X-1137.
In processing, factor X (Stuart factor) is converted to Xa by cleavage of a glycopeptide from the amino-terminal end of the heavy chain. It then acts as a serine protease in converting prothrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/protein_id="AAA52486.1"
/brotein_id="182821"
/db_xref="GDB.GOO-119-890"
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DNGKACIPTGPYPCGKQTLERRKRSYAQATSSSEAPBDSTTWKPYDAADDPTENPFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLDFNQTQPERGDNNLTRIVGGQECKDĞECPWQALLINEENEGFCGGTILSEFYILTA
ANAYAPACLIPER ANAYAREGDRNTEQEEGGEA'VHEVENVIKHNRFTKETYDFDIAVLRIKTPITFR
MNVAPACLIPERDWAESTLMYQYIGIVSGFGRTHEKCRQSTRLKMLEVPYVDRNSCKLS
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YTKVTAFLKWIDRSMKTRGLPKAKSHAPEVITSSPLK"
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                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 1126)
Leytus, S.P., Chung, D.W., Kisiel, W., Kurachi, K. and Davie, E.W. Characterization of a cDNA coding for human factor X Proc. Natl. Acad. Sci. U.S.A. 81 (12), 3699-3702 (1984)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide"
    Stuart factor, factor X; serine protease.
Homo sapiens (human)
Homo sapiens
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47.9%; Pred. No. 1.3e+02;
tive 0; Mismatches 61;
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Sequence 15 from Patent W09747737.
A93124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/map="13q34"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product="factor X mRNA"
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1. .1126
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/gene="F10"
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Best Local Similarity
Matches 56; Conserv
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                                 SOURCE
ORGANISM
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COMMENT
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A93124/c
LOCUS
DEFINITION
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KEYWORDS
SOURCE
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KEYWORDS
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CREFFRKLOSLDNGDCDQFCHERGONSVCSCARGEYTLADNGKACIPTGDPSPPGGKQTLE
RKRSVAQATSSSGEAPDST TWREYDAADLDPTSPPEDLLDFNQTOFERGDNUTTRIV
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GGAATHEVBVVIKHNRFTKETYDFDIANDLAKPTPFRAMAAGACLEFBRAAESTLMT
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ACQGDSGGPHVTRFKDTYFVTGIVSWGEGCARKGYGIYTKVTAFLKHIDRSMKTRGL
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Location/Qualifiers
                                                                                                                                                                                                                                                                       Query Match 1.0%; Score 19.4; DB 1; Length 1404; Best Local Similarity 47.9%; Pred. No. 1.3e+02; Matches 56; Conservative 0; Mismatches 61; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMCFX 11near 1
Human blood-coagulation factor X mRNA, complete cds.
unidentified
unclassified.
1 (Dassa 1 to 1404)
Kopetzki, E. and Hopfner, K.
RECOMBINANT BLOOD-COAGULATION PROTEASES
PATENT: WO 9747737-A 15 18-DEC-1997;
KOPETZKI ERHARD (DE); BOEHRINGER MANNHEIM GMBH (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="coagulation factor X precursor'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 41 (2-3), 311-314 (1986)
86221713
                                                                                                                                               Location/Qualifiers
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<1. .66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coagulation factor X.
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="F10"
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    ORGANISM
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                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Characterization of a cDNA encoding murine coagulation factor VII Thromb. Haemost. 75 (3), 481-487 (1996) 96276538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                       Ouery Match
1.0%; Score 19.4; DB 1; Length 1414;
Best Local Similarity 47.9%; Pred. No. 1.3e+02;
Matches 56; Conservative 0; Mismatches 61; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MMU44795 1850 bp mRNA linear ROD 23-MAY
Mus musculus coagulation factor VII (fVII) mRNA, complete cds.
U44795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1448 HGCATGTGGTGCCTGTGTGTGTTGCTGTTGCTCATTGTTGCTTC 1500
                                                                                                                                                                                                     /product="coagulation factor X activation peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Levine, Z., David, A., Azar, I., Khosravi, R. and Bernstein, J. Variants of alternative splicing Patent: WO 0136632-A 59 25-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.0%; Score 19.4; DB 1; Length 1551;
Best Local Similarity 60.4%; Pred. No. 1.3e+02;
Matches 32; Conservative 0; Mismatches 21; Indels 0;
                                                                              /product="coagulation factor X light chain"
                                                                                                                                  /product="coagulation factor X heavy chain" 493. .648
                    'note="coagulation factor X signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AX147505 1551 bp Sequence 59 from Patent WO0136632.
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Location/Qualifiers
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'gene="F10"
                                        .483
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Schaefer, C.F., Bhat, N.K.,
Habtschul, S.F., Zeeberg, B., Morec, T., Max, S.I., Wang, J., Hsneh, R.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsneh, R.,
Diatchenko, L., Martsina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldó, M.F., Casavant, T.L.,
Scheetz, T.B. Brownstein, M.J., Uddin, T.B., Toshiyuki, S.,
Carninci, P., Parage, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosk, S.A., McEwan, P.M.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, E.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Yourghan, R.D.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
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Mus musculus coagulation factor VII, mRNA (cDNA clone MGC:74281

MAGB:30305571), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="coagulation factor VII"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGAVLLDARMIVTAAHCFDNIRYMGNITVVMGEHDFSEKDGDEGVRRVTQVIMPDKXI
RGKTNHDIALLRHRPVTFTDVVVPLCLPEKSEFSBNTLARIRFSRVSGWGLLDRGAT
ALEMSIEVPRLMYDDCLEHAKHSSNYPKITENMFCAGYMDGTKDACKGDSGCPHATH
YHGYWYLGVVSMGEGCARIGHGVYTRVSQYIDMIVRHDDSKLGVGVFLPLL"
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                          2 (bases 1 to 1850)
Rosen,E.D., Idusogie,E., Carmeliet,P., Collen,D. and
Castellino,F.J.
Direct Submission
Submitted (05-JAN-1996) Elliot D. Rosen, Chemistry, Univ. of Notre
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 1869)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.0%; Score 19.4; DB 1; Length 1850; Best Local Similarity 60.4%; Pred. No. 1.3e+02; Matches 32; Conservative 0; Mismatches 21; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coagulation; serine protease"/codon start=1
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                                                                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                  Dame, Notre Dame, IN 46556, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                           Ltype="mRNA"
xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="liver"
1. .1850
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BC061149
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DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
Contect: (Dickson, Mark) med@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 53 Row: n Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6753805. Location/Qualifiers
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Submitted (03-NOV-2003) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Michael Brownstein / Ted Usdin
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/db xref="CDD:smart00069"
268. 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement; Dr. Michael Brownstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="MGC:74281 IMAGE:30305571"
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/clone_lib="NIH_MGC_177"
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/mol_type="mRNA"
/db_xref="taxon:10090"
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Genomics 11 (4), 828-834 (1991)
92147126
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protein C; blood coagulation-related; serine protease zymogen;
vitamin K-dependent serine protease.
Capra hircus (goat)
Capra hircus
Capra hircus
Capra hircus
Capra hircus
Capra hircus
Capra hircus
Capra hircus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bovidae; Caprinae; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
1 (bases 1 to 471)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Goat gene for protein C (precursor of vitamin k-dependent serine protease), partial cds (catalytic region).
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Kremling, H., Keime, S., Wilhelm, K., Adham, I.M., Hameister, H. and
/db_xref="CDD:cd00054"
589: .1302
/hote="TYOED: Region: Trypsin-like serine protease"
/db_xref="CDD:cd00190"
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                                                                                                                                                           1.0%; Score 19.4; DB 1; Length 1869; 60.4%; Pred. No. 1.3e+02; Live 0; Mismatches 21; Indels 0
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order(M96426.1:1170. .1291,1. .62)
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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Mosera Masser
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/gene="acrosin"
/number=2
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1732 GACCAAGGIATCCATTTCTTTCTTGTCTTCACTGCCTGAGATTCTCTCTTCTATCTC 1791
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         A comparative study of partial primary structures of the catalytic Br. J. Haematol. 86 (3), 590-600 (1994)
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Mus musculus
Mus musculus
Mus musculus
Mus musculus
Musipura, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 596)
Musu,J., Liao,G., Cheng,J., Nguyen,A., Bach,C., Puech,A.,
McPherson,J.D., Foernzler,D. and Peltz,G.
Mus musculus SNPs
Unpublished (2003)
                                                                                                                                                                                                                 Murakawa, M.
Direct Submission
Direct Submission
Submitted (06-D94) Masahiro Murakawa, Harasanshin General
Hospital, Division of Hematology, 1-8 Taihaku-machi, Hakata-ku,
Fukuoka, Fukuoka 812, Japan (Tel:092-291-3434, Pax:092-291-3266)
Location/Qualifiers
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1.0%; Score 19.2; DB 1; Length 471;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 48; Conservative 0; Mismatches 48; Indels 0; Gaps
Murakawa, M., Okamura, T., Kamura, T., Kuroiwa, M., Harada, M. and
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Roche Palo Alto
3431 Hillview Ave, Mailstop S3-1, Palo Alto, CA 94024, USA
THEL 650855807
Email: Jonathan Usuka@roche.com
Primer A: No primer submitted
Primer B: No primer submitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        function="regulation of blood coagulation"
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                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Capra hircus"
/mol_type="genomic DNA"
/db_xref="taxon:9925"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="catalytic region"
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/db_xref="taxon:10090"
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/product="protein C"
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/db_xref="taxon:9031"
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/map="18-10064-9474-AC126686.3.1.232817"
/clone lib="Roche Palo Alto"
/note="SNPs developed from assay sequences derived from 15
different strains-of mice (as of October 1, 2003). Those
strains include A/J, A/HeJ.-129/Sv, AKR/J, B10.D2-H2/oSnJ,
BALB/CBYJ, BALB/CJ, C3H/HeJ, C57BL/GJ, CAST/El, DBA/2J,
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Partial characterization of vertebrate prothrombin cDNAs:
amplification and sequence analysis of the B chain of thrombin from
nine different species
Proc. Natl. Acad. Sci. U.S.A. 89 (7), 2779-2783 (1992)
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RSRYPBRWBEISTLEKII ITHOSTWARSRILDBICALMKLKEWAFSDYTHPVCLEPKQI
VTSLLQAGHKGRYTWGWSILKEWYTWNWBYQPSVLQWYNLPLVRBPICKASTGIRVTD
NMFCAGYKPEBGKRGDACEGDSGGPFVMKNPYNNRWYQMGIVSWGEGCDRDGKYGFYT
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Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
1 (bases 1 to 826)
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                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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49.5%; Pred. No. 1.40+02;
tive 0; Mismatches 49; Indels 0
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Oryccolagus cuniculus thrombin mRNA, 3' end.
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/mol_type="mRNA"
/db_xref="taxon:9986"
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/product="thrombin"
/protein_id="AAA31477.1"
/db_xref="GI:165741"
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Oryctolagus cuniculus
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/dev stage="adult"
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/gene="thrombin"
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Eelkpgsverecnbercnfeeaseifetkeatlefwskyvdgdqcaqkpcsngackdn
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DHNMCTPVVEFPCGRVKMDYTEGKAEFNIRLIGGNSGGRGFSPWRVMLQNLKGKFLCG
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NDAMJALBEPWYNIKXALPICLPFROLEHELTTKGRQMLVTGWGSTSDEMRNYSAL
ISYIEIPIVERNEGQYMTWISDINLLCAGSLGDRKDSCSGSGSGGPMATKYKDTWFLV
GLVSWGEGGGKKEKFGVYTKVSQYLEWIQHINKKSGSWRG"
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I (bases 1 to 1302)
Davidson, C. J., Hirt, R. P., Lal, K., Snell, P., Elgar, G.,
Tuddenham, E.G.D. and McVey, J.H.
Comparative sequence analyais and molecular evolution of blood Coagulation genes from Gallus gallus and Fugu rubripes
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/function="inactivates factors Va and VIIIa in the
presence of Ca++ ions and phospholipids"
/note="vitamin K dependent serine protease;
autoprochrombin IIa; coaquilation factor XIV; contains 2
BGF-like domains; member of peptidase family Si/trypsin
family; synthesized in the liver and found in plasma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (04-JAN-2002) Haemostasis Group, MRC Clinical Sciences Centre, The Faculty of Medicine, Imperial College, Hammersmith Campus, Du Cane Road, London W12 ONN, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                Gallus gallus anticoagulant protein C precursor (PROC) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McVey, J.H., Davidson, C.J., Lal, K., Snell, P. and Elgar, G. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.0%; Score 19.2; DB 1; Length 1302; 56.2%; Pred. No. 1.46+02; tive 0; Mismatches 28; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/prodouts="anticoagulant protein C precursor"
/protein id="AAO33465.1"
/db_xref="GI:28194012"
    linear
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/ DOCUMENT 164 = 74A3 06 85 . 1"

// DOCUMENT 164 87 . 1"

// EXACT 1654 87 . 1"

// LATING 18 . 1 . 1654 87 . 1"

// LATING 18 . 1 . 1654 87 . 1"

LATING 18 . 1 . 1654 87 . 1"

ELRPGNUER 26 CEBCE EREARE I FQNTED TWAFWSKY SDGDCCEDR PSGS PCDL PCC

GRACK 10 LGGGGRECO FCLEHEVRE ROWS ARMOND CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT CRAPT 
                                                                                  MAM 27-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Original source text: Bovine liver, cDNA to mRNA, clones pBC-2 and pBC-7.
The sequence reported in [1] included homopolymeric tails on the 5' and 3' ends (not shown here).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1732 GACCAAGGTATCCATTTCTTCTATCTTGTCTTCACTGCCTGAGATTCTCTTCTATCTC 1791
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                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Cetartiodactyla, Ruminantia; Pecora, Bovoidea, Bovidae; Bovinae; Bos (Los 100) (Lases 1 to 1373) (Lases 1 to 1373) (Long, C.L., Belagaje, R.M. and MacGillivray, R.T. Cloning and sequencing of liver cDNA coding for bovine protein C Proc. Natl. Acad. Sci. U.S.A. 81 (18), 5653-5656 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1619 bp mRNA linear MAM 08-FEB-2.
U77477 S56300
U77477.1 GI:1698964
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50.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 48; Indels
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                                                                                  linear
                                                                                                                                                                                      K02415.1 GI:163486
autoprothrombin IIA; protein C; serine protease.
Bos taurus (cow)
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/product="protein C light chain"
588. .1367
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/note="protein C signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="protein C prepropeptide"
                                                                                  mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
                                                                              1373 bp
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                                                                                                            Bovine protein C mRNA.
K02435
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Best Local Similarity 50.0%
Matches 48; Conservative
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                                                                              BOVPBC
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                                                                              LOCUS
DEFINITION
ACCESSION
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OCU77477/c
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RESULT 136
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PUBMED
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KEYWORDS
                                       BOVPBC/c
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Oryctolagus cuniculus (rabbit) Oryctolagus cuniculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

ORGANISM

ACCESSION

VERSION KEYWORDS

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/ LTAINS 14 LIONE - 1. 1999.99.1

/ LTAINS 14 LIONE - 1. 1999.99.1

PELREGELERECKEELCSFERREVPOSTERTKOFWITTYNDSDOCKSNPCONGGSCED

OLOSY ICFOLDFRENCESKNWDOLL CWYENGGEGEOCYCSDHVGSORSCRCHEGYTLL

PNGVSCTPTYDZYPCGKYPALERKRGASNPOGRIVGEKCOPKGECPWOAALMNGSTLLCG

GSILDTHWVVSAAHCFDKISSIRNITIVLGEHDLSEHEGDEOVRHVAQLINPDKYVPG

STENDIALLOPALALNINVYPLCLEBRRPSESTIATINFSSRVSGWGGLIYRGALAR

ELMAIDVPRIMTOGVVEGSEBKRGSSPVTGMNFCAGYLDGSKGDSGGFHATSYH

GTWYLTGVVSWGEGCAAVGHVGVYTRVSRYTEWLSRLMRSKLHHGIQRHFFP"
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Bukaryotes, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryotes, Metazoa; Chordata; Catarthini; Hominidae; Homo.
1 (bases 1 to 244)
Litt, M., Carrero-Valenzuela, R., LaMorticella, D.M., Schultz, D.W.,
Mitchell, T.N., Kramer, P. and Maumenee, I.H.
Autosomal dominant certlean cataract is associated with a chain termination mutation in the human beta crystallin gene CRYBB2
Upublished (1996)
2 (bases 1 to 244)
Litt, M., Carrero-Valenzuela, R. and LaMorticella, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (25-SEP-1996) Molecular and Medical Genetics, Oregon
Health Sciences University, 3181 SW Sam Jackson Pk. Rd., Portland,
                                                                                                                                                                                                       Losses 1 to 1619)

Buiz, S.R., Blajdchman, M.A. and Clarke, B.J.

Buiz, S.R., Blajdchman, M.A. and Clarke, B.J.

Buizect Submission
Submitted (05-NOV-1996) Pathology, McMaster University, 1200 Main
St. West, Hamilton, ONT L8N 325, Canada
On Feb B, 2002 this sequence version replaced gi:266294.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
1 (bases 1 to 1619)
Brothers, A.B., Clarke, B.J., Sheffield, W.P. and Blajchman, M.A. Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
Thromb. Res. 69 (2), 231-238 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.0%; Score 19.2; DB 1; Length 1619;
ilarity 67.5%; Pred. No. 1.44+0.4;
Conservative 0; Mismatches 13; Indels 0;
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Human beta B2 crystallin (CRYBB2) gene, exon 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="coagulation factor VII"
/protein_id="AAB37326.1"
/db_xref="G1:1698965"
                                                                                                                                                                                                                                                                                                                                                                                     1 .1619
Coganism="Oryctolagus cuniculus"
/mol type="mRNA"
/db_xref="taxon:9986"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue type="liver"
22. .1356
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HSCRYBB2S3
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                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                          AUTHORS
TITLE
                                                                                                                            JOURNAL
MEDLINE
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AUTHORS
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VERSION
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                              REFERENCE
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DMUSB868
352 bp mRNA linear VRT 16-MAY-1997
Dissostichus mawsoni antifreeze glycopeptide precursor (DM-AFGP)
mRNA, partial cds, 3' region.
US8868
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterrygii; Percomorpha; Perciformes; Notothenioidei; Nototheniidae; Dissostichus.

1 (bases 1 to 352)
Chen,Lu., DeVries,A.L. and Cheng,C.H.
Evolution of antifreeze glycoprotein gene from a trypsinogen gene in Antarctic notothenioid fish
Proc. Natl. Acad. Sci. U.S.A. 94 (8), 3811-3816 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1884 TAATTCTATTTCCACTTTCAGGTCCTGAAATGTTTTACTCATTTTCCTCCCAGTATTTAC 1943
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                                        249 rahaganariaccaciriarritoricacricoccacigericacaccecerderina 308
                                                                        156 daraccerddagrinacacagaagringrincracagaaargaarianigarcacerga 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (21-MAY-1996) Liangbiao Chen, Molecular and Integrative Physiology, diversity of Illinois, 524 Burrill Hall, 407 S. Goodwin Ave, Urbana, IL 61801, USA Location/Qualifiers
  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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/product="antifreeze glycopeptide precursor"
/protein_id="AAB730.1"
/bxref="G1:1399809"
/trānslation="AATPAINFVATPATAATAATAATAARG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.9%; Score 18.8; DB 1; Length 352; Best Local Similarity 52.6%; Pred. No. 1.7e+02; Matches 41; Conservative 0; Mismatches 37; Indels C
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    0; Mismatches 37; Indels
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/function="inhibits ice crystal growth"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Dissostichus mawsoni"
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Seguence 931 from Patent WO0149716.
AX193364
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Chen, L., DeVries, A. and Cheng, C.
Direct Submission
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/db_xref="taxon:36200"
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                                                                                                                  524 GATGACCTAACTGTTGGA 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="DM-AFGP"
                                                                                                                                                        96 GACAAGCTTCCTGTTTGA 79
                                                                                                                                                                                                                                                                                                                              U58868.1 GI:1399808
                                                                                                                                                                                                                                                                                                                                                                      Dissostichus mawsoni
Dissostichus mawsoni
    41; Conservative
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SOURCE
ORGANISM
    Matches
                                                                                                                                                                                                                                                                       DEFINITION
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DMU58868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    464 GGTCCACTTGGTTTATGACATCAGTTAGCTCCAGCATTTCTCTGTTTTTTGTTGA 523

156 GATACCCTGGAGTTTACACAGAAGTTAGTTTCTACAAGAAATGGATTATTGATCACCTGA 97
                                                                                                                                                                                                                                                        0;
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llarity 52.6%; Pred, No. 1.7e+02;
Conservative 0; Mismatches 37; Indels (
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                                                                                                                                                                                                                Length 244;
                                                                                                                                                                                                              0.9%; Score 19; DB 1; Length 244
65.1%; Pred. No. 1.4e+02;
tive 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                          152 GGCACTACCGCATTCCCTCTTCCAAACACTTCTATTTCT 194
                                                                                                                                                                                                                                                                                                                 193 GCCATCACCCTACTCCCTCTCTGCCCATCATCTTTCT 235
/map="22q11-22q12.1"
/clone="YAC clone M686F7 from CEPH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protease homologs
Patent: US 6331427-A 28 18-DEC-2001;
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Robison, K.B.
Pactease homologs
Patent: US 6331427-A 29 18-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28 from patent US 6331427. AR263850
                                                                                                                                                  complement (223. .244)
/note="reverse PCR primer"
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Sequence 29 from patent US 6331427.
AR263851
                                                                        'note="forward PCR primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
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    .340
    /organism="unknown"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     524 GATGACCTAACTGTTGGA 541
                                                                                                              /gene="CRYBB2"
                                                         /gene="CRYBB2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AR263850.1 GI:28075854
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Robison, K.E.
                                                                                                                                     /number=4
                                                                                                                                                                                                                                                    28; Conservative
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Best Local Similarity
Matches 41; Conserva
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AR263850/c
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Padigaru, M., Li, L., Zerhusen, B.D., Casman, S.J., Shenoy, S., Spytek, K.A., Zhong, M., Gangolli, E.A., Burgess, C.E., Patturajan, M., Vernet, C.A., Taylor, S., Tchernev, V.T., Miler, C.E., Guo, X., Boldog, F.L., Grosse, W.M., Alsobrook, J.P., Gelach, V., Edingermark, S., Rothenberg, M.E., Ellerman, K., Macdougall, J., Malyankar, U., Millet, I., Peyman, J., Smithson, G., Gunther, E. and
                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                 Proteins, polynucleotides encoding them and methods of using the
                                                                                                                                                                                                                                                                                                                     Patent: WO 02055704-A 31 18-JUL-2002;
Curagen Corporation (US)
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                          Stone, D.J.
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ACCESSION
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AX523898/c
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                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                       Xu,J., Iodes,M.J., Secrist,H., Benson,D.R., Meagher,M.J., Stolk,J.A., King,G.E., Wang,T. and Jiang,Y. Compounds for immunotherapy and diagnosis of colon cancer and methods for their use Patent: WO 01491i6-A 931 12-JUL-2001; CORIXA CORPORATION (US)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 GGCGTCCATGTGTGTGCTGCTCTCTCTGTGTCTGAGCAGTGGGTGCTGTCAGCT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 GGTTTCCATAAGTTTGTAAGTTTTCTGTTGTTTCTGTTGTTGTTGTTGTTATCT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 GGCGTCCATGTGTGTGGTGGCTCTCTCGTGTCTGAGCAGTGGGTGCTGTCAGCT 323
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0.9%; Score 18.8; DB 1; Length 882;
Best Local Similarity 59.3%; Pred. No. 1.8e+02;
Matches 32; Conservative 0; Mismatches 22; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       0.9%; Score 18.8; DB 1; Length 596; 59.3%; Pred. No. 1.7e+02; Live 0; Mismatches 22; Indels (
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Sequence 33 from Patent WO02055704..
AX675583
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/db_xref="taxon:9606"
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Location/Qualifiers
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    AX193364.1 GI:15211315
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Homo sapiens
                                                 Homo sapiens (human)
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                                                                          Homo sapiens
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Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
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                                                                                                                                                                                                                                                                                    403 GGCGFCCAFGTGTGTGTGGCTCTCTCGTGTCTGAGCAGTGGGTGCTGTCAGCT 456
                                                                                                                                                                                                                              239 GGTTTCCATAAGTTTGTAAGTTTTCTGTTGTTGTTGTTGTTGTTATCT
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                                                                                                             Query Match

0.9%; Score 18.8; DB 1; Length 1161;
Best Local Similarity 59.3%; Pred. No. 1.88+02;
Matches 32; Conservative 0; Mismatches 22; Indels 0;
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Patent: WO 02064799-A 105 22-AUG-2002;
TRANSKARYOTT THERAPIES, INC. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 105 from Patent WO02064799,
AX523898
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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150 ATCAGGATAACCAGCACAAATCATATTTGGGTAATTATTAGTCCTTCATTTCCATATAT 91
                                                                                                                                                                                                                                                                                                                                                                                                            Plea serine protease nucleic acid molecules
Patent: US 5972645-A 28 26-OCT-1999;
Location/Qualifiers
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Sequence 28 from patent US 6077687.
AR098999
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Sequence 28 from patent US 5972645.
AR081819
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/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                    Submitted (14-JUN-2001) Cellular and Structural Biology, University of Texas Health Science Center at San Antonio, 7703 Floyd Curl Drive, San Antonio, TX 78229, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /trānslation="MSLILVFSILMSLHYCHSAAVFVHRDEAHEVLIRSKRANSGWFE
ELKTGWLERCEDEKCSYEEAREVFEHTBATNERKIYDVKOHCASSPCENDGLCTYQ
NALDSYMCLLAPGRSGRHUEDGAIADHOUDSCHENGTGEFOTTBORRNGSCADGYYLD
NSGQKCRSHEVFFOGKVPLLQAGAGAADHQVDLASRIYGGSECFKGHCPWQVLLKYGEK
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VSETABLDLALLFIYTYYAYAVYVOLLPERABRELBMAYKHTVSGWGKRSEDGP
TSRLLRRLLVPRITTGECVQVSNLTLISNMFCAGYIEGRQDSCKGDSGGELVTRYRDT
AFLLGIVSWGKGCARPGSYGIYTRVSNYLQWIRQTTNTIH"
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Cypriniformes; Cyprinidae; Danio.
(Dases 1 to 1671)
Sheehan, J., Templer, M., Gregory, M., Hanumanthaiah, R., Troyer, D., Phan, T., Thankavel, B. and Jagadeeswaran, P.
Demonstration of the extrinsic coagulation pathway in teleostei: identification of zebrafish coagulation factor VII
Proc. Natl. Acad. Sci. U.S.A. 98 (15), 8768-8773 (2001)
                                                                                                                                                                            2 (bases 1 to 1671)
Sheehan, J., Templer, M., Gregory, M., Hanumanthaiah, R., Troyer, D.,
Phan, T., Thankavel, B. and Jagadeeswaran, P.
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Grieve, R.B., Rushlow, K.B., Hunter, S.Wu., Frank, G.R. and
Stiegler, G.L.
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Best Local Similarity 47.8%; Pred. No. 1.8e+02;
Matches 54; Conservative 0; Mismatches 59; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="coagulation factor VII"
/protein_id="AAK74192.1"
/db_xref="GI:15020318"
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Patent: US 5962257-A 28 05-0CT-1999;
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Sequence 28 from patent US 5962257.
AR077689
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/db_xref="taxon:7955"
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Direct Submission
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1552 ACCTTGATAGGCATCTTTCTCAAGGTTAGGAAATTTTTCTTTTT

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Grieve, R.B., Rushlow, K.E., Hunter, S.Wu., Frank, G.R., Stiegler, G.L. and Gaines, P.U.
Flea aminopeptidase nucleic acid molecules and uses thereof
Patent: US 6077687-A 28 20-JUN-2000;
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47.8%; Pred. No. 1.8e+02;
tive 0; Mismatches 59; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
1612 ATAITITICCTIGCTTTIGACCIGCCTICTTCCCCTICCTCTATICCTTIGGIT 1664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unclassified.
1 (bases 1 to 168)
Grieve, R.B. Rushlow, K.E., Hunter, S.Wu., Frank, G.R. and
Stiegler, G.L.
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AR141647.1 GI:15101163
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AR151537/c
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                                                                                                                                                 Unclassified.

1 (bases 1 to 168)
Strieger, G. L. Rushlow, K.E., Hunter, S.W., Frank, G.R. and Strieger, G.L.
Methods of eliciting an antibody response using flea protease proteins and homologe thereof Patent: Use 5138840-A. 28 31-00T-2000;
Location/Qualifiers
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1 (bases 1 to 168)
Grieve, R.B., Rushlow, K.E., Hunter, S.Wu., Frank, G.R. and Stiegler, G.L.
Stiegler, G.L.
Flea leucine aminopeptidase proteins and uses thereof Patent: US 6180383-A 28 30-JAN-2001;
Location/Qualifiers
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                                              linear
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Best Local Similarity 47.8%; Pred. No. 1.8e+02;
Matches 54; Conservative 0; Mismatches 59
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AR127061
AR127061.1 GI:14113654
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Sequence 28 from patent US 6146870.
AR141647
                                       Sequence 28 from patent US 6139840.
AR116830
                                                                                                                                                                                                                                                                                       /organism="unknown"
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/organism="unknown"
                                                                                         AR116830.1 GI:14097736
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Best Local Similarity 47.8
Matches 54; Conservative
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AR141647/C
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AR116830/c
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(bases I to 168)
Grieve, R.B., Rushlow, K.E., Hunter, S.Wu., Frank, G.R., Stiegler, G.L., Gaines, P.J. and Silver, G.
Flea serine protesse nucleic acid molecules and uses thereof Patent: US 623096-A 28 15-WAY-2001;
Location/Qualifiers
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Unknow...
Unclassified.
Unclassified.
1 (bases 1 to 168)
Grieve,R.B., Rushlow,K.B., Hunter,S.Wu., Frank,G.R. and Stiegler,G.L.
Stiegeler,G.L.
Flea protease proteins
Patent: US 6146870-A 28 14-NOV-2000;
Location/Qualifiers
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1 (bases 1 to 168)
Grieve, R.B., Rushlow, K.E., Hunter, S.Wu., Frank, G.R. and
                                                                                                                                                                                                                                                                                     Length 168;
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0.9%; Score 18.6; DB 1;
Best Local Similarity 47.8%; Pred. No. 1.8e+02;
Matches 54; Conservative 0; Mismatches 59;
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ARIS1537
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/organism≈"unknown"
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Sequence 28 from patent US 5712143.
182435
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/mol_type="unassigned DNA"
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Best Local Similarity
Matches 54; Conserv
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116 TCTTCGATGCATTCTCTTTCAAGATTACCCTGTTTGGTTTCTTCAAGTAAAGAACTT 60
                                                                                              linear
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AY135778S14
189 bp DNA
DOPERINTION GOTILLS GOTILLS HCR (HCR) gene, exon 14.
ACCESSION AY135791.1 GI:21296123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Gorilla gorilla"
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1..189
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1. 189
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Pongo pygmaeus
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Gorilla gorilla
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2 (bases 1 to 189)
Asumalahti, K. and Kere, J.
Direct Submission
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/number=14
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2 (bases 1 to 189)
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AY135778S1/c
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Biochemistry 29 (34), 7853-7861 (1990)
                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 174)
Stiegler, G.L. Flea proteins, nucleic acid molecules, and uses thereof Patent: US 5712143-A 28 27-JAN-1998; Location/Qualifiers
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Original source text: Human DNA.
Draft entry and computer-readable sequence for [Biochemistry 29, 7853-4861 (1990)] kindly submitted 7853-4861 (1990)] Kindly submitted 7853-4861 (1990)] Amstel, 13-JUL-1990.
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0.9%; Score 18.6; DB 1; Length 174;
Best Local Similarity 57.9%; Pred. No. 1.8e+02;
Matches 33; Conservative 0; Mismatches 24; Indels 0; Gaps
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    >174
    /note="protein S pseudogene beta mRNA and introns"

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                                                                                                                                              0.9%; Score 18.6; DB 1; Length 168; ilarity 47.8%; Pred. No. 1.8e+02; Conservative 0; Mismatches 59; Indels C
                                                                                          /organism="unknown"
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/gene="PROS2"
/note="intron 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (25-UUL-2002) Department of Medical Genetics, Biomedicum, University of Helsinki, PO Box 63 (Haartmaninkatu 8), Helsinki FIN-00014, Finland
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Direct Submission
Submitted (25-JUL-2002) Department of Medical Genetics, Biomedicum,
University of Helsinki, PO Box 63 (Heartmaninkatu 8); Helsinki
FIN-00014, Finland
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1 (bases 1 to 189)
1 HCR gene orthologs in chipanzee, pygmy chimpanzee, gorilla, and orangutan
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1. Similarity 61.2%; Pred. No. 1.8e+02;
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/gene≈"HCR"

/number=14

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Schlueter,T.
Gene library and method for its production
Parent: EP 1236798-A 314 04-SEP-2002;
LION Bioscience AG (DE)
Location/Qualifiers
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Sequence 314 from Patent EP1236798.
AX524284
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CpG island; genomic Msel fragment.
HOmo sapiens (human)
Homo sapiens
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/mol_type="genomic DNA"
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I (bases 1 to 200)
Gundling.6.J.
Rapid RNA isolation procedure in the presence of a transition metal
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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ilarity 61.2%;
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Dactors 1 to 241)
MacDonald, M., Huckle, E., Wilkinson, P. and Micklem, G.
MacDonald, M., Huckle, E., Wilkinson, P. and Micklem, G.
Bubmitted (16-0CT-1995) The Sanger Centre, Hinxton, Cambridgeshire,
Vector: pGBM-52f(-)
Clones are available from the UK MRC Human Genome Mapping Project
Resource Centre, Hinxton, Cambridgeshire CB10 1RQ, UK. See URL:
http://www.hgmp.mrc.ac.uk/ for details
or contact: blothelp@lignm.mrc.ac.uk.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Cross,S.H., Charlton,J.A., Nan,X. and Bird,A.P.
Purification of CpG islands using a methylated DNA binding column
Nat. Genet. 6 (3), 236-244 (1994)
94282070
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/organism="Homo sapiens"
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Best Local Similarity 57.94
Matches 33; Conservative
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AX277375/c
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                                                                                                                                                                                                                  115 ricingicricinal accada cacceririn coccalina accidida and carringa general
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Novel proteins and nucleic acids encoding same
Patent: WO 0174897-A.7, 11-OCT-2001,
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0.9%; Score 18.6; DB 1; Length 427;
Best Local Similarity 49.5%; Pred. No. 1.9e+02;
Matches 48; Conservative 0; Mismatches 49; Indels 0; Gaps
                                                                                                                                          0; Gaps
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                                                                                              0.9%; Score 18.6; DB 1; Length 427;
49.5%; Pred. No. 1.96+02;
tive 0; Mismatches 49; Indels C
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Gene library and a method for producing the same
Patent: WO 02074953-A 314 26-SEP-2002;
LION Bioscience AG (DE)
                                                                                                                                                                                                                                                           251 TITGIAAGITTTCTGTTCTGTTGTTGTTGT 287
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Sequence 314 from Patent W002074953.
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/mol_type="unassigned DNA"
/db_xref="taxon:10090"
                                   /mol_type="unassigned DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  439 bp
Sequence 7 from Patent WO0174897.
AX277349
                   /organism="Mus musculus"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
Mus musculus
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                                                                                         Query Match
Best Local Similarity 49.54
Matches 48; Conservative
  1. .427
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DEFINITION
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/codon start=1
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/protein id="CAD1033.1"
/brotein id="CAD1033.1"
/db xref="RinfEMBL:CAD10333"
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GDSGGPLVCQERRLWXLVGATSFGIGCAEVNKPGVYTVSPPSWTGSTSRWRET"
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Rheeus monkey gene for coagulation factor X, partial cds.
D21214
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Bur. J. Haematol. 52 (3), 162-168 (1994)
94222160
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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Murakawa,M., Okamura,T., Kamura,T., Kuroiwa,M., Harada,M. and
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                                                                                                                                                                                                                    /note="unnamed protein product"
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Sequence 33 from Patent WO0174897.
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Macaca mulatta (rhesus monkey)
Macaca mulatta
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Location/Qualifiers
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PAT 09-JAN-2002

linear

DNA

AX335885 Sequence 6394 from Patent WO0194629. AX335885.1 GI:18126604

LOCUS DEFINITION ACCESSION VERSION

Submitted (18-OCT-1993) Masahiro Murakawa, Harasanshin General Hospital, Division of Hematology; 1-8 Taihaku-machi, Hakata-ku, Pukuoka, Fukuoka, Fukuoka 812, 1092-291-3434, Fax:092-291-3266) Submitted (18-Oct-1293) to DDBJ by: COMMENT

Masahiro Murakawa Division of Hemorology Harasanshin General Hospiral I-8 Taihaku-machi, Hakata-ku Fukuoka, Fukuoka 812

Japan Phone: 092-291-3434

Fax : 092-291-3266

organism="Macaca mulatta" Location/Qualifiers FEATURES

/mol\_type="genomic DNA" /db\_xref="taxon:9544" .>484

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ó. ch 1 Similarity 61.2%; Pred. No. 1.99+10; 30; Conservative o; Mismatches 19; Indels o Query Match Best Local Similarity Matches

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DNA AX775014 546 bp Di Sequence 330 from Patent WO03038129. DEFINITION RESULT 166 AX775014/c

AX775014.1 GI:32486530 Homo sapiens (human) Homo sapiens KEYWORDS SOURCE ORGANISM ACCESSION VERSION

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. Methods for assessing and treating leukemia Patent: WO 03038129-A 330 08-MAY-2003; Ortho-Clinical Diagnostics, Inc. (US) 10-cation/Qualifiers Raponi, M. TITLE JOURNAL AUTHORS REFERENCE

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FEATURES

Gaps Query Match
0.9%; Score 18.6; DB 1; Length 546;
Best Local Similarity 57.9%; Pred. No. 1.9e+02;
Matches 33; Conservative 0; Mismatches 24; Indels (

336 Addendencherneacadaddaddaceceeeraneereeraneeraddaddaa 37 AGCCTCTGCTGCCAATACTTCTGGGGCTGCTGCCTTTCTCCCTGTCTGATTCCTAGG 93

RESULT 167 AX335885/c

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L29433. M.4327 N00045
L29433.1 G1:459809
Stuart factor; blood coagulation factor, factor X; glycoprotein; serine protease. Leytus, S.P., Foster, D.C., Kurachi, K. and Davie, E.W. Gene for human factor X: a blood coagulation factor whose gene organization is essentially identical with that of factor IX and 0; Gaps Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. 264 TGTTGTTTCTGTTGTTGTTGTTATCTAGATTTAAGCTGTGGTC 312 351 idricigacidardardandericciaacaderingeadericidardedard 303 ch 0.9%; Score 18.6; DB 1; Length 624; Similarity 61.2%; Pred. No. 2e+02; 30; Conservative 0; Mismatches 19; Indels C factor Xa heavy chain. /product="coagulation factor X" /protein id="AAA52764.1" /db\_xref="GI:182831" gene sets gene sets Patent: WO 0194629-A 6394 13-DEC-2001; Avalon Pharmaceuticals (US) Location/Qualifiers Biochemistry 25 (1.8), 5098-5102 (1986) /note="preprofactor X" (codon start) /organism="Homo sapiens" /mol\_type="unassigned DNA" /db\_xref="taxon:9606" /organism="Homo sapiens" /mol\_type="genomic DNA" /db\_xref="taxon:9606" Location/Qualifiers codon start=1 /map="13q34" Homo sapiens (human) Homo sapiens Homo sapiens (human) .624 13 Query Match Best Local Similarity 87026600 protein 3768336 ORGANISM DEFINITION ORGANISM RESULT 168 HUMFX8/c ACCESSION VERSION KEYWORDS AUTHORS TITLE Matches MEDLINE PUBMED JOURNAL REFERENCE AUTHORS REFERENCE JOURNAL KEYWORDS FEATURES FEATURES TITLE SEGMENT COMMENT . 0 .. 0 linear PAT 09-JUL-2003

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PAT 12-DEC-2003
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/note="unnamed protein product; trypsinogen (1 is 3rd base
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MacDonald, R.J., Stary, S.J. and Swift, G.H.
Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of the cloned cDNAs
J. Biol. Chem. 257 (16), 9724-9732 (1982)
82265624
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Rattus norvegicus (Norway rat)
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/mol_type="mRNA"
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Sequence 552 from Patent BP1344834.
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GKACIPTGPYPCGKQTLERRKRSVAQATSSSGBAPDSITWKPYDAADLDPTENPFDLL
DFNQTQPERGUNLTTIVGGOBCKDGBCPWQALLINEBNEGFCGGTLISETYILTAAH
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1 (Dases 1 to 711)

Nakamura, Y., Sugano, S., Matsusue, T., Okamoto, A. and Okawa, K.
Novel serine protease MP493

Patent: WO 02054295-A 3 01-AUG-2002;

MOCHIDA PHARMACEUTICAL CO LTD, YUSUKE NAKAMURA, SUMIO SUGANO,

TOMOKAZU MATSUSUE, ATSUSHI OKAMOTO, KAZUFUMI OKAWA

S. Homo sapleans (Human)

PN WO 02059295-A/3

PD 01-AUG-2002
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PI KAZUTUNI OKAWA
PC CL2NN5/12,CL2N9/64,CL2N1/15,CL2N1/19,CL2N1/21 PC
CL2NS/10,CO7K16/40,
PC CL2Q1/02
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23-JAN-2001 JP 01P 014963
YUSUKE NAKAMURA,SUMIO SUGANO,TOMOKAZU MATSUSUE,ATSUSHI
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0.9%; Score 18.6; DB 1; Length 624;
Best Local Similarity 61.2%; Pred. No. 2e+02;
Matches 30; Conservative 0; Mismatches 19; Indels C
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1. Similarity 57.9%; Pred. No. 2e+02;
33; Conservative 0; Mismatches ;
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/db_xref="taxon:9606"
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/note="FX intron G"
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WO 02059295-A/3.
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ð g 836 GTCTATCCATGGTAGGTTGTCTTTTGG

INV 01-0CT-1996 ö AF465268 12.78 bp mRNA linear VRT 02-FEB-2003 Gallus gallus coagulation factor VII precursor (F7) mRNA, complete Eukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca, Eumalacostraca, Eucarida, Decapoda, Dendrobranchiata, Penaeoidea, Xlein, B., Le Moullac, G., Sellos, D. and Van Wormhoudt, A. Molecular cloning and sequencing of trypsin cDNAs from Penaeus vannamie (Crustacea, Decapoda): use in assessing gene expression during the moult cycle (1810). 28 (5), 551-563 (1996) Submitted (18-APR-1995) A.E. Van Wormhoudt, College de France / CNRS, Laboratoire de Biologie Marine, BP 225, 29182 Concarneau, FRANCE Gaps ; 0 613 TGTTTTATGAACTTGGGTGACATTGTGTTTGGTGCATAGACATTAAGAA 661 797 idititakicakdindititakdangtaktitaccingaakgcakiakagak 845 Query Match 0.9%; Score 18.6; DB 1; Length 854; Best Local Similarity 61.2%; Pred. No. 2e+02; Matches 30; Conservative 0; Mismatches 19; Indels ( linear (Pacific white shrimp) /organism="Litopenaeus vannamei" /mol\_type="mRNA" |
/db\_xref="taxon:6689" |
/tissue type="hepatopancreas" |
/dev\_stage="adult" |
3..803 |
/EC\_number="3.4.21.4" mRNA 591 AAGGACTCCTGCCAGGGTGACTCTGGTGG 619 854 bp P.vannamei mRNA for trypsin. X86369 X86369.1 GI:785034 Location/Qualifiers Penaeidae; Litopenaeus. AF465268.1 GI:28194007 Gallus gallus (chicken) Gallus gallus Litopenaeus vannamei Litopenaeus vannamei 2 (bases 1 to 854) Van Wormhoudt, A.E. Direct Submission .854 PVTRYPSIN AF465268 96252881 trypsin. 8697100 VERSION KEYWORDS SOURCE ORGANISM SOURCE source DEFINITION AF465268/c DEFINITION ACCESSION VERSION AUTHORS TITLE REFERENCE AUTHORS TITLE RESULT 173 ACCESSION PVTRYPSIN JOURNAL REFERENCE JOURNAL CDS KEYWORDS FEATURES RESULT à

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GKQTLERRKESVAQATSSSGBAPDS:TWKPYDAADLDFTENPPDLLDFNQTQPERGDN
NLTRIVGGQECKDGECPWQALLINEBNEGFCGGTILSBFYILTAAHCLYQAKRFKVRV
GWRNTEQEBGGBAVHRVBVYTKHNRFYKETYDFDIAVLRKFPTJFRMYVAPACLPER
DADASTLMTQKTGIVGGFRTHEKGROSTRLKMLEVPYVDRNSCKLSSFIITQNMFC
AGYDTKQEDACQGGOBHYTRFKDTYFVTGIVSMGESCARKGKYGIYTKVTAFLKM
DRSMKTRGLPKAKSHAPEVIISSPLK"
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CMEBTCSYEBAREVPEDSDXTNBFWNKYKDGDQCETSPCQNQGKCKDGLGEYTCTCLE
GFEGKNCELFTRKLCSLDNGDCDQFCHEBQNSVVCSCARGYTLADNGKACIPTGPYPC
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                                                                                                                      A polyadenylation signal is located at position 1424-1429. This sequence was kindly submitted over electronic mail by R.T.A.MacGillivray (23-SEP-1985).
Location/Qualifiers
                       pcH\bar{X}[5,8,14]. During conversion of factor X to factor X-a, a glycopeptide of amino acids (encoded by positions 513-668 in this sequence) is
     Original source text: Human adult liver, cDNA to mRNA, clones
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Falkner, F. and Himmelspach, M.
Facror X Deletron WUTANTS AND ANALOGUES THEREOF
Patent: WO 9638318-A 43 03-SEP-1998;
FALKO GUENTER (AT); HIMMELSPACH MICHELE (AT)
Location/Qualifiers
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/note="a in pcHX8; t in pcHX5"
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/db_xref="GI:182841"
/db_xref="GDB:G00-119-890"
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A86859
                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                           'product="X mRNA"
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PEPENKLGPLERKCSFEBAREIYRDDERTKEFWHIYSDPNOCDSSPCONGGSCD
DQFOOTWCROPPEXEKSCETAVAERIKCIYDNGGCEQYCADBGSERRVCFCAEGYAL
ASDGVSCIPQVKEYCGTIPVLARRNTTRAGGRIVGGVTCPPGECFWQALIIQDQKGKCG
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VNHDIALLKLETPVNLTDFVVPICLPEKRFAVYELSSIKFSMVSGWGRLLDGGATSTF
LMRVHLPRVKTQECEKQANLNITENMFCAGDLTGKKDSCKGDSGGPHATKYKNTWFLT
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
Phasianinae, Gallus.
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[Dases 1 to 2)

MacGillivray,R.T.A.

MacGillivray,R.T.A.

[Dases 3 to 1443)

Fung,M.R.; Hay,C.W. and MacGillivray,R.T.

Characteriation of an almost full-length cDNA coding for human blood coagulation factor X

Proc. Natl. Acad. Sci. U.S.A. 82 (11), 3591-3595 (1985)
                                                                                                                                                                                                                2 (bases I to 1278)
McVey, "H., Davidson, C.J., Lal, K., Snell, P. and Elgar, G.
Direct Submission
Submitted (04-JAN-2002) Haemostasis Group, MRC Clinical Sciences
Centre, The Faculty of Medicine, Imperial College, Hammersmith
Campus, Du Care, London W12 ONN, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /EC_number="3.4.21.21"
/function="serum prothrombinconversion accelerator"
/function="witnamin K dependent serine protesse; contains 2
FGF-like domains; member of peptidase family S1/trypsin
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                                                                 1 (bases 1 to 1278)
Davidson, C.J., Hirt, R.P., Lal, K., Snell, P., Elgar, G.,
Tuddenham, E.G.D. and Movey, J.H.
Comparative sequence analysis and molecular evolution of blood coagulation genes from Gallus gallus and Fugu rubripes
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/protein_id="AAO33363.1"
/db_xref="GI:28194008"
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0; Mismatches 24; Indels
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blood coaquiation factor; factor X.
Homo sapiens (human)
Homo sapiens
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57.9%; Pred. No. 2e
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/db_xref="taxon:9031"
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source

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/organism="unknown"
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                                                                                                    AR316969.1 GI:33696092
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Homo sapiens
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Unclassified.
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Matches 30; Conserv
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SSSFIITQMMFCAGYDFYKGEDACQGDGGPHVTRFKDTYFYTGIVSWGESCARKGKYG

IYTKVTAFLKMIDRSMKTRGLPRAKSHAPEVITSSPLK"
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1 (bases 1 to 1467)

1 mmestpach, M. and bibl, J.
FACTOR X ANALOGUES WITH A MODIFIED PROTEASE CLEAVAGE SITE
PACENT: WO 9838317-A 26 03-SEP-1998;
HIMMELSPACH MICHELE (NT); FIBL JOHANN (AT)
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0.9%; Score 18.6; DB 1; Length 1467;
Best Local Similarity 61.2%; Pred. No. 2e+02;
Matches 30; Conservative 0; Mismatches 19; Indels 0;
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Pred. No. 2e+02;
0; Mismatches 19; Indels
                                                                                    'note="unnamed protein product"
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                                                                                                   /codon_start=1
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1. .1467
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                'organism="unidentified"
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1. .1467
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Matches 30; Conservative
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  PAT 17-AUG-2003
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Unclassified.
1 (bases 1 to 1467)
Himmelspach, M., Pfleiderer, M., Falkner, F.-G., Eibl, J., Dorner, F.
and Schlokat, M.
Factor X deletion mutants and analogues thereof
Factor X deletion Qualifiers
Location/Qualifiers
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Himmelspach,M., Schlokat,U., Dorner,F., Fisch,A. and Eibl,J.
Factor X analogues with a modified protease cleavage site
Patent: US 653071-A 26 03-UUN-2003;
Location/Qualifiers
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Factor x analog with an improved ability to be activated
Patent: WO 0110896-A 1 15-FEB-2001;
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0.9%; Score 18.6; DB 1; Length 1467;
Best Local Similarity 61.2%; Pred. No. 2e+02;
Matches 30; Conservative 0; Mismatches 19; Indels 0;
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AR316969 1467 bp n
Sequence 43 from patent US 6562598.
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Sequence 1 from Patent W00110896.
AX082959 GI:13184880
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JOHANN EIBL,
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Unpublished
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AF191307/c
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Himmelspach,M., Pfleiderer,M., Falkner,F.G., Eibl,J., Dorner,F. and
Schlokat,U.
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Himmelspach,M., Schlokat,U., Dorner,F., Andreas, Fisch and Bibl,J.
Factor X-analogues With modified protease cleavage site
Patent: JP 2001513631-A 26 04-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PI MICHELE HIMMELSPACH, UWE SCHLOKAT, FRIEDRICH DORNER, ANDREAS PIFISCH, JOHANN EIBL
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Factor X-analogues with modified protease cleavage site.
BD070392
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61.2%; Pred. No. 2e+02;
ative 0; Mismatches 19; Indels 0;
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Factor X deletion mutants and analogues thereof.
BD070435
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61.2%; Pred. No. 2e+02;
tive 0; Mismatches 1
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Strandedness: Single,
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/db_xref="taxon:32644"
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JP 2001513631-A/26
JP 2001513601
Z7-FEB-1998 JP 1998537062
Z7-FEB-1997 AT A 335/9
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Baxter Aktiengesellschaft (AT)
              Location/Qualifiers
1. .1467
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JP 2001513632-A/43.
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Matches 30; Conservative
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BD070435/c
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CCGROTCIDGLGGFREDCAGGWEGSFCHEVTSFONGSTBOGCAHVCLDEEGGRRCA
CCGROTCIDGLGGFREDCAGGWEGSFCHEVTSFONGSTBOGCAHVCLDEEGGRRCA
CSPGYRLGDDHLQCPEKVRS PCGRLCHRWEKKRRIKRDTDQVDKKEDOLDPELVNGS
QSPWGESPWQVILLDSKKKLACGAVIJHVSWVLTAAHCLDDYKKLTVRLGEYDLRRE
KWEDVDLDIFFETVHPRYTRSFSDNDTALLRALBAFTFSQTITVBICLDGGLSREHTR
VGCGTVYTGWGYRSBKTNGSFILNFIKVPVAPHNEVVQAMHNKISBWLCGGLGBEJTRG
RDACEGDSGGPWVASFRGTWFLVGLVSWGEGCGRLHNYGVYTKVSRYLDWIHGHIRME
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Grimm, D.R., Colter, M.B. and Kim, H.
Cloning of the complete cDNA sequences encoding porcine factor V
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                                                                                                                                                27-FEB-1998 JP 1998537063
27-FEB-1997 AT A 336/97
MICHELE HIMMELSPACH, MICHAEL PFLEIDERER, FALKO GUNTER FALKOER,
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0.9%; Score 18.6; DB 1; Length 1467;
Best Local Similarity 61.2%; Pred. No. 2e+02;
Matches 30; Conservative 0; Mismatches 19; Indels 0;
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Patent: JP 2001513632-A 43 04-SEP-2001;
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C12N15/57, C12N9/64, A61K38/48
Strandedness: Single;
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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JP 2001513632-A/43
04-SEP-2001
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Homo sapiens (human)
                  Homo sapiens
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HUMDPBA/c
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                                                                                                      1854 CAGATTICCTICAGTITIGGGTTTTGTTTAATTCTATTTCCACTTTCCAGGTCCTGAAA 1913
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Evans, B.A., Yun, Z.X., Close, J.A., Tregear, G.W., Kitamura, N., Nakanishi, S., Callen, D.F., Baker, E., Hyland, V.J., Sutherland, G.R. and Richards, R.I.
                               Query Match 0.9%; Score 18.6; DB 1; Length 1514; Best Local Similarity 51.9%; Pred. No. 2e+02; Matches 42; Conservative 0; Mismatches 39; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Structure and chromosomal localization of the human renal kallikrein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Original source text: Human parotid gland, cDNA to mRNA. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="kallikrein mRNA and introns"
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/gene="KLK1"
/note="kallikrein intron D"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .193
/organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Example DNA"
/db xref="taxon:9606"
/map="19q13.3"
                                                                                                                                                                                                                                                                                              HUMKALR4 193 bp
Human renal kallikrein, exon 4.
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/note="G00-120-118"
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/gene="KLK1"
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Homo sapiens
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167. .>193
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HUMDPB1A/c
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 249)
Gao,X., Veale,A. and Serjeantson,S.
ABI: a novel HLA-DPB1 allele found in one third of an Australian population.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (sites)
Mitsunaga,S., Kuwata,S., Tokunaga,K., Uchikawa,C., Takahashi,K., Akaza,T., Mitomi,Y. and Juji,T.

Ramily study on HLA-DPB1 polymorphism: linkage analysis with HLA-DR/DQ and two 'new' alleles
Hum. Immunol. 34 (3), 203-211 (1992)
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Homo sapiens gene for HLA-DP beta, partial cds, clone:SSKl.
D10478
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HLA-DP beta; DPB1; MHC; human leukocyte antigen; major
histocompatibility complex class II molecule.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
0.9%; Score 18.4; DB 1; Length 249;
Best Local Similarity 56.7%; Pred. No. 2.1e+02;
Matches 34; Conservative 0; Mismatches 26; Indels 0
                                                                                                                                                                                                                                                 Original source text: Homo sapiens blood DNA. Location/Qualifiers
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Dept. of Transfusion Medicine and
Immunobmatology, Faculty of Medicine
The University of Tokyo
7-3-1 Hongo, Bunkyo-ku
                                                                                                                                                    Immunogenetics 36 (1), 64-66 (1992) 92267574
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Mitsuraga. S.
Mitsurada. S.
Submitted (17-Feb-1992) to DDBJ by:
                                                                                                                                                                                                                                                                                               1. 249
/organism="Homo sapiens"
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/map="6p21.3"
/map="6p21.3"
/tissue_type="lymphocyte"
/tissue_type="blood"

    .249
    /organism="Homo sapiens"

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/isolate="THKK"
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03-3816-2516.
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/gene="HLA-DPB1"
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DPB1 protein.

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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Bases I to 249)

Bugawan, T.L., Horn, G.T., Long, C.M., Mickelson, E., Hansen, J.A., Ferrara, G.B., Angelini, G. and Erlich, H.A.
Analysis of HAA-DP allelic sequence polymorphism using the in vitro enzymatic DNA amplification of DP-alpha and DP-beta loci

J. Immunol. 141 (11), 4024-4030 (1988)
                                                                                                                                                                                                        .
/db_xref="G1:219607"
/translation="VYQLRQECYAFNGTQRFLERYIYNREELVRFDSDVGEFRAVTEL
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/db_xref=[G1:188071]
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/db_xref="G1:00-120-636"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRI 07-JAN-1995
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HLA-DP antigen; cell surface glycoprotein; class II gene; integral membrane protein; major histocompatibility complex.
Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                   /cell_type="peripheral blood mononuclear cell"
1. .249
/gene="DPB1"
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Human MHC class II HLA DP-beta gene, exon 2 allele DPB5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.9%; Score 18.4; DB 1; Length 249; Best Local Similarity 56.7%; Pred. No. 2.18+02; Matches 34; Conservative 0; Mismatches 26; Indels 0
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Ab xxef="c1:213602"

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Homo sapiens gene for HLA-DP beta, partial cds, clone:SSK2.
D10479
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Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mitsunaga.S., Kuwata.S., Tokunaga.K., Uchikawa,C., Takahashi,K.,
Akaza,T., Mitomi,Y. and Juji,T.
Family study on HiA-DPB1 polymorphism: linkage analysis with
HIA-DR/DQ and two 'new' alleles
HUM. Immunol. 34 (3), 203-211 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 0; Gaps
                                                               type="peripheral blood mononuclear cell"
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HLA-DP beta, DPB1; MHC, human leukocyte antigen; major
histocompatibility complex class II molecule.
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Ratsushi Tokunaga
Dept. of Transfusion Medicine and
Immunohematology, Faculty of Medicine
The University of Tokyo
7-3-1 Hongo, Bunkyo-ku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (17-Feb-1992) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
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03-3816-2516.
                    chromosome="6"
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/gene="DPB1"
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## RESULT 191 HUMDPB1KT/c source DEFINITION ORGANISM ACCESSION VERSION AUTHORS TITLE JOURNAL REFERENCE AUTHORS mRNA exon JOURNAL gene REFERENCE AUTHORS JOURNAL JOURNAL PUBMED REFERENCE CDS KEYWORDS FEATURES COMMENT TITLE TITLE SOURCE ઠે a /product="MHC class II HLA-DP-beta-1" /protein\_id="AAA59726.1" /db\_xref="G1:53549" /db\_xref="G0:53549" /db\_xref="G0:500-120-636" /db\_xref="GD8:G00-120-636" /translation="HFGRQBCYAFNGTQRFLERYIYNREELVRFDSDVGEFRAVTEL GRPEAEYWNSQKDILEERRAVPDRMCRHNYELDBAVTLQRR" Lower spains MHC class II antigen (HLA-DPB1) gene, HLA-DPB1 variant AF180970 HUMMHDPIH 256 bp DNA linear PRI 07-JAN-1995 Human MHC class II HLA DP-beta (allele DPBS), partial cds. M62333 ö 1812 TIGICICIGAGGIICCIGIIGGGIICTIAAITITITICATITICCAGAITICCITCAGTIIG 1871 1812 ITGICTCTGAGGTTCCTGTTGGGTTCTTAATTTTTTCATTTCCAGAITTCCTTCAGTTTG 1871 218 TIGIGICTGCACATCCTGTCCGGCACTGCCCGCTTCTCCTCCAGGATGTCCTTCTGGCTG 159 HLA-DP antigen; cell surface glycoprotein; class II gene; integral membrane glycoprotein; major histocompatibility complex. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 257) Xu,A., Huang,H., Liu,Z., Chen,W., Pan,D., Lin,J., Xu,K., Chen,S., Wang,X. and Chen,R. Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammallai, Eutheria, Primates; Catarrhini, Hominidae, Homo. 1 (Dases 1 to 256) Bugawan, T. L., Begovich, A. B. and Brlich, H. A. Rapid HAA-DPB typing using enzymatically amplified DNA and nonradioactive sequence-specific oligonucleotide probes Gaps 0; Gaps ., Query Match 0.9%; Score 18.4; DB 1; Length 256; Best Local Similarity 56.7%; Pred. No. 2.1e+02; Matches 34; Conservative 0; Mismatches 26; Indels Query Match 0.9%; Score 18.4; DB 1; Length 249; Best Local Similarity 56.7%; Pred. No. 2.1e+02; Matches 34; Conservative 0; Mismatches 26; Indels ( GRPEAEYWNSQKDILEEKRAVPDRMCRHNYELDEAVTLQ" Original source text: Human DNA allele DPB5. 'organism="Homo sapiens" /mol\_type="genomic\_DNA" /db\_xref="taxon:9606" /map="6p21.3" Location/Qualifiers gene="HLA-DPB1" gene="HLA-DPB1" AF180970.1 GI:14279142 codon\_start=1 Homo sapiens (human) Homo sapiens Homo sapiens (human) M62333.1 GI:188026 . 256 Homo sapiens RESULT 189 HUMMHDP1H/c SOURCE source RESULT 190 AF180970/c LOCUS DEFINITION SOURCE ORGANISM AUTHORS TITLE MEDLINE PUBMED ACCESSION ACCESSION REFERENCE gene REFERENCE AUTHORS JOURNAL KEYWORDS KEYWORDS FEATURES VERSION COMMENT VERSION

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/product="WHC class II antigen"
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Human MHC classII HLA-DPB1 gene allele DPB1*KT.
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Hid-DP antigen; cell surface glycoprotein; class II gene; integral
membrane protein; major histocompatibility complex.
Homo sapiens (human)
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Industries, Ltd., 14-15 Kobuchi 2-chome, Sagamihara, Kanagawa 229,
Japan (Tel:0427-51-7568) Fax:0427-51-7519)
Submitted (06-Apr-1992) to DDBJ by:
A novel HLA-DPB1 allele in Chinese people Unpublished 257)
Zu, A., Huang, H., Liu, Z., Chen, W., Pan, D., Lin, J., Xu, K., Chen, S., Wang, X. and Chen, R.
Direct Submission
Submitted (25-Aug. 1999) Biochemistry, School of Life Science, 135 Xingangxi Road, Guangzhou, Guangdong 510275, P.R.China Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 TIGIGLICIGACATCTIGIC COGCTICICCCCCAGAIGICCTTCTGGCTG
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14-15 Kobuchi 2-chome
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Direct Submission
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Brachyramphus marmoratus
Brachyramphus marmoratus
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TITLE
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AUTHORS
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Brachyramphus marmoratus haplotype MMC ribosomal protein 40 gene,
inton 5 and partial sequence.
AF306907
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                                                                                                                                                                                                                                                                                                                                                      0
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Backco, N. m. and Friesen, V.L.

Direct Submission

Submitted (21-SEP-2000) Department of Biology, Queen's University,

Kingston, ON K7L 3N6, Canada

1. 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachyramphus marmoratus
Brachyramphus marmoratus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Charadriiformes; Alcidae;
Brachyramphus.
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Pacheco, N. M. and Friesen, V.L.
A molecular investigation of hybridization in Brachyramphus
                                                                                                                                                                                                                                                                                                            Query Match
0.9%; Score 18.4; DB 1; Length 264;
Best Local Similarity 56.7%; Pred. No. 2.1e+02;
Matches 34; Conservative 0; Mismatches 26; Indels 0
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15. .262
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                                             Location/Qualifiers
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               0427-51-7568
                                  0427-51-7519
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/number=5
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RESULT 193

AF306908

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279 bp DNA linear VRT 23-JAN-2001 Exchyramphus marmoratus haplotype MMH ribosomal protein 40 gene, 1ntron 5 and partial sequence.
                       VRT 23-JAN-2001
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Pacheco, N.M. and Friesen, V.L.
Pacheco, N.M. and Friesen, V.L.
Direct Submission
Submitted (21-SEP-2000) Department of Biology, Queen's University,
Kingston, ON K7L 3NG, Canada
Location/Qualifiers
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Pacheco,N.M. and Friesen,V.L.
Direct Submission
Submitted (21-58P-2000) Department of Biology, Queen's University,
Kingston, ON K7L 3NG, Canada
Location/Qualifiers
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Brachyramphus marmoratus haplotype MAD ribosomal protein 40 gene, intron 5 and partial sequence.
AR30690R
                                                                                                                                                                                                           Brachyramphus marmoratus
Brachyramphus marmoratus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Charadriiformes; Alcidae;
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Archosauria, Aves, Neognathae, Charadriiformes, Alcidae,
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Pacheco, N. M. and Friesen, V. L.
A molecular investigation of hybridization in Brachyramphus
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Pacheco, N. M. and Friesen, V. L.
A molecular investigation of hybridization in Brachyramphus
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0.9%; Score 18.4; DB 1; Length 279;
Best Local Similarity 56.7%; Pred, No. 2.1e+02;
Matches 34; Conservative 0; Mismatches 26; Indels 0
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exon 2 and partial cds.
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                                                                                                                                                                                                                                  Unpublished
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LOCUS AF492638 285 bp DNA linear PRI 01-APR-2003
DEFINITION Homo sapiens MHC class II antigen (HLA-DPB1) gene, HLA-DPB1*0501
                                                                                                                                                                                                                                        283 bp DNA linear PRI 22-MAR-2001 alone sapiens WHC class II antigen (HLA-DPB1) gene, HLA-DPB1*3801 AF336224
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                                                                                                                                             250 GITTGIAAGITTTCTGTTGTTGTTGTTGTTGTTATCTAAGATTTAAGCTGTGGTG 309
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I toases I to 28, Man, W., Jia, Z., Pan, D. and Xu, A.
Sequence of complete exon 2 and partial intron 2 of HLA-DPB1*3801
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2 (bases 1 to 283)

2 (bases 1 to 283)

2 Liu,Z., Lin,J., Chen,W., Jia,Z., Pan,D. and Xu,A.

Direct Submission
Submitted (16-JAN-2001) Biochemistry Department, Zhongshan (Sun Xat-sen) University, 135 W. Xingang Rd, Guangzhou, Guangdong 510275, P.R. China
Location/Qualifiers
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Pred. No. 2.1e+02;
0; Mismatches 26; Indels
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gene="HLA-DPB1"
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                                                                        ch 0.9%;
1 Similarity 56.7%;
34; Conservative
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                                                                            Query Match
Best Local
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DEFINITION
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AF336224/c
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/gene="HiA-DPB1"
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                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 285)
Luo,M., Mao,X., Shehzad,I., Jacobson,K., Kwan,L., Shroeder,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 285)
                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 285)
Luo,M., Mao,X., Shehzad,I., Jacobson,K., Kwan,L., Shroeder,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (14-MAR-2002) Medical Microbiology, University of
Manitoba, R507 BMSB, 730 William Avenue, Winnipeg, Manitoba R3B
                                                                                                                                                                                                                                                                              Sequence-Based DPB Typing Fills the Missing Exon 2 Sequences of Multiple HLA-DPB1 Alleles
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Original source text: Homo sapiens (individual_isolate SASBE41)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1812 ITGTCTCTGAGGTTCCTGTTGGGTTCTTAATTTTTTCATTTCCAGATTTCCTTCAGTTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.9%; Score 16.4; DB 1; Length 285; 56.7%; Pred. No. 2.1e+02; Live 0; Mismatches 26; Indels
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Human MHC HLA-DPB1 gene, exon 2, clone DPB new A.
M83912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'product="MHC class II antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /allele="HLA-DPB1*0501"
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/gene="HLA-DPB1"
/number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="HLA-DPB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="HLA-DPB1"
allele, exon 2 and parti
AF492638
AF492638.1 GI:29422764
                                                                                                            Homo sapiens (human)
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/protein_id="AAA31520.1"
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                                                                                                                                                                                                                                                                                                                  linear MAM 27-APR-1993
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AGYHBGGKDSCQGDSGGPHVTEVBGTSFLTGIISWGESCAMKGKYGIYTKVSRYEV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     832 bp mRNA linear VRT 09-SEP-1997
nogen Bl (TRYPBI) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Original source text: Sheep liver, cDNA to mRNA.

Draft entry and computer-readable sequence for [1] kindly provided by G.Sarkar, 18-JUL-1989.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 ATTICTIGATITCTAICTIGGCICATITITAACICAGIAGIGAGITGITIGGITICCAIA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 AATTGCTGCATTCTGTGGAGGTTCCATCGTTAATGAAAATGGGTTGTAACTGCTGCCCA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Petromyzon marinus
Eukaryota; Meteazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
1 (bases 1 to 832)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 823)
Sarkar,G., Koeberl,D.D. and Sommer,S.S.
Direct sequencing of the activation peptide and the catalytic domain of the factor IX gene in six species
Genomics 6 (1), 133-143 (1990)
0; Gaps
                                                                    517 ITGITGAGAIGACCTAACTGITGGAGAAAIGGGGTAITGAAGIAGCCCACT 568
                                                                                                                                    Roach,J.C.
The Wolecular Evolution of the Vertebrate Trypsinogens
Unpublished
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49.0%; Pred. No. 2.2e+02;
tive 0; Mismatches 51; Indels 0
21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 CIGCATCAAGCCIGGIGITAAAATTACTGTIGTIGCAGGT 306
                                                                                                                                                                                                                                                                                                                  mRNA
0; Mismatches
                                                                                                                                                                                                                                                                                               823 bp
Sheep factor IX mRNA, partial cds.
M26233
M26233.1 GI:165878
factor TV
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/db_xref="taxon:9940"
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Best Local Similarity 49.0%
Matches 49, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ovis aries (sheep)
Ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . >823
31; Conservative
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   Matches
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                                                                                                                                                                                                                                          RESULT 199
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JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Luidia foliolata sea star regeneration-associated protease SRAP
                                                                                                                                                                                                                                                                                                                                                                                                            /translation="NYVYQLRQECYAFNGTQRFLERYIVNREELVRFDSDVGBFRAVT
ELGRPEAEYWNSQKDILEEKRAVPDRMCRHNYELDEAVTLQRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1812 ȚIGICȚCIGAGGITCCIGITGGGITCIIAAITITITCAITICCAGAITICCAGAITIG 1871
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VMFRKRYWAGDYQFCGGTLISDEWAYSAAHCFHNYGNINHYTAYVGAHBRDSYDSTQT
TVGLGKVFVHESYDTSGTLISDEWAYSAAHCFHNYGNINHYTAYVGAHBRDSYDSTQT
GDGETAVDPFTLQSVYVPIISSEQCHRATWYGGEINDNMICAGFKEGGKDSCGGDSGG
PFVCQSASGEYELVGVVSWGYGCADARKPGVYAKVLNYVSWINNLVARN"
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'protein_id="AAKI5274.1"
'db_xref="G1:3183620"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Asteroidea; Valvatacea; Paxillosida; Luidiidae; Luidia.

1 (bases 1 to 804)
Vickery,M.C., Vickery,M.S., McClintock,J.B. and Amsler,C.D.
Utilization of a novel deuterostome model for the study of regeneration genetics; molecular cloning of genes that are differentially expressed during early stages of larval sea star
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 804)
Vickery, M.C.L., Vickery, M.S., McClintock, J.B. and Amsler, C.D.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (12-OCT-2000) Department of Biology, University of Alabama at Birmingham, 1300 University Blvd., Birmingham, AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Luidia foliolata
Luidia foliolata
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Asterozoa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.9%; Score 18.4; DB 1; Length 285; Best Local Similarity 56.7%; Pred. No. 2.1e+02; Matches 34; Conservative 0; Mismatches 26; Indels C
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                                                                                                                                                                                                                                                                                                                                        /protein_id="AAA36266.1"
/db_xref="GI:553571"
                                                                                              'celi_type="granulocyte"
                                                                                                                                                                                                                                                                            label=exon 2
product="MHC HLA DPB1"
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/db_xref="taxon:105861"
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                              /db_xref="taxon:9606"
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/isolate="SASBE41"
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                                                                                                                                                                                                    <20. .>283
/codon_start=3
/label=exon_2
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/number=2
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APVLSDTSCRNSYPGDITTNNNICLGYLEGGGRDSGGSPVVCNGQLQGIVSWGRGC
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Takifugu rubripes coagulation factor VIIc precursor, mRNA, complete
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Takifugu rubripes
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Meopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
1 Chases 1 to 1293
Davidson, C.J., Hirt, R.P., Lal, K., Snell, P., Elgar, G.,
Comparative sequence and McVey, J.H.
Comparative sequence analysis and molecular evolution of blood coagulation genes from Gallus gallus and Fugu rubripes
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                     Roach,J.C.
Direct Submission
Submitted (01-JUL-1997) Molecular Biotechnology, University of
Washington, Seattle, WA 98195, USA
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AF465275.1 GI:28194021
   (bases 1 to 832)
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/EC_number="13.4.21.21"
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/Indiction="serum prochrombincon"
/Indiction="serum prochrombincon"
/Indiction="serum"
// redon start=1
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PTRRANFLEBELKAGNLERECIEBKSYEBAKEIFALPODEAFWRTYTAVDOCKLSP

CKNGATCTRRFETYACKCANGFHGHNCDKVBLISNGCRFRNGGCEHFCREFPDRSVT

FOAPGYKLDKDNSTOLDØVKVPCGRLOILFSPRVINGLICPKGHCPWQAMLSENNIYT

CGTIILSEQWYLTAAHCWWRRAHLENVTVGEHDREIFEKTEGHRRYIKVLIHPGYNK

TSDKOLAAMLKHRFWYGLGIVVVPCICAAONSTISRIANIRGSTVSGWGRLSRFGPP

ATILORITERRPPLOGCRIHTKLNITRNMLCAGLKTGGRDAGEGDSGGSPLVTYYEKTW

FLIGGVVSWGKGCANENLYGVVVVVTNFLDMIGNIIATN"
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Mammalia, Eutheria, Primates, Catarrhíni, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 171)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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0.9%; Score 18.4; DB 1; Length 1505;
Best Local Similarity 59.6%; Pred. No. 2.2e+02;
Matches 31; Conservative 0; Mismatches 21; Indels 0
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Patent: WO 02064799-A 105 22-AUG-2002;
TRANSKARYOTIC THERAPIES, INC. (US)
Location/Qualifiers
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AX523898
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Homo sapiens
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$78934.1 GI:244109
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Cercopithecinae, Macaca.
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/gene="TCR-b"
                                                                                                                                                                                                                                            1. .251
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Solera,J., Magallon,M., Martin-Villar,J. and Coloma,A.
Pactor IXMadrid 2: a deletion/insertion in factor IX gene which
abolishes the sequence of the donor junction at the exon IV-intron
d splice site
                                                                                                                                                                                                                                                                                                                                                                                              427 CTTTGTGTTTTGGTGAAATAGTCTGTAAATATCTCTAGGTCCACTTGGTTTATGACATCA 486
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Patent: WO 0177155-A 73 18-OCT-2001;
Curagen Corporation (US)
On Jul 8, 2002 this sequence version replaced gi:17900986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca mulatta (rhesus monkey)
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                       GenBank staff at the National Library of Medicine created this entry [NCB1 gibbsq 78934] from the original journal article. This sequence comes from Fig 3A.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                   Query Match

0.9%; Score 18.2; DB 1; Length 171;
Best Local Similarity 51.9%; Pred. No. 2.2+40;
Matches 41; Conservative 0; Mismatches 38; Indels (
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0.9%; Score 18.2; DB 1; Length 240;
Best Local Similarity 58.2%; Pred. No. 2.3e+02;
Matches 32; Conservative 0; Mismatches 23; Indels (
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                                                                               Am. J. Hum. Genet. 50 (2), 434-437 (1992) 92133619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AX318568 240 bp
Sequence 73 from Patent WO0177155.
                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          487 GTTAGCTCCAGCATTTCTC 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 CTTTGAACCATGAGTATTC 162
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DEFINITION
ACCESSION
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AY083553
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MEDLINE
PUBMED
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Norgen, R. B. Ur., Zink, M.A., Jia, Y., Ojeda, S.R. and Spindel, E.R. Norgen, R.B. Ur., Zink, M.A., Jia, Y., Ojeda, S.R. and Spindel, E.R. Unstruction of a targeted rhesus macaque microarray Unpublished
2 (bases 1 to 251)
Norgen, R.B. Ur., Zink, M.A., Jia, Y., Ojeda, S.R. and Spindel, E.R. Direct Submission
Submitted (11-MAR-2002) Molecular and Cellular Biology Core, Oregon Regional Primate Research Center, 505 NW 185th Avenue, Beaverton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRI 22-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          900 TICTGTTACCCAGIATCTTTTTCTAGAGAAATTAAGATCATTGAGTCATTGATGATGTTGAGA 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 TTTTGTTTCTTGGTGTTTTTTGGCGAGTTTTTGGTAATGATGATTCAATCATTTTGGGA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 265)
Jores, R. and Meo, T.

Grees, R. and Meo, T.

Few V gene segments dominate the T cell receptor beta-chain repertoire of the human thymus

J. Immunol. 151 (11), 6110-6122 (1993)
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Submitted (11-AUG-1993) R. Jores, Institut Pasteur, Unite
d'Immunogenetique, Dept d'Immunologie, 25, rue du Dr. Roux, 75015
Paris, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.9%; Score 18.2; DB 1; Length 251; Best Local Similarity 55.6%; Pred. No. 2.38+02; Matches 35; Conservative 0; Mismatches 28; Indels C
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H.sapiens (3.2) mRNA for T-cell receptor beta chain.
X74849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <1. .>251
/gene="GAP43"
/product="growth associated protein 43"
<1. .>251
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clone_lib="human thymus cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X74849.1 GI:407455
T-cell receptor beta chain; TCR-b gene.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                               /organism="Macaca mulatta"
/mol_type="genomic DNA"
/db_xref="taxon:9544"
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/clone="3.2"
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/gene="GAP43"
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38,
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2 (bases 1 to 265)
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/translation="MLSPDLPDSAWNTRLLCRVMLCLLGAGSVAAGVIQSPRHLIKEK
RETATLKCYPIPRHDTVYWYQQAEDLKNVFPP"
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Petromyzon marinus
Eukaryyota; Metazoa, Chordata, Craniata, Vertebrata, Hyperoartia,
Eutromyzontiformes; Petromyzontidae, Petromyzon.

1 (bases 1 to 836)
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Submitted (Ol-JUL-1997) Molecular Biotechnology, University of
Washington, Seattle, WA 98195, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1076 TGTCTGTGTGTGTGTGTGTGTGTGTCTCTCCCCTCTTTTGATTTTTGGCCTGGAA 1130
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Petromyzon marinus trypsinogen b2 (TRYPB2) mRNA, partial cds.
AF011901
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0.9%; Score 18.2; DB 1; Length 265
Best Local Similarity 58.2%; Pred. No. 2.3e+02;
Matches 32; Conservative 0; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="T-cell receptor beta chain"
125. .238
/gene="TCR-b"
/note="VD23"
/codon_start=1
/product="r-call receptor beta chain"
/protein_id="CAA52841.1"
/db_xref="GI:407456"
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/mol_type="mENA"
/db_xref="taxon:7757"
/db_xref="taxoncoete"
/tissue_lib="anterior intestine"
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/gene="TRYPB2"
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/gene="TRYPB2"
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/gene="TCR-b"
/note="Cb2"
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                                                                                                                                                                                                                                                                                            38. .124
/gene="TCR-b"
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                                                                                                                                                                                                                                                                                                                                                                       125. .>265
/gene="TCR-b"
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2 (bases 1 to 836)
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/protein_id="AAO27572.1"
/db_xxef="fg12792333"
/tdaxaslation="#xgPHTAALLLLELLLRSGTEGARTLRACGHPKWFNRWVGGENA
LEGEWPWQVSIQRNGIHFCGGSLIAPTWVLTAAHCFSNTSDISIYQVLLGALKLQQPG
HALLYVPWCWYCSNPQYYGGASSADYALVELGOBTFTWYLIPWCLDPSYIFESGMN
CWYTGWGSFSEQDRLPPRYLQKLAYPIIDTPRCNLLYNKDVESDFQLKTIKDDMLCA
GFAEGKKDACKGDSGGFLVCLVDQSWVQAGVISWGEGCARRNRPGVYIRVTSHHKWIH
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J. Biol. Chem. 5, 3363-3371 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                  836 TTTTTTTTTTTAACTTTTCAAAGGTTTTTATTCGTTTCATGGCATTACAACCATCATAGTG 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1492 AIGCACIGIGGGGAGITICTITICCGGICCAATCIAITIGGIGITITIGIAIGCITCTIG 1550
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Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 987)
Ehagwandin,V.J., Hau,L.W., Mallen-St Clair,J.; Wolters,P.J. and
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Bhagwandin,V.J. and Caughey,G.H.
Bhagwandin,V.J. and Caughey,G.H.
Surect Submission
Submisted (29-40G-2002) Cardiovascular Research Institute,
University of California San Francisco, 90 Medical Center Way,
Surge Building, Room 206, Box 0911, San Francisco, CA 94143, USA
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                                                                                                                                      th 18. Score 18.2; DB 1; Length 836; I Similarity 47.18; Pred. No. 2.58+102; Pred. S6; Conservative 0; Mismatches 63; Indels 65; Conservative 10; Mismatches 63; Indels 64; Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pred. Pr
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/codon start=1
/product="pancreasin"
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Mus musculus pancreasin mRNA, complete cds.
AF542056
/product="trypsin b2"
/evidence=not_experimental
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/strain="C57BL/6"
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Mus musculus
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                                                                                                                                                                              Best Local Similarity
Matches 56; Conserv
                                                                                                                                      Query Match
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AF542056/c
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                                                                                                     OCU49933 1558 bp mRNA linear MAM 27-MAR-1996 Oryctolagus cuniculus vitamin K-dependent protein C precursor mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSPWQVILLDSKKKIACGAVLIHVSWVLTAAHCMEEPKKLFVRLGEYDLRRKERWELD
LINIGEVLIHENYSRSTTDNDIALLRAADPATUSGTIVVPICHONGLAERELMOAGGET
LINIGEVLHESREKERKRRYRFILDINFITYPVAPQNECEQWGNIISENMLCALIGDRR
DACDGDSGGPWVASFRGTWFILVGLVSWGEGCGDLINVYGVYTKVSRYLDINIHSHIEEKE
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GTCADSIGGFSCQCHGGWEGSFCQYEVRFSNCSVDNGGCAHYCLEEBAGRSCSCAPGY
BLADDHLQCEPAVRFFCGRLGWKRIEKKRGNVKRDLEQVDEMDEVDFRLIDGKLTRRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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(bases 1 to 1558)
Shen,L., He,X. and Daalback,B.
Molecular cloning of rabbit vitamin K-dependent protein C and demonstration of its mRNA in the reproductive organs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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Submitted (26-PEB-1996) Lei Shen, Clincal Chemistry, Lund
University, University Hospital, Malmo S-205 02, Sweden
Location/Qualifiers
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548 ITCTGCAGGACCCGTGGGTTGGGTAGTCGGTCTTGTTCACTGG 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109. .1374
/product="vitamin K-dependent protein C"
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/tissue_type="laver"
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                                                                                                                                                                                                                             Oryctolagus cuniculus (rabbit)
Oryctolagus cuniculus
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m,L., He,X. and Dahlback,B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
                                                                                                                                                                                      U49933.1 GI:1236620
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                                                                                                                                              partial cds.
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                                                            RESULT 209
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/protein_id="To1:545021"
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AREVFENTERT"
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                        1 (bases 1 to 199)
de la Salle,C., Charmantier,J.L., Ravanat,C., Ohlmann,P.,
Hartmann,M.L., Schuhler,S., Bischoff,R., Ebel,C., Roecklin,D.,
Balland,A. et al.
The Arg-4 mutant factor IX Strasbourg 2 shows a delayed activation
by factor XIa
Nouv. Rev. Fr. Hematol. 35 (5), 473-480 (1993)
94126308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strasbourg 2, Arg-4 to Gln transition, Method: conceptual translation with partial peptide sequencing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 TGTTCTTTCAGTGTTTTCAAAAACTTCTCGTGCTTCTTCAAAACTACACTTTTCTTCCAT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 ACATTCTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCTGAATTATACCTCTT 49
                                                                                                                                                                                                                                                                                                                        GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 143652] from the original journal article. G6365 to A transition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="blood"
<4. .>168
/note="cross reacting material positive factor IX
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Unknown.
Unclassified.
Unclassified.
I (bases 1 to 276)
Apple,R.J., Bugawan, T.L. and Erlich,H.A.
Methods and reagents for HLA class I A locus DNA typing
Methot: US 5451512-A 123 19-SEP-1995;
Location/Qualifiers
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0.9%; Score 18; DB 1; Length 276;
Best Local Similarity 52.7%; Pred. No. 2.6e+02;
Matches 39; Conservative 0; Mismatches 35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic_DNA"
/isolate="hemophilia B patient J-C L"
/db xref="taxon:9606"
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Sequence 123 from patent US 5451512.
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                                                                                                       Homo sapiens MHC class I antigen (HLA-A) gene, HLA-A*3401 variant allele, exon 3 and partial cds.
AY267910
AY267910.1 GI:30525804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 CTGCGGAGCCACTCCACGCACGTGCCCTCCAGGTAGGCTCTCCACTGCTCCGCCTCATGG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 CTGCGGAGCCACTCCACGCACGTGCCCTCCAGGTAGGCTCTCCACTGCTCGCCTCATGG 179
                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 276)
Steiner,N.K., Fernandez-Vina,M. and Hurley,C.K.
Novel HiA.A, Allele
Unpublished
                                                                                                                                                                                                                                                                                                                                                        Creases 1 to 276)
Steiner, N.K., Fernandez-Vina, M. and Hurley, C.K.
Direct Submission
Submission
Submitted (03-APR-2003) Lombardi Cancer Center, Georgetown University Medical Center, 3970 Reservoir Rd. NW, Washington, DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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order(AY267909.1:<1. .270,1. .>276)
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join(AY267909.1:<1. .270,1. .>276)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  location/Qualifiers
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/gene="HLA-A"
/number=3
                              123 TITCTCTAACACTI 136
                                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
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                                                           178 GCCGTCTCCCACTT 165
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Matches 39; Conserva
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AY267909S2/c
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HSHLAAGN2 276 bp DNA linear PRI 20-OCT-2000 Human MHC class I antigen HLA-A gene (A*2601 variant), exon 3 and partial cds.
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Submitted (10-SEP-2002) Lebedeva T.V., HLA laboratory, American Red
Cross New England Region, 180 Rustcraft Rd, Dedham, MA 02026, USA
Location/Qualifiers
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Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 276)
Hurley, C.K., Stainer, N., Kosman, C., Mitton, W., Koester, R., Bei, M.,
Bush, J., McCormack, J., Hahn, A., Henson, V., Hoyer, R., Made, J.A.,
Novel HiA-A and HiA-B alleles
Tissue Antigens 52 (1), 84-87 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 CIGCIGCCTITCTCCCCTGICTGAITCCTAGGGIGAGGGITACCACTGCTCTCTCTCTCTCCC 122
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                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo,
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Bei,M. and Hurley,C.K.

Direct Submission

Submitted (20-FEB-1997) Microbiology & Immunology, Georgetown University Medical Center, 3970 Reservoir Rd. NW, Washington, DC
                                                                                                                                                                                                                                                                Lebedeva, T.V., Huang, A., Janzen, M. and Yu, N. Identification of novel HLA Class I alleles using single allele
AJ507648 GI:23304865
AJ507648.1 GI:23304865
HLA-A gene; HLA-A*34 allele; human leucocyte antigen A; major histocompatibility complex; MHC class I antigen.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 52.7%; Pred. No. 2.6e+02;
Matches 39; Conservative 0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /number=3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /map="6p21.3"
1. .276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="HLA-A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .276
/gene≂"HLA-A"
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090243.1 GI:1905858
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2 (bases 1 to 276)
Lebedeva,T.V.
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linear
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0.9%; Score 18; DB 1; 1

Best Local Similarity 54.5%; Pred. No. 2.6e+02;

Matches 36; Conservative 0; Mismatches 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=3
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                                                                                                                                                                                                                           iocation/Qualifiers
                                                                                                                                                                 Leach, M.D. and Shimkets, R.A.
                                                       AX312474.1 GI:17897467
                                                                                       Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <1. .>302
/gene="hp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "gene="hp"
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                                                                                                        Homo sapiens
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                             DEFINITION
                                                                                                      ORGANISM
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 217
                                           ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
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TITLE
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JOURNAL
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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Lalgadi,R.V., Ito,L.Y. and Sherman,B.K.
Polynucleotides and polypeptides derived from corn ear
Patent: US 6476212-A 4503 05-NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.9%; Score 18; DB 1; Length 276; Best Local Similarity 52.7%; Pred. No. 2.66+02; Matches 39; Conservative 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.9%; Score 18; DB 1; Length 290; 51.2%; Pred. No. 2.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40;
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/gene="HLA-A"
                                                                                                                                |Oin(U90242.1:<1. .270,1. .>276)
|gene="HLA-A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4503 from patent US 6476212. AR249144 GI:27297018.
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                                                                                                                                                                                                                                                                                                                                GTCVEWLRRYLENGKETLORT"
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           Location/Qualifiers
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Matches 42; Conserv
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AR249144/c
LOCUS
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RESULT 216

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PAT 14-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lavery, K.S., Gabler, C. and Killian, G.J.
Expression and localization of haptoglobin in the bovine female reproductive tract
Unpublished
2 (bases 1 to 302)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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Submitted (28-JAN-2000) Lavery K.S., Dairy & Animal Science,
Submitted (28-JAN-2000) Lavery K.S., Dairy & Animal Science,
Pennsylvania State University, The John O. Almquist Research
Center, Pox Hollow Road, University Park, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  Human polynucleotides and polypeptides encoded thereby
Patent: WO 0190366-A 5459 29-NOV-2001;
Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus partial mRNA for haptoglobin (hp gene). AJ771156.1 GI:9581738 haptoglobin, hp gene. Bos taurus (cow)
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GGSLVNAEWVVSAAHCYKSRVEVRLGEHNIRLTEGTEQFISSSRVIRHPNYSSYNIDN
                                                                                                                                                                                                                                                                           AF266240 383 bp mRNA linear VRT 15-FEB-2001 Gillichthys seta trypsinogen 2 precursor, mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gillichthys seta
Gillichthys seta
Gillichthys seta
Bukaryota; Metzea, Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neoperygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
Gobioidei; Gobiidae; Gillichthys.
1 (bases 1 to 383)
Gracey, A.Y., Troll, J.V. and Somero, G.N.
Hypoxia-induced gene expression profiling in the euryoxic fish
Gillichthys mirabilis
Proc. Natl. Acad. Sci. U.S.A. 98 (4), 1993-1998 (2001)
                                                                                                                                                                                                                                                                                                                        297 draggeadardedecarracirrerearracadegracerrererereagricadragagee 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 TCACTTCTGTGGAGGCTCTCTGGTCAACGCGGAATGGGTTGTGTCTGCTGCTCACTGCTA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cracey, A.Y., Troll, J.V. and Somero, G.N.
Direct Submission
Submitted (10-MAX-2000) Biological Sciences, Stanford University,
Hopkins Marine Station, Oceanview Blvd., Pacific Grove, CA 93950,
                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                     0.9%; Score 18; DB 1; Length 302;
52.7%; Pred. No. 2.6e+02;
tive 0; Mismatches 35; Indels
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33. .>383
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                                                                                                                                                                                                                                                                                                                                                                                                                           237 CAATGICTACCITG 224
                                                                                                                                                                   Query Match
Best Local Similarity 52.7%
Matches 39, Conservative
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Matches 39; Conserv
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ACCESSION
VERSION
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AUTHORS
TITLE
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PUBMED
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/translation="NANKILARPKY YNSGKLEBFVGGNLERECMEEKCSFEBARBVFE
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PPDVDYVNSTEAETILDNITQSTQSFNDFTRVVGGEDAKPGGFPRQVVLNGKVDAFCG
GSIVNEKMITYAAHCVETGVKITVVAGEHNIEETEHTEQKRNVIRIIPHHNYNAAINK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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         linear PAT 18-DEC-2003
                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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HUMAN coagulation factor IX mRNA, partial cds.
M35672
M35672.
M35672.
M35672.
GI:180287
coagulation factor IX; serine protease.
Homo sapiens (human)
Homo sapiens (human)
Mammalia; Eutheria; Primates; Cararrini; Hominidae; Homo.
I (bases I to 873)
Jagadeeswaran, P., Lavelle, D.E., Kaul, R., Mohandas, T. and
Warren, S.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isolation and characterization of human factor IX cDNA: identification of Tag I polymorphism and regional assignment SGmat. Cell Mol. Genet. 10 (5), 465-473 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Original source text: Human adult liver, cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.9%; Score 18; DB 1; Length 815; Best Local Similarity 64.3%; Pred. No. 2.7e+02; Matches 27; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1664 TITIGCATAGIGICTCTGGCTTCCTGGATGTTTTATGCCTGG 1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 TCTTGCAGAGTGTGGCTTGCAGCCTGCCTGGAGGATGGCCGG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="coagulation factor IX"
                                                                                                                                                                                                                                                               Patent: WO 02068649-A 101 06-SEP-2002;
815 bp Dr
Sequence 101 from Patent WO02068649.
AX921761
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                   Curagen Corporation (US)
Location/Qualifiers
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                                                                            AX921761.1 GI:40215332
                                                                                                                         Homo sapiens (human)
Homo sapiens
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/gene="F9"
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                             DEFINITION
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RESULT 219 AX921761

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PAT 29-SEP-1997
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                     Artificial gene
Artificial sequence, Genes.
Homo sapiens (human)
JP 1990167096-A/1
27-JUN-1990
13-JUL-1989 JP 1989179140
26-JUL-1988 JP 88P
1484519070 TAMOTSU, ASTO MASAHIRO
C12P21/02,C07K13/00,C12N15/12//A61K37/465,(C12P21/02, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Ampk-related serine/threonine kinase, designated snark
Patent: WO 012456-A 51 14-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.9%; Score 18, DB 1, Length 1389;
60.0%; Pred. No. 2.7e+02;
tive 0; Mismatches 20; Indels
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/product='protein c mutant'
replace(592. .594, ')
/product='protein c mutant'
replace(592. .594, ')
/product='protein c mutant'
replace(595. .597, ')
/product='protein c mutant'
/product='protein c mutant'
/product='protein c mutant'
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                                                                                                                                                                                                                                           1 (bases 1 to 1389)
Hashimoto, T. and Sato, M.
Hushimoto, T. and Sato, M.
Human PROTEIN C MUTAWY AND ITS PRODUCTION
Patent: JP 1990167096-A 1 27-JUN-1990;
HOBCHST JAPAN LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. 1389
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="texon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                        DNA
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AX381010
                                                                             DNA encoding protein C mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strandedness: Single;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   topology: Linear; anti-sense: No;
                                                                                                                                                                          synthetic construct
synthetic construct
artificial sequences.
                                                                                                                          E02492.1 GI:2170722
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Homo sapiens
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Matches 30; Conservative
                                                                                                                                                     JP 1990167096-A/1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sig_peptide
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FH Key
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                                                                                                                                                                                                                                                                        AF465274 1inear VRT 02-FEB-2003 Takifugu rubripes coagulation factor VIIb precursor, mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1397 ICTAATAÇATÇTGCCTTTATATGTTAATTGGTCTTTTTTCCCTTGCATCTTTTAATATTC 1456
                                                                                                                                                                                                                                                                                                                                                                                                                                             Takifugu rubripes

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Actinopterygii, Teleostei, Euteleostei, Neoteeleostei, Acanthomorpha, Acanthomorpha, Acanthomorpha, Acanthomorpha, Acanthomorpha, Tetradontoidea, Tetradontoidea, Tetradontidea, Tetradontoidea, Tetradontidae, Takifugu.

Tetradontoidea, Tetradontidae, Takifugu.

Davidson, C.J., Hirt, R.P., Lal, K., Shell, P., Elgar, G.,
Tuddenham, E., G.D. and Movey, J.H.

Comparative sequence analysis and molecular evolution of blood coagulation genes from Gallus gallus and Fugu rubripes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /EC_number="3.4.21.21"
/function="serum prothrombinconversion accelerator"
/function="vitamin K dependent serine protease; similar to
/note = "vitamin K dependent serine protease; similar to
Fugu rubripes FVII; synthesized in liver; contains 2
EGF-like domains; member of peptidase family S1/trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 1329)
McVey, J.H., Davidson, C.J., Lal, K., Snell, P. and Blgar, G.
Direct: Submission
Submitted (04-JAN-2002) Haemostasis Group, MRC Clinical Sciences
Centre, The Faculty of Madicine, Imperial College, Hammersmith
Campus, Du Cane Road, London M12 ONN, UK
                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="coagulation factor VIIb precursor"
protein id="AA033369.1"
db_xref="GI:28194020"
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Query Match 0.9%; Score 18; DB 1; Length 873; Best Local Similarity 64.3%; Pred, No. 2.7e+02; Matches 27; Conservative 0; Mismatches 15; Indels
                                                                                                     263 CTGTTGTTTCTGTTGTTGTTGTTATCTAGATTTAAGCTG 304
                                                                                                                                                  476 chéthrhrechdardredactarenalamatrerachdadeche 517
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/db_xref="taxon:31033"
                                                                                                                                                                                                                                                                                                                                                                                                                           Takifugu rubripes (Fugu rubripes)
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Matches 39; Conserv
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Dp δ

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/organish- now suprems
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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RESULT 226 AX524243 ð g ö linear PAT 08-AUG-2001 linear PAT 18-NOV-2000 Gould-Rothberg, B.E. and Dipippo, V.A. Method of identifying toxic agents using differential gene express Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 239)
Coben, M. Colpitts, T.i., Friedman, P.N., Granados, E., Klass, M.R.,
Russell, J.C., Stewart, K.D. and Stroupe, S.D.
Serine protease reagents and methods useful for detecting and
treating diseases of the prostate
reating diseases of the prostate
Patent: US 6223456-A 3 15-MAY-2001;
Location/Qualifiers Query Match

0.9%; Score 17.8; DB 1; Length 177;

Best Local Similarity 58.5%; Pred. No. 2.8e+02;

Matches 31; Conservative 0; Mismatches 22; Indels 0; Gaps 93 ccecaegraciarieres de recipio de la contra del la contra della cont 42 CIGCIGGCAATACTICIGGGCTGCTGCCTTICICCCTGTCTGATTCCTAGGG Query Match
0.9%; Score 17.8; DB 1; Length 239;
Best Local Similarity 55.7%; Pred. No. 2.98+02;
Matches 34; Conservative 0; Mismatches 27; Indels 0 DNA DNA Patent: WO 0063435-A 33 26-OCT-2000; Curagen Corporation (US) /mol\_type="unassigned DNA" /organism="Rattus sp." /mol\_type="unassigned DNA" /db\_xref="taxon:10118" AR152169 239 bp Sequence 3 from patent US 6232456. AR152169 GI:15118219 Sequence 33 from Patent WO0063435. AX040017 Location/Qualifiers /organism="unknown" AX040017.1 GI:11230031 Unknown. Unclassified. Rattus sp. Rattus sp. AX040017 Unknown. 197 A 197 136 A 136 Rattug. AR152169/c LOCUS DEFINITION ORGANISM DEFINITION ORGANISM RESULT 224 RESULT 225 ACCESSION VERSION REFERENCE AUTHORS TITLE ACCESSION JOURNAL VERSION KEYWORDS REFERENCE AUTHORS JOURNAL KEYWORDS SOURCE AX040017 FEATURES FEATURES TITLE SOURCE δ ઠે

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Query Match 0.9%; Score 17.8; DB 1; Length 1125; Best Local Similarity 53.6%; Pred. No. 3e+02; Matches 37; Conservative o Mismatch
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Hau,L.W.T and Caughey,G.H.
Direct Submission
Submitted (11-AFF-2001) Medicine, UCSF, 90 Medical Center Way, San Francisco, CA 94143-0911, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Structure and activity of human pancreasin, a novel tryptic serine peptidase expressed primarily by the pancreas J. Biol. Chem. 278 (5), 3363-3371 (2003)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Bayer Aktiengesellschaft (DE)
Location/Qualifiers
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Homo sapiens pancreasin mRNA, complete cds.
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                                      DNA
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                                  AX375719 927 bp
Sequence 26 from Patent W00196378.
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AB056161 1125 bp mRNA linear PRI 04-MAR-2003
Homo sapiens PRSS27 mRNA for serine protease 27, complete cds.
AB056161
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EMPWQVSIQENGSHRADALOLLILCFGSQRAKAATACGRPRMLNRMVGGQDTQEG
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BGKKDACKGDSGGPLVCLVGQSWLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRII
                                                                                                             1225 TICTITACALCIGALITITATCITAGAAIGICTITICITICICCAACIATIGIGACAGAAAG 1284
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Query Match 0.9%; Score 17.8; DB 1; Length 1077; Best Local Similarity 53.6%; Pred. No. 3e+02; Matches 37; Conservative 0; Mismatches 32; Indels 0;
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/protein_id="BAB85497.1"
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/cell_type="pool"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Molecular toxicology modeling
Patent: WO 0210453-A 1575 07-FEB-2002;
Gene Logic, Inc. (US)
                                                             Rattus norvegicus (Norway rat)
AX401899.1 GI:21338079
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Okafuji,T.
Direct Submission
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FBEIKLGPLERECIBEKCSFEEAREIVRDDBRTKEFWHIYSDPNGCDSSPCONGGSCD
DQFQDYVCRCPPEYEGKSCETAVAENLKCIYDNGGCEQYCADEQSEKRVCFCAEGYAL
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                                                                                                                                                             AF465268 1278 bp mRNA linear VRT 02-FEB-2003
Gallus gallus coagulation factor VII precursor (F7) mRNA, complete
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1 (bases 1 to 1278)
Davidson, C.J., Hirt, R.P., Lal, K., Snell, P., Elgar, G., Comparative sequence analysis and molecular evolution of blood coagulation genes from Gallus gallus and Rugu rubripes

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wavey, J.H., Davidson, C.J., Lal, K., Snell, P. and Blgar, G. Direct Submission
Submitted (04-JAN-2002) Haemostasis Group, MRC Clinical Sciences Centre, The Faculty of Medicine, Imperial College, Hammersmith Campus, Du Cane Road, London W12 ONN, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="serum prothrombinconversion accelerator"
/note="vitamin K dependent serine protease; contains 2
EGF-like domains; member of peptidase family S1/trypsin
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51.9%; Pred. No. 3e+02;
tive 0; Mismatches 37; Indels 0;
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/protein id="AA033363.1"
/db xref="GI:28194008"
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1. ...1278
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                                                                                                                                                                                                                                                                                                  AF465268.1 GI:28194007
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                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (chicken)
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AX401899
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Daiichi Pharmaceutical Co LTD, 16-13 Kitakasai 1-Chome, Edogawa-ku,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butberia, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tokyo 134, JABAN
On Nov 19, 2003 this sequence version replaced gi:251769.
Location/Qualifiers
                                                                                                                                                                                                           0
                                                                                                                                                         Score 17.8; DB 1; Length 1543;
Pred. No. 2.9e+02;
                 1.1543
/organism="Rattus norvegicus"
/mol type="unassigned DNA"
/db_xref="taxon:10116"
/note="EMBL/GenBank Accession No. NM_012803"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 1543)
Okafuji,T., Maekawa,K., Nawa,K. and Marumoto,Y.
The CDNA cloning and mRNA expression of rat protein C
Biochim. Biophys. Acta 1131 (3), 329-332 (1992)
                                                                                                                                                                                                                                                     1792 TIGIATICIGICAGIGAGGCITGICTCGAGGTICCTGTGGGTT 1836
                                                                                                                                                                                                                                                                                                     1268 TGGTCTTCTTTCGGGGTACCTGGTTTCTGGTGGGGCCTGGTGAGCT 1312
                                                                                                                                                                                                           17; Indels
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/product="protein C precursor"
/protein_da="CAAA5617.1"
/db_xref="G1:56963"
/db_xref="G0:56963"
/db_xref="G8YISS-PROT:P31394"
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/organisem="Rattus norvegicus"
/mol_type="mRNA"
/strain="Wistar"
                                                                                                                                                                             62.2%; Pred. No. 2.9e-
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/clone="28000"
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Location/Qualifiers
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Kmiec,E.B., Gamper,H.B. and Rice,M.C.
Targeted chromosomal genomic alterations with modified single stranded oligonucleotides
Patent: NO 0173002-A 2392 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
                                                       /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                        Location/Qualifiers
    UNIVERSITY OF DELAWARE (US)
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Best Local Similarity
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AX265001/c
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WELDLDIKEVLVHPNYTRSNSDNDIALLRLSQPATLSKTIVPICLPNSGLAQELSQAG
QETVVTGWGYQSDKVKDGRRNRTFILFFIRIPLAARNDCMQVMNNVVSENMLCAGIIG
DTRDACDGDSGGPMVVFFRGTWFLVGLVSWGBGCGHLNNYGVYTKVGSYLKWIHSYIG
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Mammalia, Eutheria, Primates, Cararrhini, Hominidae, Homo.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Prinates; Catarrhini; Hominidae; Homo.
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Targeted chromosomal genomic alterations with modified single
Stranded oligonucleotides
Patent: WO 0173002-A 238B 04-OCT-2001;
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Patent: Wo 0.136532-A 59 25-MAY-2001,
Compugen Ltd. ([Lb]
Location/Qualifiers
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                                                                                                                                                                       Query Match 0.9%; Score 17.8; DB 1; Length 1543; Best Local Similarity 62.2%; Pred. No. 2.96+02; Matches 28; Conservative 0; Mismatches 17; Indels 0;
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15.0%; Pred. No. 2.9e+02;
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/mol_type="unassigned DNA"
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Sequence 59 from Patent WO0136632.
                                                                            49. .147
169. .1431
/product="protein C"
1514. .1519
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Matches 67; Conserva
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mat_peptide
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AX147505/c
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1919 TACTCATTTTCCTCCCAGTATTTACATTTTCATAGGTTTCTTTAATGGATTTATTCATTT 1978
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Targeted chromosomal genomic alterations with modified single stranded oligonucleotides
Patent: WO 0173002-A 2389 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
Location/Qualifiers
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Query Match 0.9%; Score 17.6; DB 1; Length 121; Best Local Similarity 54.7%; Pred. No. 3.1e+02; Matches 35; Conservative 0; Mismatches 29; Indels (
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Sequence 2389 from Patent WO0173002.
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Location/Qualifiers
                   source
FEATURES
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ö 1919 TACTCATTTTCCTCCCAGTATTTACATTTTCATAGGTTTCTTTAATGGATTTTATTCATTT 1978 115 TACTCACTGTTCTTTCAGTGTTTTCAAAAACTTCTCGTGCTTCTTCAAAACTACACTTTT 56 Query Match 0.9%; Score 17.6; DB 1; Length 121;
Best Local Similarity 54.7%; Pred. No. 3.1e+02;
Matches 35; Conservative 0; Mismatches 29; Indels 0; Gaps 1979 CCTC 1982 55 CTTC 52 a ò a

linear AX265002 Sequence 2393 from Patent WO0173002. AX265002 AX265002.1 GI:16513801 Homo sapiens (human) DEFINITION RESULT 238 ACCESSION VERSION AX265002 KEYWORDS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens ORGANISM REFERENCE AUTHORS TITLE

Kmiec,E.B., Gamper,H.B. and Rice,M.C.
Targeted chromosomal genomic alterations with modified single
stranded oligonuclectides
Patent: wo 0173002.A 2393 04-OCT-2001;
UNIVERSITY OF DELAWARE (US) JOURNAL

/mol\_type="unassigned DNA" /db\_xref="taxon:9606" /organism="Homo sapiens" Location/Qualifiers source FEATURES

Query Match Best Local Similarity Matches 35; Conserva

1919 TACTCATTTTCCTCCCAGTATTTACATTTTCATAGGTTTCTTTAATGGATTTATTCATTT 1978 7 TACTCACTGTTCTTTCAGTGTTTTCAAAACTTCTCGTGCTTCTTCAAAACTACACTTTT 66 염

1979 CCTC 1982 CTTC 70 g ò

RESULT 239 AX265005/c

AX265005 Seguence 2396 from Patent WO0173002. AX265005 AX265005.1 GI:16513804 Homo sapiens (human) DEFINITION ACCESSION VERSION KEYWORDS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens ORGANISM REFERENCE

Kmiec, B.B., Gamper, H.B. and Rice, M.C.
Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 113002-A 356 04-OCT-2001;
UNIVERSITY OF DELAMARE (US)
Location/Qualifiers AUTHORS TITLE JOURNAL

FEATURES

source

0; Gaps Query Match

0.9%; Score 17.6; DB 1; Length 121;
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RESULT 240 AX265006

PAT 26-OCT-2001

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Homo sapiens (human) KEYWORDS

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. Homo sapiens ORGANISM REFERENCE

Kmiec,E.B., Gamper,H.B. and Rice,M.C.
Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002-A 2397 04-OCT-2001;
UNIVERSITY OF DELAWARE (US) JOURNAL

1. .121 /organism="Homo sapiens" Location/Qualifiers FEATURES

Query Match 0.9%; Score 17.6; DB 1; Length 121;
Best Local Similarity 54.7%; Pred. No. 3.1e+02;
Matches 35; Conservative 0; Mismatches 29; Indels 0; Gaps /mol\_type="unassigned DNA" /db\_xref="taxon:9606"

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1979 CCTC 1982 ò

68 CTTC 71

RESULT 241 AX265009/c

PAT 26-OCT-2001

linear

DNA

linear PAT 26-OCT-2001 DNA 121 bp DN Sequence 2400 from Patent WO0173002. AX265009 AX265009.1 GI:16513808 DEFINITION ACCESSION VERSION KEYWORDS

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. Homo sapiens ORGANISM

Homo sapiens (human)

Kmiec, E.B., Gamper, H.B. and Rice, M.C.
Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002-A 2400 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
Location/Qualifiers REFERENCE AUTHORS TITLE

JOURNAL FEATURES

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KEYWORDS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Targeted chromosomal genomic alterations with modified single
stranded oligonuclectides
Patent: WO 0173002-A 2401 04-0CT-2001;
UNIVERSITY OF DELAMARE (US)
Location/Qualifiers
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Targeted chromosomal genomic alterations with modified single stranded oligonucleotides
Patent: Wo 0173002.A 2404 04-OCT-2001,
UNIVERSITY OF DELAWARE (US)
                                                                   . Match 0.9%; Score 17.6; DB 1; Length 121; Local Similarity 54.7%; Pred. No. 3.1e+02; les 35; Conservative 0; Mismatches 29; Indels 0
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1919 TACTCATTTTCCTCCCAGTATTTACATTTTCATAGGTTTCTTTAATGGATTTATTCATTT 1978
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002-A 2405 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
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Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002-A 2416 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
ch 0.9%; Score 17.6; DB 1; Length 121; 1 Similarity 54.7%; Pred. No. 3.18+02; 35; Conservative 0; Mismatches 29; Indels C
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Sequence 2405 from Patent WO0173002.
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Sequence 2416 from Patent WO0173002.
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1919 TACTCATTTTCCTCCCAGTATTTACATTTTCATAGGTTTCTTTAATGGATTTATTCATTT 1978

0.9%; Score 17.6; DB 1; Length 121; 54.7%; Pred. No. 3.1e+02; Live 0; Mismatches 29; Indels (

Query Match
Best Local Similarity 54.7%

0; Gaps

102 TACTCACTGTTCTTTCAGTGTTTTTCAAAACTTCTCGTGCTTCTTCAAAACTACACTTTT 43

1979 CCTC 1982

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42 CTTC 39

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Targeted chromosomal genomic alterations with modified single stranded oligonuclectides
Patent: WO 0173002-A 2417 04-OCT-2001;
UNIVERSITY OF DELAMARE (US)
Location/Qualifiers
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Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002.A 2408 04-0CT-2001;
UNIVERSITY OF DELAWARE (US)
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Sequence 2417 from Patent WO0173002.
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Sequence 2408 from Patent WO0173002.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Targeted chromosomal genomic alterations with modified single
Stranded oligonucleotides
Patent: WO 0173002-A 2420 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
Location/Qualifiers
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Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0133002-A 2409 04-0CT-2001;
UNIVERSITY OF DELAMARE (US)
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Sequence 2409 from Patent WO0173002.
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Matches 35; Conservative 0; Mismatches 29; Indels 0; Gaps
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Targeted chromosomal genomic alterations with modified single
stranded oligonuclectides
Patent: WO 0173002-A 221 04-OCT-2001;
UNIVERSITY OF DELAMARE [US)
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Search completed: August 9, 2004, 16:48:35 Job time : 634 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

August 9, 2004, 16:48:23; Search time 786 Seconds (without alignments) 3.881 Million cell updates/sec Run on:

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Scoring table: IDENTITY NUC Gapext 0.5 Sequence:

1612 seqs, 761539 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4
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Annual Munich Mu

1826 TCCATGTGTGT 1816

## ALIGNMENTS

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AAV02230 standard; cDNA; 2422 BP.
                                                                 AAV02230;
 RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1946 TGTGCATATCTCTATGTGCGTGTGCATCGGTGTGTTTGCGTÄTCTCTGTGTGGACCATCTG 1887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibition of tissue factor, vascular restenosis and platelet deposition - using modifier factor VII unable to activate factors IX and X_i e.g. for treating thrombosis, embolism, stroke etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ80296 shows the cDNA encoding human Factor VII. Factor VII is a trace plasma glycoprotein that circulates in blood as a single-chain zymogen. The zymogen is catalytically inactive, and is converted into a two-chain active mol. by cleavage of an internal peptide bond located approx. In the middle of the mol. Factor VII a rapidly activates Factor X or Factor IX by limited proteolysis. Modified Factor VII has anticoaqulant properties, for preventing the coagulation cascade. The modified Factor VII has an active site modified by at least one amino acid substitution, and in its modified form is capable of binding tissue factor and inhibiting its action. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                               Factor VII, plasma glycoprotein, derivative, tissue factor, TP; inhibition; vascular restenosis; platelet deposition; catalytic centre, factor IX; factor X; inactivation; thrombosis; embolism; stroke; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%; Score 43; DB 1; Length 2422;
8.0%; Pred. No. 4.3e-05;
ve 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2422 BP; 596 A; 712 C; 692 G; 422 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                     /*tag= a
/note= "wild type Factor VII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 39-40; 51pp; English.
                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berkner KL, Petersen LC, Hart CE;
                              AAQ80296 standard; cDNA; 2422 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-US005779.
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                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ZYMO ) ZYMOGENETICS INC. (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                       41. .1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 58.0 es 76; Conservative
                                                                                                                                                    cDNA encoding Factor VII.
                                                                                                   (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-022464/03.
                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAY-1994;
                                                                                                 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                        WO9427631-A1
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                                                                                                                  17-JUL-1995
                                                                 AAQ80296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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              AAQ80296/
RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that encoding a Ser344Ala modified factor VII which can be used as part of a method for inhibiting thrombus formation. The method is used to maintain or improve vascular patency, to prevent or minimise myocardial injury associated with post-ischaemic reperfusion and to improve regional myocardial blood flow during post-ischaemic reperfusion. The method is particularly used where the site of thrombus or reduced patency is associated with (micro) surgery, angioplasty or trauma or where the myocardial injury is myocardial necrosis. Particular applications are in treatment or prevention of intimal hyperplasia or restences caused by acute (e.g. mechanical) injury, deep vein thrombosis, pulmonary embolism, stroke, disseminated intravascular coagulation; fibrin deposition
                                                                                                                                      Factor VII, modified, Ser344Ala mutant; vascular patency, prevention, myocardial injury, blood flow; angioplasty; trauma; intimal hyperplasia; restencesis; deep vein thrombosis; treatment; pulmonary embolism; stroke; disseminated intravascular coagulation; fibrin deposition; endotoxaemia; myocardial infarction; anticoagulant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      factor VII - also used to maintain vascular patency, prevent myocardial injury and improve regional myocardial blood flow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1946 IGTGCATATCTCTATGTGCGTGTGCATCGGTGTGTTTTGCGTATCTCTGTGTGACCATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting thrombus formation by topical administration of modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2422;
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58.0%; Pred. No. 4.3e-05;
iive 0; Mismatches 55; Indels
                                                                   Homo sapiens cDNA encoding Ser344Ala modified factor VII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "Ser344Ala modified factor VII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      associated with endotoxaemia and myocardial infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rasmussen ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 69-73; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hedner U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-DK000251.
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08-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41. .1375
/*tag= a
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Best Local Similarity 58.09
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hart CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZYMO ) ZYMOGENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-052245/05.
P-PSDB; AAW31687.
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                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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The present invention describes a method for the inhibition or minimisation of myocardial injury associated with post-ischaemic repertusion by administering factor VII, which has at least I modification in its catalytic triad (therefore inhibiting the ability of factor VII to activate plasma factor X or IX). The method can be used for inhibiting or minimising myocardial injury and for imparting regional myocardial blood flow associated with post-ischaemic reperfusion. It can also be used for inhibiting blood coagulation, platelet deposition, thrombus formation and maintaining or improving vascular potency. Factor VII can be administered at relatively low doses and does not produce undesirable side effects. Further it acts specifically at sites of injury. The present sequence encodes Factor VII
                                                                                                                                                                                                                                                                    Factor VII, catalytic active site, blood coagulation, plasma, Factor X; Factor IX; vasotropic, antischaemic, anticoagulant, myccardial injury, post-ischaemic reperfusion, platelet deposition; thrombus formation; vascular potency; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibition or minimization of myocardíal injury associated with post-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.1%; Score 43; DB 1; Length 2422; Best Local Similarity 58.0%; Pred. No. 4.3e-05; Matches 76; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2422 BP; 596 A; 712 C; 692 G; 422 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a /product= "Factor VII"
                                                                                                                                                                                                                                        Factor VII encoding cDNA SEQ ID NO:1.
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                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                           AAZ57385 standard; cDNA; 2422 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-00662920.
93US-00065725.
94WO-US005779.
94US-0047289.
95US-00472895.
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                                                                                                                                                                                                          05-APR-2000 (first entry)
                             1072 TCTGTGTCTGT 1082
                                                             1826 rccardrdrdr 1816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ischemic reperfusion
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                                                                                                                                                                                                                                                                                                                                                          Unidentified.
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07-JUN-1995;
07-JUN-1996;
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                                                                                                                                                                           AAZ57385;
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AAZ57385/c
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952 TGTIGAGAATTATCAATGAGCAGTGTTIGTGGATTCTTGTTATCTTGCACTTGTGAAGTG 1011
                     1946 TGTGCATARCTCTATGTGCGTGTGCATCGGTGTTTGCGTATCTCTGTGTGACCATCTG 1887
                                                Use of modified human factor VIIa with a covalent modification in its catalytic center, to inhibit thrombus formation or to maintain vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to the use of modified human Factor VIIa for inhibiting thrombs formation, or maintaining or improving vascular patency in a patient. The modified factor VIIa comprises a covalent modification in its catalytic center which effectively interrupts the blood cosquiation cascade. The modifications render Factor VIIa substantially unable to activate plasma factor IX or X. The modified Factor IX or X. The modified
                                                                                                                                                                                                                                                                                       Factor VIIa, thrombus, vascular patency, blood coagulation, Factor X, plasma factor, Factor IX, myocardial injury, human, Factor VII, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rasmussen ME;
                                                                                                                                                                                                                                                                Human Factor VII polypeptide encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                    location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Col 43-48; 34pp; English.
                                                                                                                                                                                     AAF57099 standard; cDNA; 2422 BP.
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95US-00475845.
96US-00660289.
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93US-00065725.
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155. .1372
/*tag= c
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                                                                                              1072 TCTGTGTCTGT 1082
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P-PSDB; AAB61992.
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07-JUN-1995;
07-JUN-1996;
06-JUN-1997;
                                                                                                                                                                                                                                                                                                                            Homo sapiens
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21-MAY-1993;
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                                                                                                                                                                                                                                                                                                                                                                                         sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
                                                                                                                                                                                                              AAF57099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dermatological; anorectic; immunosuppressive; cytostatic; antiinflammatory; antiinflammatory; antiinflammatory; antiinflammatory; antiinflammatory; antiinflammatory; antiinflammatory; antiinflammatory; antiinflammatory; antiinflammatory; antiinflammatory; cardiomyopathy; atherosclerosis; hypertension; congenital heart defect; plumonary stenosis; scleroderma; obesity; metabolic disturbance; obesity; transplantation; adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer; diabetes; metabolic disorder; neoplasm; adenocarcinoma; fertility; haemophilia; graft versus host disease; AIDS; hronchial asthma; Crohn's disease; multiple sclerosis; infectious disease; anorecagenerative disorder; alzebener; disease; multiple sclerosis; and sease; barkinson's disease; immune disorder;
associated with post-ischemic reperfusion, for improving regional myocardial blood flow during reperfusion and maintaining or improving vascular patency in a parient. The present sequence represents the cDNA encoding a human Factor VII polypeptide
                                                                                                                                                                                                                                                                                                                                       0; Gaps
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Stone DJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human; NOVX; cardiant; antiarteriosclerotic; hypotensive; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 haematopoietic disorder; dyslipidaemia; wasting disorder; gene; ss.
                                                                                                                                                                               Sequence 2422 BP; 596 A; 712 C; 692 G; 422 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                       2.1%; Score 43; DB 1; Length 2422;
58.0%; Pred. No. 4.3e-05;
trive 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alsobrook JP, Burgess CE, Edinger SR, Gerlach VL, Ji M, Li L, Macdougall JR, Miller CE, Millet I, Patturajan M, Rieger DK, Schore P, Shenoy SG, Smithson G, Spytek KA, Voss EZ, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human NOV8a encoding cDNA SEQ ID NO:33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "NOV8a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADC24226 standard; cDNA; 2422 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAR-2002; 2002US-0361974P.
19-MAR-2002; 2002US-0365477P.
22-MAR-2002; 2002US-036561F.
66-AUG-2002; 2002US-0401661P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAR-2003; 2003WO-US006951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAR-2003; 2003US-00401661.
                                                                                                                                                                                                                       Query Match
Best Local Similarity 58.01
Best Local 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1072 TCTGTGTCTGT 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1826 rccardrdrdr 1816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .1375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003076584-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-SEP-2003.
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   8X333333
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The present invention describes novel human proteins, designated NOVX proteins. The NOVX sequences have cardiant, antiarteriosclerotic, proteins. The NOVX sequences have cardiant, antiarteriosclerotic, hypotensive, vasotropic, dermacological, anorectic, immunosuppressive, cytostatic, antiinfertility, haemaclogical, anorectic, immunosuppressive, cytostatic, antiinfertility, haemaclogical, anorectic, immunosuppressive, cytostatic, antiinfertility, haemaclogical, anorectic, inductor an expension as thereby and can be used in gene therapy. The NoVX sequences can be used with NoVX. The NoVX proteins and nucleic acids pathology associated with NoVX sequences, including cardiomyopathy, conditions associated with NoVX sequences, including cardiomyopathy, conditions associated with NoVX sequences, including cardiomyopathy, stenosis, scleroderma, obesity, metabolic disturbances associated with Compenital adrenal hyperplasia, prostate cancer, diabetes, metabolic discorders, neoplasm, adenocarcinoma, fertility, haemophilia, graft versus host disease, AlDS, corportial asthma, crofn's disease, multiple sclerosis, infectious disease, anorexia, neurodegenerative disorders (e.g. Alzheimer's disease, compenied proteins can also be used as immunogens to produce antibodies and as vaccines. The sequences may further be used in chromosome mapping, and in forensic identification of a biological sample. The present typing), and in forensic identification of a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             952 TGTTGAGAATTATCAATGAGCAGTGTTTGTGGATTCTTGTTATCTTGCACTTGTGAAGTG 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New NOVX polypeptides and nucleic acids, useful for diagnosing or treating e.g. cardiomyopathy, atherosclerosis, hypertension, scleroderma, obesity, prostate cancer, AIDS, bronchial asthma, Crohn's disease, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Truncated tissue factor; tissue factor binding ligand; coagulation; disease-associated vasculature; tumour; benign prostatic hyperplasia; diabetic-retinopathy; vascular restenosis; arteriovenous malformation; AVM; meningioma; hemangioma; neovascular glaucoma; psoriasis; synovitis; dermatitis; endometriosis; angicilaroma; rheumatoid arthritis; atheore, atheore, corneal graft neovascularisation; haemophilic joint; hypertrophic scar; Osler-Weber syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1946 IGTGCATATCTCTATGTGCGTGTGCATCGGTGTTTTGCGTATCTCTGTGTGACCATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2422 BP; 596 A; 712 C; 692 G; 422 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
2.1%; Score 43; DB 1; Length 2422;
Best Local Similarity 58.0%; Pred. No. 4.3e-05;
Matches 76; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding coagulation factor VII/VIIa.
                                                                                                                                                                                                               Claim 20; SEQ ID NO 33; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX15425 standard; DNA; 2462 BP.
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                    WPI; 2003-722330/68.
                                                                                                                                                                multiple sclerosis.
                                         P-PSDB; ADC24227.
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2007 IGIGCATATCTCTATGTGCGTGTGCATCGGTGTGTTTGCGTATCTCTGTGTGACCATCTG 1948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a coagulation factor. The specification which comprises a binding region which binds to vasculature, particularly of tumours, and a tissue factor construct. The binding ligands can be used for stimulating coagulation in disease-associated vasculature, particularly for the treatment of tumours. The products can also be used for treating e.g. benign prostation hyperplasia, diabetic-retinopathy, vascular restenosis, arteriovenous malformations (AWM), meningioma, neovascular glaucoma, psoriasis, symovitis, dermatitis, endometriosis, angiotibroma, rheumatoid arthritis, atheroscelotic plaques, corneal graft neovascularisation, haramophilic joints, hypertrophic scars, OSEL-Meber syndrome, pyoganic aranuloma retrolental fibroplasia, scleroderma, trachoma, or vascular adhesions. The products can also be used in binding assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            952 TGTTGAGAATTATCAATGAGCAGTGTTTGTGGATTCTTGTTATCTTGCACTTGTGAAGTG 1011
                                                                                                                                                                                                                                                                                                                                                                                       Tissue factor binding ligands - comprising first binding region which binds to vasculature, particularly of tumours, and tissue factor
pyogenic granuloma retrolental fibroplasia, scleroderma, trachoma, vascular adhesion, coagulation factor, factor VII/VIIa, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Truncated tissue factor; tTF; human; blood coagulation; tumour vasculature; bispecific antibody; targetting; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2462 BP; 590 A; 724 C; 721 G; 427 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1%; Score 43; DB 1; Length 2462;
58.0%; Pred. No. 4.3e-05;
ive 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding Factor VII/VIIa, SEQ ID NO:25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA12968 standard; DNA; 2462 BP.
                                                                                                                                                            95US-00479733.
                                                                                                                                                                                             92US-00846349.
                                                                                                                                                                                                             94US-00205330.
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es 76; Conservative
                                                                                                                                                                                                                                                               (SCRI ) SCRIPPS RES INST. (TEXA ) UNIV TEXAS SYSTEM.
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                                                                                                                                                                                                                                                                                                                       Thorpe PE;
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                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-189722/16.
                                                                                                                                                                                                                                                                                                                       Edgington TS,
                                                    Homo sapiens
                                                                                                                                                            17-JUN-1995;
                                                                                                                                                                                             05-MAR-1992;
                                                                                                                                                                                                                 02-MAR-1994;
                                                                                                                                                                                                                                  11-JUL-1994;
                                                                                       US5877289-A.
                                                                                                                          02-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                  construct.
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Db
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The invention relates to the induction of blood coagulation specifically within tumour vasculature. This is achieved by the use of a bispecific molecule, which comparises a region capable of binding to intratumoral vascular or stromal celle linked to a coagulation factor or to a region capable of binding to a coagulation factor. An example of such a region capable of binding to a coagulation factor. An example of such a tumour antigen, and the other arm binds a coagulation factor. The capable of certain proteins (tumour antigens) is upreplated in tumour vasculature; such proteins (tumour antigens) is upreplated in tumour vasculature; such proteins (tumour antigens) is upreplated in tumour vasculature. The capable for bispecific molecule in order to target coagulation to the bispecific molecule in order to target coagulation to the uncorporated into the bispecific molecule in order to target coagulation to to tumour vasculature. The coagulation factor-binding portion of the bispecific molecule in order to target coagulation to the invention is a trundated form (tFF). A preferred form of TF used in the invention is a trundated form (tFF). A preferred form of TF used in the invention is a trundated form (tFF) an associated with a phospholipid surface for coagulation of cagniation to occur. However, associated with a phospholipid surface for coagulation to occur. However, and thinking of tFF to tumour vasculature via a tumour anticom/tFF bispecific anticody brings tFF into close enough proximity with the call membrane to cause benign growths, prostatic hypertrophy, restenosis, psortasis, but tumour vasculature, minimising side effects. Such kits are likely to be effective against many different types of cancer. Sequences AAAL2945- AAAL2954-AAL2954 and AAAL2971 AAL2972 represent Postpructs symmetry or the present invention to generate constructs in exemplifications of the present invention to generate constructs in the present invention to the present invention or tTF dimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            952 TGTTGAGAATTATCAATGAGCAGTGTTTGTGGATTCTTGTTATCTTGCACTTGTGAAGTG 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2007 TGTGCATATCTCTATGTGCGTGTGCATCGGTGTGTTTGCGTATCTCTGTGTGACCATCTG 1948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kit for inducing coagulation in tumor vasculature, useful for treating malignant or benign growths, contains ligand, linked to coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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58.0%; Pred. No. 4.3e-05;
ative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 2462 BP; 590 A; 724 C; 721 G; 427 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 9; Col 127-130; 86pp; English.
vascularised tumour; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 malignant or benign growths, contagent, that targets tumor marker.
                                                                                                                                                                                    95US-00479727.
                                                                                                                                                                                                                                                        94US-00205330.
94US-00273567.
                                                                                                                                                                                                                               92US-00846349.
                                                                                                                                                                                                                                                                                                                          TEXAS SYSTEM.
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                                                                                                                                                                                                                                                                                                                       (TEXA ) UNIV TEXAS SYSTEM (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-269871/23.
                                             Homo sapiens.
                                                                                                                                                                                    07-JUN-1995;
                                                                                                                                                                                                                                 05-MAR-1992;
                                                                                                                                                                                                                                                                            11-JUL-1994;
                                                                                        US6036955-A
                                                                                                                                      14-MAR-2000
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This is the coding sequence for Factor VII/VIIa, a vitamin-K-dependent coagulation factor. This coagulation factor can be used in the formation of coagulation factor. This coagulation factor can be used in the formation of coagulations. The sequence can be used in the method for delivering a coagulation to a tumour-associated vasculature binding ligand consists of a binding region that binds to a surface.

Cell, intratumoural vasculature or tumour associated strong. The binding region is linked to a coagulation second binding region of an antibody. The method is used for cell, intratumoural vasculature or tumour associated strong. The binding region of an antibody. The method is used for an antigen binding region of an antibody. The method is used for an antigen binding region of an antibody. The method is used for associated vasculature which is benign or ampligant. The method can be used to treat cancer by promoting specific blood coagulation in the vasculature which is benign or malignant. The method can be used to treat tumour relative to the vasculature in nontumour sites. Vascularised tumours are usually solid tumours, particularly carcinomas which require a vascular component to provide oxygen and nutrients. The usual to treat benign and malignant diseases with a vascular restenosis, arteriovenous malignant, hasmangiona, heavenagine, necessariated agents such as activated plastis. Certain cells and disease-associated agents such as activated plastis. Certain disease-associated agents such as activated plastises and in different tumours, making it possible to treat numerous diseases and different types of cancer with one pharmaceutical, therefore an agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vitamin-K-dependent coagulation factor; tumour associated vasculature, carcinoma; benign prostatic hyperplasia; diabetic retinopathy; vascular restenosis; arteriovenous malformation; meningoma; haemangioma; neovascular glaucoma; psoriacis; cytostatic; antidiabetic; vasotropic; ophthalmological; antipsoriatic; factor VII/VIIa; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bispecific binding ligands for promoting blood coagulation in a tumor associated vasculature are useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vitamin-K-dependent coagulation factor VII/VIIa coding sequence.
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                                                                                                                                                                                                             AAZ56118 standard; DNA; 2462 BP
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94US-00273567.
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                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
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1887 TCCATGTGTGT 1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thorpe PE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Edgington TS,
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11-JUL-1994;
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27-MAR-2000
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does not need to be tailored to each individual disease or specific tumour type. (Updated on 15-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 6Bi-ii; 60pp; English.
                                                                                                                                                                                                                            Human factor VII coding sequence.
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                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                            16-MAR-2000; 2000WO-US006934.
                                                                                                                                                                          AAA54032/c
ID AAA54032 standard; DNA; 2462
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                                                                                                                                           1887 rccardigidi 1877
                                            Local Similarity 58.0
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                                                                                                                                                                                                                                                                                              WO200054787-A1.
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952 TGTTGAGAATTATCAATGAGCAGTGTTTGTGGATTCTTGTTATCTTGCACTTGTGAAGTG 1011 2007 TGTGCATATCTCTATGTGCGTGTGCATCGGTGTTTGCGTATCTCTGTGTGACCATCTG 1948 Vitamin K dependent protein, VKDP; gamma-carboxylation, chimeric protein, fusion protein, coagulation factor; Factor X; Factor VII; Protein S; Factor IX; Protein C; prothrombin; blood clotting; haemophilia; human; Efficient processing and release of mature two-chain factor X into the circulation requires: removal of the signal sequence; formation of disulfide bonds; modification of amino terminal glutemic acid residues, to gamma-carboxyglutemic acid, modification of one aspartic acid, in the first epidermal growth factor (EGF) domain to Beta-hydroxyaspartic acid, removal of N- and O-linked oligosaccharides to the activation peptide; removal of an internal tripeptide to yield two-chain factor X and removal of the propeptide just prior to secretion. While some of these modifications do not appear essential for factor X function the removal of the signal sequence, propeptide, internal tripeptide and full gammacarboxylation are all steps which are important requisites for the production of biologically active factor X/FXa. Isolated chimeric Chimeric DNA for optimizing gamma carboxylation of vitamin K-dependent protein useful for treating diseases associated with the protein, comprises sequence encoding propeptide fused to sequence encoding the Gaps ö 2.1%; Score 43; DB 1; Length 2462; 58.0%; Pred. No. 4.3e-05; tive 0; Mismatches 55; Indels Sequence 2462 BP; 590 A; 724 C; 721 G; 427 T; 0 U; 0 Other; Stafford DW;

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952 TGTTGAGAATTATCAATGAGCAGTGTTTGTGGATTCTTGTTATCTTGCACTTGTGAAGTG 1011
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polymucleotides are described which encode a propeptide fused to a nucleic acid sequence encoding a vitamin K-dependent protein (VKDP). The fusion proteins encoded are vitamin K-dependent protein gamma-carboxylation enhancers and are useful for optimising the gamma-carboxylation of a VKDP to produce a fully gamma-carboxylated VKDP. The fusion proteins and recombinant cells expressing them are useful for alleviating a VKDP associated disease. The fusion constructs result in the production of fully gamma-carboxylated mature VKDPs, which are biologically active. The invention encompasses all combinations of propeptide sequences (modified or not) and VKDP's. This sequence encodes the signal, propeptide and mature protein sequence of human Factor VII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue factor protein, truncated tissue factor; tTF; cytostatic; coagulant; diabetic retinopathy; arteriovenous malformation; meningioma; hemangiona; neovascular glaucoma; psoriasis; synovitis; endometriosis; hemophylic joint; hypertrophic scar; vascular adhesion; tumour; cancer; ligand; human; factor VII; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2462;
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Local Similarity 58.0%; Pred. No. 4.3e-05;
es 76; Conservative 0; Mismatches 55; Indels
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94US-00205330.
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The present invention relates to a binding ligand with a first binding region that is operatively linked to either a coagulation factor or a second binding region that binds to a coagulation factor. The first binding region is all or part of an antibody. An example of a coagulation factor for use in the invention is human truncated tissue factor for use in the invention is human truncated tissue factor for protein (see Abhl5019). The binding ligand of the mature tissue factor protein (see Abhl5019). The binding ligand of the mature tissue factor protein (see Abhl5019). The binding ligand of the mature tissue factor simulating coagulation in vasculature associated diseases. Particularly, the binding ligand is useful for treating both benign and malignant diseases that have a vascular component. These classes include benign growths (e.g. BPH), diabetic retinopathy, arteriovenous malformations, meningioma, hemangioma, neovascular coagulations, synovitis, endometriosis, hemophylic joints, hypertrophic scars or vascular adhesions. The present binding ligands of fer the advantage that even limited damage to the tumour vasculature could produce an avalanche of tumour cell death because each capillary provides oxygen and nutrients for thousands of tumour cells. The present condition factor VII/VIIa, This factor was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2007 IGTGCATATCTCTATGTGCGTGTGCATCGGTGTGTTTGCGTATCTCTGTGACCATCTG 1948
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stomach, lung, prostate, pancreas, carcinoma, antitumour, cancerous,
cytostatic, gene therapy, antineoplastic, Wilm's tumour, adenocarcinoma,
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58.0%; Pred. No. 4.3e-05;
tive 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2462 BP; 590 A; 724 C; 721 G; 427 T; 0 U; 0 Other;
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2000US-0234009P.
2000US-0234034P.
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20-SEP-2000;
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25-SEP-2000;
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The present invention describes a method (M1) for screening for an antinoplastic agent. The method involves exposing cells to a chemical agent neoplastic activity, determining a chemical agent comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95 identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the channeal structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, concert to properties of the agent. All can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, concert to minimize the cancer, adenocardinoma, carcinoma, cancer, squamous call carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endress G, Horrigan S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2462 BP; 590 A; 724 C; 721 G; 427 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carter KC, Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 5592; 44pp; English.
                                             25-58P-2000, 200005-02350807-25-58P-2000, 200005-02350807-25-58P-2000, 200005-02350807-25-58P-2000, 200005-02350807-25-58P-2000, 200005-02350807-27-58P-2000, 200005-023511P-27-58P-2000, 200005-0235840P-27-58P-2000, 200005-0235840P-28-58P-2000, 200005-0235840P-28-58P-2000, 200005-0235840P-28-58P-2000, 200005-0235841P-29-58P-2000, 200005-0236034P-29-58P-2000, 200005-0236034P-29-58P-2000, 200005-0236034P-29-58P-2000, 200005-0236034P-29-58P-2000, 200005-0236034P-29-58P-2000, 200005-0237034P-29-58P-2000, 200005-0237034P-29-2000, 200005-0237034P-29-2000, 200005-0237034P-20005-0237034P-2000, 200005-0237034P-2000, 200005-0237034P-2000, 200005-0237034P-2000, 200005-0237034P-2000, 200005-0237034P-2000, 200005-0237034P-2000, 200005-0237504P-2000, 200005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-0237504P-20005-023
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03-OCT-2000; 2000US-0237608P.
01-NOV-2000; 2000US-0244667P.
01-NOV-2000; 2000US-0245084P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Augustus M,
Weaver Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AVAL-) AVALON PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-188264/24.
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Soppet DR,
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2.1%; Score 43; DB 1; Length 2462; 58.0%; Pred. No. 4.3e-05; tive 0; Mismatches 55; Indels

Query Match
Best Local Similarity 58.0
Matches 76; Conservative

à Db

0; Gaps

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The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumouur in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatocropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying the progression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism. Note: The sequence data obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.
                                                                                                                                                                                                      Gene, liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      952 TGTTGAGAATTATCAATGAGCAGTGTTTGTGGATTCTTGTTATCTTGCACTTGTGAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2007 IGTGCATATCTCTATGTGCGTGTGCATCGGTGTTTGCGTATCTCTGTGTGACCATCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 43; DB 1; Length 2462 llarity 58.0%; Pred. No. 4.3e-05; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vockley JG;
                                                                                                                                                               Gene #2251 used to diagnose liver cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Horne D, Alvares C, Peres-Da-Silva S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 2251; 298pp; English
                                        ABN95753 standard; DNA; 2462 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                     02-OCT-2001; 2001WO-US030589.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-OCT-2000; 2000US-0237054P
                                                                                                                         13-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENE LOGIC INC.
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Best Local Similarity
Matches 76; Conservat
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                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                 ABN95753;
                      ABN95753/C
RESULT 12
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Page 10

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It is used in a DNA construct which contains a nuclectide sequence encoding a protein which, on activation, has the same biological activity for blood coagulation as Peator Ila. The nucleotide codes at least partially for Factor VII and comprises sequence encoding a calcium binding domain joined to a sceond sequence downstream of this encoding a catalytic domain for the serine proteins activity of Factor VIII. The calcium binding domain comprises a gene encoding Factor VIII. TX, Protein C, prothrombin or Protein S. The construct is used to transfect Nots cells to produce the protein which, on activation, yields Factor VIII. (Updated on 31-oCT-2002 to add missing OS field.) (Updated on 25-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The partial factor VII cDNA sequence is from cDNA clonl lambda VII2463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gray CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA construct used to transfect hosts - to produce protein which activates to give factor VIIa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hagen FS, Murry MJ, Berkner KL, Insley MY, Woodbury RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . Match 2.1%; Score 43; DB 1; Length 2483; Local Similarity 58.0%; Pred. No. 4.4e-05; es 76; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2483 BP; 611 A; 725 C; 720 G; 427 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Factor VII; Factor VIIa; DNA construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1B; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Factor VII cDNA of lambda VII2463.
                                                                                                                                                                                                                                                                                                           AAN60064 standard; DNA; 2483 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAY-1991 (first entry)
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                                                                                               1072 TCTGTGTCTGT 1082
                                                                                                                                                       1887 rccardrdrdr 1877
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1986-326899/50,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAP60056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-APR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-APR-1985;
16-DEC-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
31-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP200421-A
                                                                                                                                                                                                                                                                                                                                                                      AAN60064;
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                                                                                                                                                                                                                                                   RESULT 13
AAN60064/c
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The partial factor VII cDNA sequence is produced by joining portions of cDNA clones lambda VII2115 and lambda VII1923. It is used in a DNA construct which contains a nucleotide sequence encoding a protein which, on activation, has the same biological activity for blood coagulation as Factor IIa. The nucleotide codes at least partially for Factor VII and comprises a sequence encoding a calcium binding domain joined to a scend sequence downstream of this encoding a catalytic domain for the serine protease activity of Factor VIIa. The calcium binding domain comprises a gene encoding Factor VII, IX, X, Protein C, prothrombin or Protein S. The construct is used to transfect host cells to produce the protein which, on activation, yields Factor VIIa. (Updated on 31-OCL2 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hagen FS, Murry MJ, Berkner KL, Insley MY, Woodbury RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2177 BP; 569 A; 624 C; 605 G; 379 T; 0 U; 0 Other;
                                                                                                                                                                                   Factor VII; Factor VIIa; DNA construct.
                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1A; 55pp; English.
              AAN60063 standard; cDNA; 2177 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                     85US-00724311.
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                                                                                (revised)
(revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                  Partial Factor VII cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1986-326899/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAP60055
                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                       17-APR-1985;
16-DEC-1985;
                                                                                                                                                                                                                                                                                                                                                                                      16-APR-1986;
                                                                                25-MAR-2003
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1935 IGCATATCTCTATGTGCGTGTGCATCGGTGTGTTTGCGTACTCTGTGTGACCATCTGTGT 1876

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1695 IGCATATCTCTATGTGCGTGTGTGTGTTTTGCGTACTCTGTGTGACCATCTGTGTGT 1636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA construct used to transfect hosts - to produce protein which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berkner KL, Insley MY, Woodbury RG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Factor VII; Factor IX; DNA construct.
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7. .1368
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Factor IX/Factor VII cDNA fusion.
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                                                                                                                                                                                                                                                                                                AAN60065 standard; DNA; 2438 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activates to give factor VIIa.
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85US-00810002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                1635 GTGCATCC 1628
                                                                                           1094 CTGTGTTC 1101
                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1986-326899/50.
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31-OCT-2002
23-MAY-1991
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16-DEC-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
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1034 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTCTGTGTCTGTGTCTTGTGTGT 1093

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The present invention describes a library of human polynucleotides comprising the sequences given in AAZ12532 to AAZ1779 Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being ancerous, where the gene product is encoded by one of the 548 polynuclectide sequences given in AAZ12522 to AAZ17779. The polynuclectides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides for experimental, diagnostic and the arrays for diagnostics (which may be used to determine function of an encays for diagnostics (which may be used to determine function of an encay and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer, The polynucleotides can also be used to screen for and lung cancer. The polynucleotides can also be used to screen for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human genes and their expression products which are differentially expressed in different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J; Jises K, Randazzo F, Kennedy GC, Pot D, Kassam A; nanac R, Crkvanjakov R, Diokson M, Drmanac S, Labat I; Kita D, Garcia V, Jones WL, Stache-Crain B;
                                                                                                                                                                                                                                                                                 Human, gene, gene expression product, diagnosis, therapy, probe, detection, mapping, tissue typing, profiling, forensic, cancer, genetic analysis, colorectal cancer, breast cancer, lung cancer, ss.
                                                                                                                                                                                                                                                Human gene expression product cDNA sequence SEQ ID NO:94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 683; 2479pp; English.
                                                                                                                                AAZ12625 standard; cDNA; 300 BP.
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98US-0080114P.
98US-0080515P.
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98US-0105234P.
98US-0105877P.
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Lamson G, Drmanac R,
Leshkowitz D, Kita D,
  1094 CTGTGTTC 1101
                                    1875 Grécarce 1868
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Reinhard C,
                                                                                                                                                                                                                                                                                                                                                                                                   WO9938972-A2.
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24-FEB-1998;
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21-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, S' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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60.6%; Pred. No. 2.1;
tive 1; Mismatches 25; Indels 0; Gaps
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Best Local Similarity 78.0%; Pred. No. 0.026;
Matches 39; Conservative 0; Mismatches 11; Indels
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                                                                                                                Sequence 300 BP; 41 A; 84 C; 105 G; 68 T; 0 U; 2 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein 5' EST, SEQ ID NO: 20254.
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peptide analogues and antagonists
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS9464 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at the printed sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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1.3%; Score 25.4; DB 1; Length 237;
Best Local Similarity 51.3%; Pred. No. 2.3;
Matches 59; Conservative 0; Mismatches 56; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 237 BP; 97 A; 34 C; 82 G; 24 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                             DNA encoding novel human diagnostic protein #4731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 4731; 103pp; English.
                                                                                                                                                AAS68927 standard; cDNA; 237 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US008631.
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                                                                                                                                                                                                                                      13-FEB-2002 (first entry)
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968 TGAGCA 973
                                     128 TGAGCA 133
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1362 CATTITIGAGITICIATIGGAAAAGICAGGIGIAATICIAAIACAICIGCCITIATAIGIT 1421

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Local Similarity 60.69

Query Match

Matches

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236 CATITITGGTTTGCATTGGGTTGCTGCTGGGAGAACCAAATGTCTGGCAGCTTCTTGGTC 177 ò g

AAA54035 standard; DNA; 1843 BP. AAA54035

AAA54035;

(first entry) 08-FEB-2001 Human protein C coding sequence.

Vitamin K dependent protein, VKDP, gamma-carboxylation, chimeric protein, fusion protein, coagulation factor, Factor X, Factor VII, Protein S, Factor IX, Protein C, prothrombin, blood clotting, haemophilia, human,

Homo sapiens.

WO200054787-A1.

21-SEP-2000.

16-MAR-2000; 2000WO-US006934.

99US-0124609F. 16-MAR-1999;

(CHIL-) CHILDRENS HOSPITAL PHILADELPHIA. (UYNC-) UNIV NORTH CAROLINA.

High KA, Camire RM, Larson PJ, Stafford DW;

WPI; 2000-638152/61.

Chimeric DNA for optimizing gamma carboxylation of vitamin K-dependent protein useful for treating diseases associated with the protein, comprises sequence encoding propeptide fused to sequence encoding the 

Disclosure; Fig 6Ei-ii; 60pp; English.

Efficient processing and release of mature two-chain factor X into the circulation requires; removal of the signal sequence; formation of circulation requires; removal of the signal sequence; formation of discultide bonds; modification of amino terminal glutamic acid residues; to gamma-carboxyglutamic acid; modification of one aspartic acid; modification of one apparent acid; modification of N- and O-linked oligosaccharides to the activation peptide; removal of an internal tripptide to yield two-chain factor X and removal of the propeptide just prior to secretion, while some of these modifications do not appear essential for factor X function the removal of the signal sequence, propeptide, internal tripeptide and full gamma-carboxylation are all steps which are important requisites for the propential and relative factor X/FXa. Isolated chimeric polymucleotides are described which encode a propeptide fused to a nucleic acid sequence encoding a vitamin X-dependent protein (WDP). The fusion proteins encoded are vitamin X-dependent protein (WDP). The fusion proteins and recombinant cells expressing them are useful for allowiating a WDP to produce a fully gamma-carboxylated which are such in the production of fully gamma-carboxylated mature WDPP, which are broduction of fully gamma-carboxylated mature WDPP, which are broduction of fully gamma-carboxylated mature WDPP, which are broduction of mid WDPP's. This sequence encodes the propertial processing them are useful in the production of fully gamma-carboxylated mature WDPP, which are processing the processing them are processed to the production of mid WDP's. This sequence encodes the processing them are processed to the propertion of mid WDP, and mid and mature worked the processing them are processed to the processing them are processed to the processed to the processed to the processed to the processed to the processed to the processed to the processed to the processed to the processed to the processed to the processed to the processed to the processed to the pro the signal, propeptide and mature protein sequence of human protein C

Sequence 1843 BP; 417 A; 530 C; 564 G; 332 T; 0 U; 0 Other;

Query Match

1.3%; Score 25.2; DB 1; Length 1843;

1063 GIGIGIGIGICIGIGICIGIGICITIGIGIGICIGIGITCTCTCCCCCCTTTTTGATTTTTG 1122 0; Gaps 38; Indels 55.8%; Pred. No. 4.3; tive 0; Mismatches 48; Conservative Best Local Similarity Matches

AAF54050

AAF54050 standard; DNA; 1843 BP.

30-MAR-2001 (first entry)

Human protein C gene, SEQ ID NO:49.

Age-related gene regulation; gene expression; human protein C; hPC; S' UTR; 5' untranslated region; age-regulatable expression construct; PEA-3 element; polyoma virus activators 3; antisense therapy; entrombosis; cardiovascular disease; diabetes; Alzheimer's disease; parkinson's disease; cancer; osteoporosis; osteoarthritis; dementia; ds.

Homo sapiens.

40200075279-A2.

06-JUN-2000; 2000WO-US015728.

09-JUN-1999; 99US-00328925.

(UNMI ) UNIV MICHIGAN.

Kurachi K, Kurachi S;

WPI; 2001-061708/07.

New regulatory elements that control age-related gene expression, useful in gene therapy and for reducing Factor IX expression.

Disclosure; Fig 12; 225pp; English.

The invention relates to nucleic acid sequences which regulate gene expression in an age-related manner and/or in a liver-specific manner. The invention identifies regions of the human factor IX (hFIX) gene, and a region of the human protein C (hPC) gene, which are age-related carginatory sequences. The hFIX age-related regulatory sequences are designated AES' (AAF54016) and AE3' (AAF54017) and are found in the 5' UTR (at position 2164-2165 of AAF54018) and are found in the 5' UTR (at position 2164-2165 of AAF54018) and are found in the 5' UTR (at position 2164-2165 of AAF54018) and are found in the 5' UTR (at position 2164-2165 of AAF54018) and are found in the 5' UTR (at position 2164-2165) and are found in the 5' UTR (at position 2164-2165) are stabiliste hFIX mRNA, and AE3' acting to increase hFIX mRNA levels, over time. AE5' also directs liver-specific expression. The hFC gene age-related regulatory sequence is found in the 5' UTR (AAF54081), and contains two PEA-3 (polyoma virus activator 3) elements 5' GAGGAA-3' and 5'-CAGGAA-3'. The age-related regulatory sequence of the invention, along with their homologues, variance and fragments, may be used in the construction of recombinant expression vectors for the expression of a desired sequence in an age-related fashion in a host coll. Preferred target genes for expression in such age-regulatable expression vectors include those encoding proteins involved in blood anti-coagulants protein and areporter proteins such as luciferase.

10664775-3.rng

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Preferred promoters for use in such age-regulatable expression vectors include the human factor IX promoter, the TJ promoter, the TJ promoter. The axpression vectors of the invention may be used in gene therapy to provide age-related and/or liver specific expression of target genes. Age-regulatable constructs may be used in the treatment of such age-related conditions such as thrombosis, cardiovascular disease, diabetes, Alzheimer's disease, Parkinson's disease, cancer, osteoporosis, osteoatrhritis and dementia. Specifically, they may be used to express factor IX antisense mRNA in the treatment of thrombotic conditions associated with the natural age-related rise in factor IX expression. Transgenic cells or animals that contain vectors of the invention are useful as models of these diseases, in screening for potential therapeutic agents and for studying normal processes such as equences, are useful as probes to detect, isolate or identify other such sequences in samples. The present sequence represents the hPC
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ö 1063 GIGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTCTCTCCCCCTCTTTTGATTTTTG 1122 0; Gaps DB 1; Length 1843; Sequence 1843 BP; 417 A; 530 C; 564 G; 332 T; 0 U; 0 Other; 38; Indels Score 25.2; Di Pred. No. 4.3; 0; Mismatches 1123 GCCTGGAATTATTTATTCATATT 1148 1778 rcgregrrererirriahrerrrr 1753 1.3%; 48; Conservative Query Match Best Local Similarity Matches

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Gene #3673 used to diagnose liver cancer. ABN97175 standard; DNA; 1843 BP 13-AUG-2002 (first entry) ABN97175; 

Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism. Homo sapiens.

WO200229103-A2.

11-APR-2002.

02-OCT-2000; 2000US-0237054P

02-OCT-2001; 2001WO-US030589.

(GENE-) GENE LOGIC INC Horne D, Alvares C,

Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample. WPI; 2002-426119/45.

Peres-Da-Silva S, Vockley JG;

Claim 1; SEQ ID NO 3673; 298pp; English.

The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepstocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient involving detection the land

probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of

The present invention provides a number of single exon nucleic acid

Example 4; SEQ ID NO 20161; 658pp + Sequence Listing; English.

Human genome-derived single exon nucleic acid probes useful for analyzing

gene expression in human bone marrow.

Rank DR;

Chen W,

Hanzel DK,

WPI; 2001-488900/53.

(MOLE-) MOLECULAR DYNAMICS INC

1063 GTGTGTGTGTCTGTGTCTTGTGTGTGTGTGTGTTCTCTCTCCCCTCTTTTGATTTTTG 1122 expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well amarkers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism. Note: The sequence date for this patent did not form part of the printed specification, but was fip.wipo.int/pub/published\_pct\_sequences 0; Gaps Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss. Human bone marrow expressed single exon probe SEQ ID NO: 20161. Score 25.2; DB 1; Length 1843; Pred. No. 4.3; 0; Mismatches 38; Indels 0; Sequence 1843 BP; 417 A; 530 C; 564 G; 332 T; 0 U; 0 Other; 1123 GCCTGGAATTATTTATTCATATT 1148 1778 rccrccrcrrrrrrrrrrrrrr AAK45604 standard; DNA; 267 BP. 1.3%; 26-WAY-2000; 2000US-0207456P-30-UTM-2000; 2000US-00608408. 31-AUG-2000; 2000US-00632366. 21-SEP-2000; 2000US-0234687P-27-SEP-2000; 2000US-0236359P-30-JAN-2001; 2001WO-US000668. 04-OCT-2000; 2000GB-00024263. 04-FEB-2000; 2000US-0180312P (first entry) Local Similarity 55.8 nes 48; Conservative WO200157276-A2. Homo sapiens. 06-NOV-2001 09-AUG-2001 AAK45604; Query Match Matches RESULT 22 AAK45604 886666666666888 g à à g

1620 CCTGCTTTTGACCTGCCTTCTTCCCCTTCCTCTATTCCTTTGGTTTTTGCATAGTGTCTC 1679 1680 TGGCTTCCTGGATGTTTTATGCCTGGATTATTTAGACTTAACATTTTCTTTGACCAAGG 1739 ó cerrefected de la contraction Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer; The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention ceréérecrecrecreéreceirecréerérecrerrerrerecreirerecritirieere 257 Single exon nucleic acid probes for analyzing gene expression in human Gaps . Example 4; SEQ ID NO 19590; 650pp + Sequence Listing; English. DB 1; Length 267; ; Score 24.2; DB 1; Length 267; Pred. No. 5.2; 0; Mismatches 103; Indels Human brain expressed single exon probe SEQ ID NO: 19590. Sequence 267 BP; 3 A; 151 C; 4 G; 109 T; 0 U; 0 Other; Rank DR; AAK19599 standard; DNA; 267 BP. (MOLE-) MOLECULAR DYNAMICS INC. Chen W, 30-JUN-2000; 2000US-00608408. 03-AUG-2000; 2000US-00632866. 21-SEP-2000; 2000US-0234687P. 27-SEP-2000; 2000US-0234687P. 04-OCT-2000; 2000GB-00024263. 04-FEB-2000; 2000US-0180312P. 26-MAY-2000; 2000US-0207456P. 30-JAN-2001; 2001WO-US000667 Similarity 45.5%; (first entry) 86; Conservative TGTCAGTGA 1808 TTCCTGGGA 266 Hanzel DK, WPI; 2001-483446/52 WO200157275-A2. Homo sapiens. 05-NOV-2001 09-AUG-2001 258 AAK19599; 78 1800 198 Query Match Best Local Penn SG, brains. Matches RESULT 23 AAK19599 X S 셤 ò g à d ò 8

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1740 TATCCATTTCTTCTATCTTGTCTTCACTGCCTGAGATTCTCTCTTCTATCTTGTATTC 1799
                                    198 CCTCCTCCTCCTCCTCCTCCTCCTCCTCCACTGTTTCTCCTCCTTCTCCTTTTTCCTC 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined mucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
                                                                                                                                                                                                                                                                                                                                Human, single exon nucleic acid probe, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia, hypercholesterolaemia, coronary heart disease, ss.
                                                                                                                                                                                                                                                                                                  Human liver single exon probe, SEQ ID No 20284.
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236559P.
04-OCT-2000; 2000GB-00024263.
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DB 1; Length 267; Indels

Score 24.2; DB 1; Pred. No. 5.2; 0; Mismatches 103;

ch 1.2%; 1 Similarity 45.5%; 86; Conservative (

Local Similarity

Query Match Matches

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Sequence 267 BP; 3 A; 151 C; 4 G; 109 T; 0 U; 0 Other;

1620 CCTGCTTTTGACCTGCCTTCTTCCCCTTCCTTTTCCTTTGGTTTTTGCATAGTGTCTC 1679

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1680 TGGCTTCCTGGATGTTTTATGCCTGGATTATTTTAGACTTAACATTTTCTTTGACCAAGG 1739

10664775-3.rng

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associated with coronary heart disease. ABS25011-ABS51005 represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                            Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomcosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease; open reading frame; ORF.
                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon probe ORF from lung SEQ ID No 19867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
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                                                                                                                                DB 1; Length 267;
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45.5%; Pred. No. 5.2;
live 0; Mismatches 103; Indels
                                                                                               Sequence 267 BP; 3 A; 151 C; 4 G; 109 T; 0 U; 0 Other;
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2000US-00608408.
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21-SEP-2000; 2000US-023468TP.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                            Local Similarity 45.5
les 86; Conservative
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Spatially-addressable set of single exon nucleic acid probes, used to

measure dene express

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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising shaingle exon nucleic acid probes having one of roughleic acid probes for measuring gene expression in a sample derived from the 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12814 open reading framed derived from the 12614 probes. Also included are a matcroarray comprising the novel set of probes of the human lung; measuring set high stringency to a nucleic acid expressed in the human lung; measuring specific production to a sample acid expressed in the human lung; measuring the label derectably bound to each probe of the array, identifying exons in a eutsavotic genome, comprising (a) and producting at least one exon from genomic sequences of the eutsavote, and (b) detecting specific hybridistation of detectably the above mentioned microarray, assigning exons to a single exon probe, laving a fragment identical to the predicted exon, the probe is included in a the above mentioned microarray, assigning exons to a single exon probe, comprising (a) identifying the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarray when any and probe with the exon, where a common pattern of a probes/open reading frames (ORF). The probes are used for gene expression of the exons in the second to the exons should be assigned to a single gene, a peptide comprising or analysis, and for identifying exons in a gene, particularly using human lung derived many and for the study of lung diseases such as assigned to a single gene, a peptide comprising on the exons in the second of the exons in the second of the exons in a gene, as the accordance of the prince of analysis, and for identifying exons in a gene, particularly using human lung derived many hypertension and hypertension and hypertension pulmonary dysplates, pulmonary dysplates, pulmonary dysplates, pulmonary dysp
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                 Claim 4; SEQ ID NO 19867; 634pp; English.
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Best Local Similarity 45.5%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' - and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence from a human clone which was used in homology searches to identify the clone. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381 ATTCAATTTTGGAGAGTTTCATAGGGTGCTGACAAGAAGGTACAGTCTTTGTGTTTTTGGT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 830 Primers useful for synthesizing full length cDNA clones and their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                         kawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
                                                                                                                                                                                                                                                                                                 Example 11; SEQ ID NO 2040; 1380pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
                   Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
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Human cDNA clone representative sequence, SEQ ID NO: 2040.
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                                                                                                                                      99JP-00194486.
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                                                                                                                                               11-JAN-2000; 2000JP-00118774
02-MAY-2000; 2000JP-00183765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       441 GAAATAGICIGIAAA 455
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                                                                                                                                                                                                         Nishikawa T,
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                                                                                                                                     08-JUL-1999;
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                                            Homo sapiens.
                                                                 EP1130094-A2.
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                                                                                        05-SEP-2001.
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Gaps

0;

DB 1; Length 868;

Sequence 868 BP; 199 A; 220 C; 254 G; 190 T; 0 U; 5 Other;

1.2%; Score 23.8; 57.3%; Pred. No. 9;

381 ATTCAATTTTGGAGAGTTTTCATAGGGTGCTGACAAGAAGGTACAGTCTTTGTGTTTTTGGT 440 

441 GAAATAGTCTGTAAA 455

167 GCTTTCCTTTTTÄÄÄ 181

0; Mismatches 32; Indels

43; Conservative

Local Similarity

Human, cytosine methylation, 5'-CpG-3', uracil, cytosine, diagnosis, drug, side effect, cancer, central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP, cell differentiation; ds.

01-SEP-2001; 2001WO-EP010074. 05-SEP-2000; 2000DE-01044543

WO200218632-A2

Homo sapiens.

01-SEP-2000; 2000DE-01043826

Ş.

Oligonucleotide for detecting cytosine methylation SEQ ID NO 34557.

ABQ47966 standard; DNA; 612 BP

12-JUL-2002 (first entry)

ABQ47966;

The invention relates to primers for synthesising full length CDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for Synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a CDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from BPO

830 Primers useful for synthesizing full length CDNA clones and their use

Claim 2; SEQ ID NO 91; 1380pp + Sequence Listing; English.

in genetic manipulation.

Hayashi K, Ishii S, Kawai Y; K, Kojima S, Otsuki T, Koga

Ota T, Nishikawa T, Isogai T, Wakamatsu A, Sugiyama T, Nagai

WPI; 2001-524255/58.

07-JUL-2000; 2000EP-00114089.

05-SEP-2001.

11-JAN-2000; 2000JP-00118774. 02-MAY-2000; 2000JP-00183765.

08-JUL-1999;

(HELI-) HELIX RES INST.

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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-0pG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligomochecides and/or peptide-nucleic acid (DNA) oligomers and the degree of hybridisation to both classes is determined from the label on the run of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP, s); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for disclosure of the invention
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drug; side effect; cancer; central nervous system; cardiovascular;
gastrointestinal; respiratory system; single nucleotide polymorphism;
SNP; cell differentiation; ds.
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                                                                                                                                                                         Olek A, Piepenbrock C, Berlin K, Guetig D;
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                                                              (EPIG-) EPIGENOMICS AG.
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methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligoners and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligoners, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gasteointesinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNPs); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. Apgl3410-ABG$121 represent genomic DNA sequences used to illustrate the method in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1499 GIGGGGAGTITCITITCCGGTCCAAICIATITGGIGTITIGIAIGCTICITGIACCTIGA 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1559 TAGGCATCTCTTTCTCAAGGTTAGGAAATTTTTCTTTTTTGGTTTTTCTTGAAAATATTTT 1618
                                                                                                                                                                                                                                                  Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 GGGGGTCGTTTTCGTTCGGGGTGATTTCGTTTTTTTGGGCGATGTTTTTATTTTTAGG 123
                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel method for determining the degree of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 pacecerritricerecerrecenareeceraterecritriararaaaaaaaaa
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46.2%; Pred. No. 11;
ive 0; Mismatches 91; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 612 BP; 236 A; 216 C; 72 G; 88 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                        Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                  Guetig D;
                                                                                                                                                                    Piepenbrock C, Berlin K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT40850 standard; cDNA; 306 BP
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                                                           01-SEP-2000; 2000DE-01043826.
05-SEP-2000; 2000DE-01044543.
                    01-SEP-2001; 2001WO-EP010074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 46.2%;
es 78; Conservative
                                                                                                                                                                                                                                                                           diagnosis and prognosis, com
from chemically treated DNA.
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                                                                                                                           (EPIG-) EPIGENOMICS AG.
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Matches
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Siphonaptera sp.

07-MAR-2002.

Vitamin K dependent protein; VKDP; gamma-carboxylation; chimeric protein; fusion protein; coagulation factor; Factor X; Factor VII; Protein S; Factor IX; Protein C; prothrombin; blood clotting; haemophilia; human;

Human factor X coding sequence.

08-FEB-2001

AAA54031;

Larson PJ, Stafford DW;

High KA, Camire RM,

CHIL-) CHILDRENS HOSPITAL PHILADELPHIA. UYNC-) UNIV NORTH CAROLINA.

99US-0124609P.

16-MAR-1999;

.6-MAR-2000, 2000WO-US006934.

WO200054787-A1. Homo sapiens.

21-SEP-2000.

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This sequence (nfSP8-299) encodes a flea midgut serine protease (PfSP8-99), and has been isolated from a flea cDNA library by PCR using primers AAT40862-63 and hybridisation with probe AAT40866, based on conserved serine protease sequences. The sequence contains sequence AAT4086 (nfSP8-186), which spans 2 conserved serine protease sequence AAT40826 (nfSP8-6), which spans 2 conserved serine protease sequence (N- and C-terminal regions) and internal sequence AAT40826, since the appropriate produce a recombinant vaccine for protection of domestic animals from flea infestation, or in isolation of protease-inhibitors which may be used in controlled release formulations to reduce the flea burden on and around the animal. The inhibitors may be included in insecticidal compositions to increase efficacy of other active compounds, by reducing proteolytic activity in the flea midgut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 CCAGGGTAGGGGCACTACCGCATTCCCTCTCTTCCAAACACTTCTATTTCTTGATTTC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 CYTGGCAAGTGTCTTTTCCACCATCCAATTCTCCTGCACACATCTGTGTTTCTACAATTC 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding Flea serine protease and aminopeptidase - useful in vaccines to protect animals from flea infestation.
                                                 *tag= a
'note= "back-translated from N-terminal part of PfSP8-99
(ARMO1205)
                                                                                                                                                             *tag= c
|hote= "back-translated from C-terminal part of PfSP8-99
|AAW01205|"
                                                                                                          /*tag= b
/note= "Corresponds to nfSP8-186 (AAT40826, claim 70)"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Hunter SW, Frank GR, Stiegler GL, Heath A; Dale B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.1%; Score 23; DB 1; Length 306; Best Local Similarity 58.5%; Pred. No. 12; Matches 38; Conservative 1; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 306 BP; 83 A; 30 C; 72 G; 56 T; 0 U; 65 Other;
               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 70; Page 182; 241pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAS4031 standard; DNA; 1507 BP.
                                                                                                                                                                                                                                                                                                                   94US-00326773.
95US-00482130.
95US-00484211.
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95US-00485455.
                                                                                                                                         299
                                                                                            91. .276
                                                                                                                                                        /*tag=
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Yamanaka M, Arfsten A,
                              1. 90
/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                 (HESK-) HESKA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAW01205
                                                                                                                                                                                                                      WO9611706-A1
                                                                                                                                                                                                                                                                                    18-OCT-1995;
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                                                                                                                                                                                                                                                                                                                   18-OCT-1994;
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                 Key
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AAA54031/c
ID AAA540:
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Efficient processing and release of mature two-chain factor X into the circulation requires; removal of the signal sequence, formation of circulation requires; removal of the signal sequence, formation of circulation of control certains globes, control control control circulation of N and olinked oligosacchaides to the activation peptide; control circulation of N and olinked oligosacchaides to the activation peptide; cemoval of an internal tripeptide to yield two-chain factor X and removal control appear essential for factor X function the removal control appear essential for factor X function the removal of the signal sequence, propeptide, internal tripeptide and full gammandications are all steps which are important requisites for the production of biologically active factor X/Fxx Isolated chimeric production of biologically active factor X/Fxx Isolated chimeric production of biologically active factor X/Fxx Isolated chimeric production of biologically active factor X/Fxx Isolated chimeric production of an WDP to produce a propebtide fused to a nucleic acid sequence encoding a vitamin K-dependent protein gamma-carboxylation enhancers and are useful for optimissing the gamma-carboxylation constructs result in the production of fully gamma-carboxylated mature WEDPs, which are the production of fully gamma-carboxylated mature WEDPs, which are propeptide sequences (modified or not) and WEDPs. This sequence encodes the signal, propeptide and mature protein sequence of human Factor X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1528 ITTGGTGTTTTGTATGCTTCTTGTACCTTGATAGGCATCTCTTTCTCAAGGTTAGGAAAT 1587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric DNA for optimizing gamma carboxylation of vitamin K-dependent protein useful for treating diseases associated with the protein, comprises sequence encoding propeptide fused to sequence encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1507 BP; 394 A; 429 C; 446 G; 238 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 6a; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-638152/61.
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Farnesyl transferase inhibitor modulated leukemia associated gene #81.

ADE84862 standard; DNA; 1507 BP

ADE84862

29-JAN-2004 (first entry)

ADE84862;

ss; cytostatic; farnesyl transferase inhibitor; gene expression;

quinolinone; leukemia; cancer.

WO2003038129-A2. Homo sapiens.

08-MAY-2003

Page 20

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The invention relates to a gene expression profile comprising one or more genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type is a coronary arery endothelium, umbilical arery vein endothelium, dermal microvascular endothelium, pulmonary artery endothelium, myometrium microvascular endothelium, prostate endothelium, renal epithelium, prostate epithelium, renal epithelium, renal proximal tubule epithelium, cell airway epithelium, renal epithelium, umbilical artery smooth muscle, menatal dermal fibroblast, pulmonary artery smooth muscle, corner smooth muscle, mesangial cells, ocronary artery smooth muscle, actrockes, corner smooth muscle, uterine smooth muscle, lung fibroblast, ocronary artery smooth muscle, or determining the level of RNA expression profile is used for determining the level of RNA expression for a sample, determining the phenotype of a cell and distinguishing cell types. The gene or a protein expression profile is useful in identifying disease pathologies involving provide meaningful information with respect to tumour type and stage, reatment methods, and prognosis. The gene or protein expression profile may provide meaningful information with respect to tumour type and stage, creatment methods, and prognosis. The gene or protein expression profile may also be used for creating microarrays. The microarray is useful for antifications and prognosis. The gene or protein expression profile mayping of organisms, confirming cell or tissue defining all angebras and in identifying promising antibiotics, antivital or antivital or antivital or antivital or antivital or antivital or antivital or antivital or antivital or antivities and in identifying promising antibiotics, antivital or antivital or antivital or antivital or antivital or antivital or antivital or antivital or antivital or antivital or antivital or antivital or antivital or antivital or antivital or antivital or antivital or antivital or antivital or antivity and prognosis antivital or antivital or antivital or antivital o
                                                                                                                                                                                                                                                                Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
gene expression; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New gene expression profile generated from primary, endothelial, epithelial, and muscle cell types, useful for identifying disease pathologies involving alterations of gene expression, e.g. cancer.
                                                                                                                                                                                                                   Human gene expression profile polynucleotide SEQ ID NO 433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1507 BP; 394 A; 429 C; 446 G; 238 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ORIM ) ORTHO CLINICAL DIAGNOSTICS INC.
                                                      ABZ35322 standard; cDNA; 1507 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAR-2002; 2002WO-US008456.
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                                                                                                                                                            05-FEB-2003 (first entry)
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Best Local Similarity
Matches 38; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wan J, Wang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200274979-A2.
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-SEP-2002.
                                                                                                         ABZ35322;
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(ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.

WPI; 2003-513497/48.

30-OCT-2002; 2002WO-US034784.

30-OCT-2001; 2001US-0338997P. 30-OCT-2001; 2001US-034081IP. 30-OCT-2001; 2001US-0340938P. 30-OCT-2001; 2001US-0341012P.

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The invention relates to a method of determining whether a patient will respond to treatment with a farnesyl transferase inhibitor (FTI), by analyzing the expression of gene that is differentially modulated in the presence of an FTI. The method is useful for determining whether a patient will respond to treatment with a FTI such as (B)-6-[amino(4-chlorophenyl)](1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl), amethyl-2-(1H)quinollinne, monitoring the therapy of a patient, treating a patient with leukemia with FII if the analysis indicates that the patient will respond. This sequence corresponds to a gene whose expression may be modulated in the presence of FTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1528 TITGGTGTTTTGTATGCTTCTTGTACCTTGATAGGCATCTCTTTCTCAAGGTTAGGAAAT 1587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining whether a patient will respond to treatment with a farnesyl transferase inhibitor, by analyzing the expression of gene that is differentially modulated in the presence of the inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1%; Score 23; DB 1; Length 1507; 60.3%; Pred. No. 17; 25; Indels tive 0; Mismatches 25; Indels
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Matches 38; Conservative
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Conservative

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08-AUG-2001 (first entry)
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AAD08286;

Human secreted protein-encoding gene 4 cDNA clone HWHIH10, SEQ ID NO: 14.

Human; secreted protein; proliferative disorder; cancer; tumour; asthma; foetal abnormality; developmental abnormality; haematopoietic disorder; limmune system disorder; ALDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; angiogenic disorder; kloney disorder; gastrointestinal disorder; allergy; pregnancy-related disorder; andocrine disorder; infection; wound healing; cell culture; chemotaxis; vulnerary; binding partner identification; gene therapy; ss.

Homo sapiens

'product= "Human secreted protein precursor" 'product= "Mature human secreted protein" Location/Qualifiers 42. .914 42. .107 /\*tag= b 108. .911 ಹ /\*tag= /\*tag= sig\_peptide mat peptide

WO200136440-A1

25-MAY-2001.

19-NOV-1999; 99US-0166414P. 21-JUL-2000; 2000US-0219665P. L5-NOV-2000; 2000WO-US031282.

(HUMA-) HUMAN GENOME SCI INC

Ruben SM, Komatsoulis GA, Birse CE, Moore PA;

WPI; 2001-343795/36. P-PSDB; AAE03821. Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.

Claim 1; Page 440-441; 553pp; English.

AND MAD08283-AAD08355 represent cDNAs corresponding to 23 human secreted

Drotein genes, and ABC03896 represent the proteins they encode.

AEC03871-AAEC03896 represent human secreted protein fragments or variants.

The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy.

CC ameliogical conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 23 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, theorem. Foetal and developmental abnormalities, hematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arbhritis), inflammation, allargies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, diaberes, athema, sathma, skin disorders, and infections. The proliferation, to prevent skin aging due to sunburn, to maintain organs or pregnancy-related disorders, endocrine disorders, and infections. The proliferation, to prevent skin aging due to sunburn, to maintain organs to regenerate tissues, to identify their cognate ligands or binding to partners, and in chemotaxis, and can be used as a food additive or

1.1%; Score 22.8; DB 1; Length 433; 54.9%; Pred. No. 15; tive 0; Mismatches 37; Indels C

Query Match
Best Local Similarity 54.34
Best Local Similarity 54.34
Conservative

0; Gaps

198 ATCAAGCACCGAGGACGTGTGCGGGAGAGTGAGATGTGCACTGAGGGACTGTTGGCCCCT 257

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AAD08286/c ID AAD08286 standard; cDNA; 1151 BP. XX

RESULT 35

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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50811, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (SST) for includentifying expressed genes or for physical mapping of the human genome, in forenside, in assessing biodiversities, or in identifying mutations in sessential as hybridisation probes, as oligomers for PCR, for circomosome and gene mapping, in the recombinant production of for circomosome and gene mapping, in the recombinant production of cortion of an enerating antisense DNA of it. The present sequence is useful for generating antisense DNA of it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data obtained in electronic format directly from USPTO at continuous production, but was obtained in electronic format directly from USPTO at sequence. The sequence data obtained in electronic format directly from USPTO at sequence thimilibocides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
                                                                                                                                                                                                                                                                           Human; ss; sequencing by hybridisation; SBH; expressed sequence tag;
genome mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stache-Crain B, Dickson MC, Jones LW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUL-2001; 2001US-00918995
                                                                                                                                                                              Human adult liver cDNA #64.
                                                                                       13-OCT-2003 (first entry)
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(STAC/) STACHE-CRAIN B.
(DICK/) DICKSON M.C.
(JONE/) JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drmanac RT, Labat I,
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                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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ACH20452;
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qq ò g

Sequence 301 BP; 100 A; 54 C; 118 G; 29 T; 0 U; 0 Other;

10664775-3.rng

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preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding cDNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 TTTTCTGTTGTTTTTGTTGTTGTTGTTATCTAGATTTAAGCTGTGGTCAGATAG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe #9609 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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                                                                                                                                                                                                                                                                                                                                              DB 1; Length 1151;
                                                                                                                                                                                                                                                                        Sequence 1151 BP; 252 A; 370 C; 336 G; 193 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                     Score 22.8; DB 1; Length 11:
Pred. No. 18;
0; Mismatches 42; Indels
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30-UUN-2000; 2000US-0060B408.
23-AUG-2000; 2000US-0053336.
21-SEP-2000; 2000US-023668PP.
27-SEP-2000; 2000US-0236359P.
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Best Local Similarity 53.3%;
Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cervical cancer; ss.
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                                       Gaps
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1.1%; Score 22.2; DB 1; Length 301; 58.2%; Pred. No. 20; ve 0; Mismatches 28; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                      Human foetal liver single exon nucleic acid probe #13007.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences
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30-JUN-2000; 2000US-00608408.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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                      Local Similarity 58.2%;
nes 39; Conservative
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Best Local Similarity 58.29
Matches 39; Conservative
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1686 CCTGGAT 1692
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                                                                         WO200157271-A2.
                                                                                                                              04-FEB-2000;
26-MAY-2000;
                                                       Homo sapiens
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ID ABA31
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AC ABA31
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                                                                                                                     Probe #13557 used to measure gene expression in human placenta sample.
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58.2%; Pred. No. 20;
tive 0; Mismatches 28; Indels
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                                                                                                                                       Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID NO 13557; 654pp; English.
                                                                                                                                                                                                                                                                                                                                         Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                        gene expression in human placenta.
                                                              AAI44871 standard; DNA; 301 BP
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03-MG-2000; 2000US-00632566.
21-SEP-2000; 2000US-02346B7P.
27-SEP-2000; 2000US-02365359P.
04-OCT-2000; 2000GB-00024263.
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2000US-0207456P.
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Best Local Similarity 58.2 Matches 39, Conservative
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1686 CCTGGAT 1692
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                 217 TČTAĞCT 211
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                                                                                                                      Human; microarray; single exon probe; gene expression; breast; disease;
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Human breast cell single exon nucleic acid probe #5517.
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1.1%; Score 22.2; D
Best Local Similarity 58.2%; Pred. No. 20;
Matches 39; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2000; 2000US-00608408.
03-MG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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2000US-0207456P.
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Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                     04-FEB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0201456P.
30-UJN-2000; 2000US-0060408
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023468PP.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                    30-JAN-2001; 2001WO-US000668
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les 39, Conservative
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                                                                                           WO200157276-A2.
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                                                        Homo sapiens.
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                                                                                                                                  09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                              Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form at directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single exon nucleic acid probes for analyzing gene expression in human
                                                      Probe #10292 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                     Human; gene expression; heart, microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.1%; Score 22.2; DB 1; Length 301
58.2%; Pred. No. 20;
tive 0; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 301 BP; 100 A; 54 C; 118 G; 29 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; SEQ ID NO 10292; 530pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                   26-MAY-2000, 2000US-0207456P.
30-JUN-2000, 2000US-00608408.
03-AUG-2000, 2000US-00623366.
21-SEP-2000, 2000US-023468FP.
27-SEP-2000, 2000US-023459P.
04-OCT-2000, 2000GS-00024263.
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                                                                                                                                                                                                                                                                                30-JAN-2001; 2001WO-US000666
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                23-JAN-2002 (first entry)
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nes 39; Conservative
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                                                                                                                                                                                                         WO200157274-A2
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1626 TTTGACCTGCCTTCTTCCCCTTCCTCTATTCCTTTGGTTTTTGCATAGTGTCTCTGGCTT 1685
Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                   probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; brain expressed exon; gene expression analysis; probe; microarray;
Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                          The present invention provides a number of single exon nucleic acid
                                                                                                                                                    Example 4; SEQ ID NO 13425; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.1%; Score 22.2; DB 1; Length 301; 58.2%; Pred. No. 20; iive 0; Mismatches 28; Indels 0
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Penn SG,

brains

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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nuclectide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be in sampled erived from human adult liver. The genes identified may be in sampled erived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinsemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS51005 represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1626 TITGAÇCIGCCITÇITÇCCCCTTCCTCTTTCCTTTTGGTTTTTGCATAGTGTCTCTGGCTT 1685
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                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 301 BP; 100 A; 54 C; 118 G; 29 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
1.1%; Score 22.2; DB 1;
Best Local Similarity 58.2%; Pred. No. 20;
Matches 39; Conservative 0; Mismatches 28;
                                                                                                                                                                                                                                                                                                Claim 4; SEQ ID NO 13443; 658pp; English
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                                                            Rank DR
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26-MX-2000; 2000US-0207456P.
30-UTN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-00024263.
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                                                                Chen W,
(MOLE-) MOLECULAR DYNAMICS INC
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                                                                   Hanzel DK,
                                                                                                                                WPI; 2001-488898/53
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                                                                   Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 44
AAI05395/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 TCTCGCCTGCTTACCTCTCGCCTCTCTTTCTTTCTCTCCTCCTCCTCTTCTCTGCCGT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for analyzing gene expression in human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; SEQ ID NO 13128; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 1.1%; Score 22.2; DB 1; Length 3 Local Similarity 58.2%; Pred. No. 20; ... 185 39; Conservative 0; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 301 BP; 100 A; 54 C; 118 G; 29 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                 Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single exon nucleic acid probes
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0224687P.
27-SEP-2000; 2000US-023459P.
04-OCT-2000; 2000GB-00024263.
                                              04-FEB-2000; 2000US-0180312P.

26-MAY-2000; 2000US-0207456P.

30-UNA-2000; 2000US-00608408.

03-AUG-2000; 2000US-023468P.

27-SEP-2000; 2000US-023468P.

04-OCT-2000; 2000US-0036359P.
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                                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC
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Query Match

Best Loc Matches

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RESULT 43
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Gaps

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28; Indels

Length 301;

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The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, particularly chose diseases with polygenic aciology. The diseases include breast cancer, disorders of development, inflammatory diseases include breast, tibrocystic changes, proliferative breast disease and non-carcinoma tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                     Novel single exon nucleic acid probe used to measuring gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277 forcectectractordecorotoantrotrococorotocrotorotord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gauder's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangicleiomyomcosis; Karagener syndrome; pulmonary histiocytosis; lymphangicleiomyomcosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; pyrimary dyspinesis; pulmonary hypertension; hyaline membrane disease; open reading frame; ORF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon probe ORF from lung SEQ ID No 12940.
                                                                                                                                                                                                                                                                                                                                                                                                                                        1.1%; Score 22.2; DB 1; Length 301; 58.2%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 301 BP; 100 A; 54 C; 118 G; 29 T; 0 U; 0 Other;
                                                                                                               Claim 25; SEQ ID NO 5386; 322pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-2000; 2000US-C0608408.
30-UTV-2000; 2000US-C0608408.
03-AUG-2000; 2000US-C0632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234589F.
04-CCT-2000; 2000GB-00024263.
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                  WPI; 2001-476286/51.
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Best Local Similarity
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                                                                            a human breast.
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes for the 1284 open reading frames derived from the 1214 complements or the 1284 open reading frames derived from the 1214 probes. Also included are a microarray comprising the novel set of probes of the complements or the 1284 open reading frames derived from the 1214 probes. Also included are a microarray comprising the novel set of probes of the numan lung, comprising the acids derived from human lung measuring gene expression in a sample derived from human lung masuring the label detectably bound to each probe of the array identifying exons in a evikaryotic genome, comprising (a) and probe of the array identifying exons in a evikaryotic genome, comprising (a) and probe in the fact of array; identifying exons in a evikaryotic genome, comprising (a) and probe in the predicted exon from genomic sequences of the everyote; and (b) detecting specific hybridiation to each probe of the aving a fregment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon in the above mentioned microarray assigning exons to a single exon microarray having a probe with the exon, where a common pattern of expression of the exons should be assigned to a single gene, a peptide comprising or probes/open reading frames (ORF). The probes are used for gene expression of the exons in the tissues and/or cell types undicated to a single gene, a peptide comprising or cancer, chronic obstructive pulmonary disease (CDP), interstitial lung cancer, chronic obstructive pulmonary disease (CDP), interstitial lung derived many and for the study disease (CDP), interstitial lung cancer, chronic obstructive pulmonary disease (CDP), interstitial lung present sequence is a cindosis, pulmonary disease, pulmonary disease, pulmonary disease, pulmonary disease, pulmonary disease, pulmonary disease, pu
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                                                                                                       Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.
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58.2%; Pred. No. 20;
iive 0; Mismatches 28; Indels 0; Gaps
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                                                                                                                                                                                    Claim 4; SEQ ID NO 12940; 634pp; English.
                    Chen W, Rank DR;
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                    Hanzel DK,
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Best Local Similarity
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                    Penn SG,
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Human secreted protein 5' EST, SEQ ID NO: 8650.

(MOLE-) MOLECULAR DYNAMICS INC

WO200218632-A2

07-MAR-2002

tag; secreted protein; cDNA isolation; ss.

chromosome mapping;

Homo sapiens EP1033401-A2

This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated diemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonachecides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of clip and of a wide range of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. The method allows the methylation interest of many C residues to be determined simultaneously. Abgülstlo. ABGS+121 represent genomic DNA sequences used to illustrate the method for the determined determined in the

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258 irrcgaaggagraridrirrrrrgrarrirrrirriraraggagircggrgrafriri 199

141 

ABQ47968

ABQ47968;

(first entry)

Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.

Homo sapiens

Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA. Query Match
1.1%; Score 22; DB 1; Length 612;
Best Local Similarity 49.2%; Pred. No. 27;
Matches 58; Conservative 0; Mismatches 60; Indels Sequence 612 BP; 232 A; 219 C; 72 G; 89 T; 0 U; 0 Other; Claim 12, 56pp + Sequence Listing; 56pp; German ä Guetig Berlin K, 01-SEP-2000; 2000DE-01043826. 05-SEP-2000; 2000DE-01044543. 01-SEP-2001; 2001WO-EP010074 disclosure of the invention υ (EPIG-) EPIGENOMICS AG Piepenbrock WPI; 2002-371829/40 olek A, ò 엄 ö The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences conversed from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design 111 TOTOTOTOTOCOTTICTOTARCACTICTGGGCCAGGGTAGGGGCACTACCGCATTCCCTC 170 135 icicacacticccaecticcacatcceadactedateadacadedacacadateadaca

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.

Duclert A, Giordano J;

Dumas Milne Edwards J,

WPI; 2000-500381/45.

21'-FEB-2000; 2000EP-00200610.

26-FEB-1999;

Claim 1; SEQ ID NO 8650; 71pp + Sequence Listing; English

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30; Indels

0; Mismatches

ch 1 Similarity 57.1%; 40; Conservative (

Query Match Best Local Similarity

Matches

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Score 22; DB 1; Length 385; Pred. No. 24;

Sequence 385 BP; 69 A; 105 C; 126 G; 80 T; 0 U; 5 Other;

expression and secretion vectors

ABQ47968 standard; DNA; 612

12-JUL-2002

Oligonucleotide for detecting cytosine methylation SEQ ID NO 34559

Human, cytosine methylation, 5'-CpG-3', uracil; cytosine, diagnosis, drug; side effect, cancer, central nervous system, cardiovascular, gastrointestinal; respiratory system; single nucleotide polymorphism; SNP, cell differentiation; ds.

Homo sapiens

Oligonucleotide for detecting cytosine methylation SEQ ID NO 34560.

(first entry)

12-JUL-2002

ABQ47969;

ABQ47969 standard; DNA; 612

171 TCTCTTCCAA 180

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75 CCACAGACAA

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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a connect sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated (C, to uracil, then part of the genomic sample of but not methylated (C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (DNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognosis of side effects of the rangentic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP, s), and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ14410- for Astransian and the method allows the methylation of ABASTAL represent genomic DNA sequences used to illustrate the method for Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Astransian and Ast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                  Berlin K,
                                                                                                                                                              01-SEP-2001; 2001WO-EP010074.
                                                                                                                                                                                                                                01-SEP-2000; 2000DE-01043826, 05-SEP-2000; 2000DE-01044543,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis and prognosis, confrom chemically treated DNA.
                                                                                                                                                                                                                                                                                                                                                                                           Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-371829/40
                                  WO200218632-A2.
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ö 355 TTTCGAAGGAGTATTGTTTTTTTTTTTTTTTTTTTTTTAGGGAGTTCGGTCGTAGTTTTT 414 472 0; Gaps Query Match 1.1%; Score 22; DB 1; Length 612; Best Local Similarity 49.2%; Pred. No. 27; Matches 58; Conservative 0; Mismatches 60; Indels 0; Mismatches 60; Indels Sequence 612 BP; 89 A; 72 C; 219 G; 232 T; 0 U; 0 Other; ò

Single nucleotide polymorphism containing sequence #258. RESULT 49 AAC70944/c ID AAC70944 standard; DNA; 253 BP. (first entry) 09-FEB-2001 AAC70944;

Single nucleotide polymorphism; SNP; human; genetic disease; disease susceptibility; cardiovascular system; endocrine system; neurological system; forensic testing; paternity testing; ds.

Homo sapiens

WO200058519-A2 

05-OCT-2000

30-MAR-2000; 2000WO-US008440.

99US-0127248P. 31-MAR-1999;

(WHED ) WHITEHEAD INST BIOMEDICAL RES (AFFY-) AFFYMETRIX INC.

Lander ES; Ireland JS, Daley GQ, Sklar P; Cargill M, Patil N, 8 Altshuler D, Lipshutz RJ,

Guetig

WPI; 2000-611722/58

Nucleic acid selected from one of 106 genes comprising single nucleotide polymorphisms, allele-specific oligonucleotides to the genes are useful for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis.

Claim 1; Fig 5; 214pp; English

The present invention is concerned with a number of human single nucleotide polymorphisms (SNPs) which the inventors identified in human genes. These SNPs can be used in disease diagnosis and prediction of an individual's susceptibility to disease, in forensic and paternity testing and in genetic mapping. In particular, the SNPs of the invention can be used to diagnose used to dispasses of the cardiovascular, endocrine and neurological systems, such as coronary artery disease, schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's diseases. Note: The degenerate codon within the sequence represents the position of an SNP, for example the letter S represents a polymorphism where the nucleotide may be C or G

Sequence 253 BP; 92 A; 41 C; 58 G; 61 T; 0 U; 1 Other;

Gaps ., 1.1%; Score 21.6; DB 1; Length 253; 53.6%; Pred. No. 28; 39; Indels 0; Mismatches Query Match
Best Local Similarity 53.67
Warches 45; Conservative ò

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82

1535 TITIGIATGCTICTIGIACCTIGATAGGCAICTCTTTCTCAAGGTTAGGAAATTTTTCTT 1594 141 raridectrarritaridecercristarenenterichescacherritarritarianagegra 1595 TITIGGITTICTICAAAATATIT 1618 Dp ð

81 rcrrcccrrrcrccacacrarrr

g

ABV98470 standard; cDNA; 254 BP

(first entry) 14-JAN-2003

Human pancreatic cancer expressed cDNA SEQ ID NO 3878.

pancreas; cancer; gene therapy; vaccine; immunostimulant; cytostatic; tumour; gene; ss Human;

Homo sapiens.

WO200260317-A2

30-JAN-2002; 2002WO-US002781.

30-JAN-2001; 2001US-0265305P

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The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences consisting of at least 20 contiguous residues of (a); (d) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596 ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides (ABP68596 antibodies, fusion proteins, T cell populations and antigen presenting cants simulating an immune response. The polymucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for inhibiting expression of the tumour cells of the polymucle format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1802 TCAGTGAGGCTTGTCTCTGAGGTTCCTGTTGGGTTCTTAATTTTTTCATTTCCAGATTTC 1861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 TCAGTTCCCTCCTCCTTGTGGCCGTTGCCTCAGGCTATGGCCCACCTTCCTCTCGCCCTT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and pancreatic tumor polypeptides, useful f
diagnosing, preventing and/or treating cancer, particularly pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1742 TCCATTTCTTCTATCTTGTCTTCACTGCCTGAGATTCTCTTCTTCTATCTCTTGTATTCTG
                                                                                                                                                                                                            Lodes MJ, Persing DH, Hepler WT, Jiang Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 254;
                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 3878; 300pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 254 BP; 61 A; 74 C; 84 G; 35 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 1.1%; Score 21.6; Di Similarity 47.7%; Pred. No. 28; 63; Conservative 0; Mismatches
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31-JAN-2001, 2001US-0265682P.
09-FEB-2001, 2001US-0267568P.
28-APR-2001, 2001US-0278631P.
16-MAY-2001, 2001US-0291131P.
12-JUL-2001, 2001US-033544P.
20-MUS-2001, 2001US-0313999P.
27-NOV-2001, 2001US-0313626P.
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                                                                                                                                                                                                          Benson DR, Kalos MD,
                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                               WPI; 2002-627435/67.
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Best Local &
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This PCR fragment was used as a probe to screen a rat hypothalamus cDNA library. 2 Independent clones, named 27A (see AAV82828) and 16.6, were obtained. Clone 27A codes for a novel full-length rat galanin receptor, designated GALR2 (see AAW61461). The invention provides methods for identifying ligands particular to mouse GALR2 (see AAW61463). Such ligands may be useful therapeutically e.g. to treat obesity or cognitive disorders involving excess galanin or to treat pain or anorexia involving

Sequence 283 BP; 27 A; 116 C; 84 G; 56 T; 0 U; 0 Other;

insufficient galanin

New mouse galanin receptor, GALR2, - useful to identify agonists and antagonists to treat conditions involving galanin, e.g. for treating

obesity, pain or cognitive disorders.

Example 1; Fig 6; 56pp; English.

(MERI ) MERCK & CO INC. (UYTE-) UNIV TEXAS HEALTH SCI SAN ANTONIO.

fan CP, Kolakowski LF;

WPI; 1998-388038/33.

P-PSDB; AAW61461.

for

97WO-US023891. 96US-0033851P

18-DEC-1997; 27-DEC-1996;

WO9829440-A1.

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58 TGGGGCTGCTGCCTTTCTCCCCTGTCTGATTCCTAGGGTGAGGGTTACCACTGCTC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New galanin receptor, GALR2 - useful, e.g. to identify agonists and antagonists, therapeutically to treat conditions involving excess or
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                          o,
                                                                                                                                                                                                                                     Galanin receptor; GALR2; rat; ligand; obesity; anorexia; pain;
DB 1; Length 283;
                        0; Mismatches 21; Indels
Score 21.4; I
Pred. No. 33;
                                                                                                                                                                                                                                                  cognitive disorder; therapy; probe; ss.
                                                                                                                                                                                                              Galanin receptor GALR2 DNA probe.
                                                                                                                                      AAV32651 standard; cDNA; 283 BP.
1.1%;
                                                                                                                                                                                                                                                                                                                                                    97WO-US023890.
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                                                                                                                                                                                      (first entry)
                        34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sullivan K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-388037/33
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                          Rattus sp.
                                                                                                                                                              AAV32651;
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                          Matches
                                                                                                                          AAV3265
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0

Gaps

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21; Indels

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Sequence 283 BP; 27 A; 116 C; 84 G; 56 T; 0 U; 0 Other;
                                                                    insufficient galanin
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DB 1; Length 283;

1.1%; Score 21.4;

Query Match

Human cDNA sequence encoding for PRO4327 polypeptide.

. 0

Gaps

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DB 1; Length 283;

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The invention relates to mouse galanin receptor 2 (GALR2) and the nucleic acid encoding the novel polypeptide. The sequences are useful in assays for identifying GALR2 ligands that are useful for treating obesity, pain and cognitive disorders. The sequences are also useful for identifying agonists, antagonists, suppressors or inducers of GALR2. This sequence represents a CDNA probe used to isolate rat GALR2, used in the methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding mouse galanin receptor 2, useful in assays fidentifying galanin receptor 2 ligands for treating obesity, pain and cognitive disorders.
                                                                                                                        58 TGGGGCTGCTGTTCTCCCTGTCTGATTCCTAGGGTGAGGGTTACCACTGCTC 112
                                                                                                                                                                                                    112 recesececreterececerererecereracereseceasesereceracerace 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Galanin receptor 2; GALR2; probe; ss; rat; obesity; pain; anorectic; cognitive disorder; analgesic; neuroprotective.
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                                                      0; Mismatches
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            61.8%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat galanin receptor 2 (GALR2) cDNA probe.
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                                                                                                                                                                                                                                                                                                                                                                                                        ABK14060 standard; cDNA; 283 BP
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(TEXA ) UNIV TEXAS SYSTEM.
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Best Local Similarity
Matches 34; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human galanin receptor, GALR2, - useful to identify agonists and antagonists to treat conditions involving galanin, e.g. for treatment of obesity or cognitive disorders.
                                                                                                                                                              This PCR fragment was used as a probe to screen a rat hypothalamus cDNA library. 2 Independent clones, named 274 (see AAV35648) and 16.6, were obtained. Clone 27A codes for a novel full-length rat galanin receptor, designated GALR2 (see AAW49002). The invention provides methods for identifying ligands particular to GALR2. Such ligands may be useful therapeutically e.g. to treat obesity or cognitive disorders involving excess galanin or to treat pain or anorexia involving insufficient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 TGGGGCTGCTGCCTTTCTCCCTGTCTGATTCCTAGGGTGAGGGTTACCACTGCTC 112
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cognitive disorder; therapy; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 21.4; DB 1; Length 283; Pred. No. 33; 0; Mismatches 21; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 283 BP; 27 A; 116 C; 84 G; 56 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (WERI ) MERCK & CO INC.
(UYTE-) UNIV TEXAS HEALTH SCI CENT SAN ANTONI.
(UTOR ) UNIV TORONTO.
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            insufficient galanin such as obesity.
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                                                                                           Example 1, Fig 6, 57pp, English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.1%;
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nes 34; Conservative
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WO9829441-A1

Rattus sp.

09-JJL-1998

24-NOV-1998

AAV44930;

RESULT 53 AAV4493

Query Match

ð ΩP

galanin

27-DEC-1996;

Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.

Homo sapiens.

07-JUN-2001.

01-DEC-2000; 2000WO-US032678

99WO-USO28564. 99WO-USO28565. 99WO-USO30095. 99WO-USO30095. 99WO-USO30999. 30-DEC-1999;

99WO-US031274. 2000WO-US000219. 2000WO-US000277. 2000WO-US00376. 2000WO-US003565. 06-JAN-2000; 2 11-FEB-2000; 2 18-FEB-2000; 2 06-JAN-2000;

18-FEB-2000; 2000WO-US004341. 18-FEB-2000; 2000WO-US004342. 22-FEB-2000; 2000WO-US004414. 24-FEB-2000; 2000WO-US005004. 24-FEB-2000; 2000WO-US005004. 01-MAR-2000; 2000WO-US005004.

02-MAR-2000; 2000WO-US005841. 03-MAR-2000; 2000US-0187202P. 10-MAR-2000; 2000WO-US005819. 12-MAR-2000; 2000WO-US005884. 20-MAR-2000; 2000WO-US007377. 21-MAR-2000; 2000WO-US007532.

30-MAR-2000; 2000MO-US008439. 17-MAY-2000; 2000WO-US013705. 30-MAY-2000; 2000WO-US014041. 02-JUN-2000; 2000WO-US015264. 02-JUN-2000; 2000WO-US015264. 28-JUL-2000; 2000WO-US02329. 23-AUG-2000; 2000WO-US02352. 23-AUG-2000; 2000WO-US02352. 24-AUG-2000; 2000WO-US02352. 24-AUG-2000; 2000WO-US02352. 10-NOV-2000; 2000WO-US03352.

(GETH ) GENENTECH INC.

Gao Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G: Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

2001-408281/43. WPI; 2001-408281/ P-PSDB; AAU12282. Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung, breast, prostate, cervical.

Claim 3; Fig 221; 813pp; English.

AAS21244-AAS21518 encode for novel human secretory and transmembrane PRC polypeptides. The PRC polypeptides are useful to detect other PRC polypeptides, to link bioactive molecules to cells expressing PRC polypeptides, to modulate biological activities of cells expressing PRC

polypeptides, and to detect the presence of mammalian lung, colon, breat, prostate, rectal, cervical or liver tumours by comparing FRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TMF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in perioryce cells, the release of proceedycans from cartilage, the proliferation of inner aar unticular supporting cells or of Thompsphides and modulate glucose or free farth acid uprake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polymulochtides encoding PRO polypeptides can be used to generate probes, antienne RNA/DNA, transgenic or knock out animals and can be used in gene therapy ö Gaps 0 Query Match
1.1%; Score 21.4; DB 1; Length 1129;
Best Local Similarity 66.0%; Pred. No. 45;
Matches 31; Conservative 0; Mismatches 16; Indels 0; 1835 ITCTIAATITITCATITICCAGATITICCTTCAGTITIGGGTTTTGTTT 1881 rirrirrirrirrirricasciescacacasserisserirrirari 1083 Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; 1129 ò

ACD23963 standard; cDNA; 1129 BP ACD23963/c RESULT 56

26-AUG-2003 (first entry)

ACD23963;

Novel human secreted and transmembrane protein PRO4327 cDNA.

Human; secreted and transmembrane protein, PRO; antiinflammatory, anti-treinosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic; antidiabetic; gene therapy, tumour necrosis factor (TNF) alpha release; TNF-alpha release; cell proliferation; cell differentiation; gene expression modulator; proteoglycan release; cytokine release; tumour; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; acquired immunodeficiency syndrome, cancer; diabetic complication; chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor; tissue typing; gene; ss.

Homo sapiens.

JS2003032156-A1.

13-FEB-2003.

98WO-US012456. 98WO-US014552. 98WO-US017888. 98WO-US018824. 98WO-US019093. 98WO-US019094. 98WO-US019177. 98WO-US021141. 06-MAY-2002; 2002US-00140474. 98WO-US019330 98WO-US019437 10~SEP-1998; 14~SEP-1998; 14~SEP-1998; 14~SEP-1998; 14-JUL-1998; 28-AUG-1998; 16-SEP-1998; 07-OCT-1998; 

98WO-US022991. 98WO-US022992. 98WO-US024855. 98WO-US025108. 99WO-US000106. 29-0CT-1998; 29-0CT-1998;

20-NOV-1998; 01-DEC-1998; 05-JAN-1999;

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99WO-US012252.
99WO-US020111.
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10-MAY-2001, 2001US-00854280,
18-MAY-2001, 2001US-00860216,
25-MAY-2001, 2001US-00866023,
25-MAY-2001, 2001US-00866034,
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06-JAN-2000;
11-FEB-2000;
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30-DEC-1999;
30-DEC-1999;
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21-MAR-2000;
30-MAR-2000;
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35-APR-2001;
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The invention describes an isolated nucleic acid (I) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, one of 55 mucleotide sequences, and which encodes a corresponding comparation of polypeptide selected from 275 amino acid sequences, where all sequences of cerect PRO polypeptides, link a bloactive molecule to a cell expressing a ROO polypeptide, modulate a biological activity of a cell, stimulate the release of tumour necrosis factor (TNF)-alpha from human blood, modulate of glucose or free fatty acid by cells, stimulate or inhibit the proliferation or differentiation of cells or gene expression, stimulate the release of proteoglycans, stimulate the release of cytokine to proliferate blood monounclear cells, inhibit the binding of A-peptide to factor VIIA, or detect the presence of tumour in a mammal. The nucleic acid and polypeptide encoded by it, are useful for treating inflammatory birth defects, premature aging, acadiac injury, infertility, birth defects, premature aging, acadiac injury, infertility, birth defects, premature aging, acquired immunodeliciency syndrome (AIDS), cancer, or diabetic complications. The nucleic acid is useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, consistence encodes a novel human secreted and transmembrane PRO
                                                                                                                                                                                                                                                                                 Gao W;
                                                                                                                                                                                                                                                                                                                                                                                                                               New secreted and transmembrane PRO nucleic acids, for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, axquired immunodeficiency
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Goddard A, Godowski PJ, Gurney AL, Sherwood S;
art TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, PRO polypeptide, secreted and transmembrane protein;
anti-PRO antibody, diagnostic assay, gene expression, diabetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA encoding human PRO polypeptide #111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Fig 221; 660pp; English.
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ACA67104/c
ID ACA67104 standard; cDNA; 1129 BP.
                21-JUN-2001; 2001US-00887879.
22-JUN-2001; 2001WO-US020116.
99-JUN-2001; 2001WO-US021735.
18-JUL-2001; 2001US-00908827.
66-AUG-2001; 2001US-00924419.
09-AUG-2001; 2001US-00924836.
16-AUG-2001; 2001US-00921836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 syndrome (AIDS), or cancer.
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Best Local Similarity 66.0
Matches 31, Conservative
                                                                                                                                                                                                                                                                                 Baker KP, Beresini M,
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P-PSDB; ABO17726.
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Smith V, Stew
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MAKE XEX EXE
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bone disorder, cartilage disorder, rheumatoid arthritis, obesity, sports injury, osteoarthritis, hyper-insulinaemia, hypo-insulinaemia, hearing loss, coagulation disorder, stroke, hear attack, cardiant, antidiabetic, anorectic, vulnerarty, antiarthritis, osteopathis, antirheumatic, auditory, cerebroprotective, angiogenic, gene, ss.
                                                                                                                                    9708-0056974P
9708-0059113P
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98WO-US017888.
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98WO-US019094
                                                                        US2003004311-A1.
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07-NOV-1997,
17-NOV-1997,
21-NOV-1997,
24-NOV-1997,
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24-NOV-1997,
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11-DEC-1997,
                                                       Homo sapiens
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11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004414.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US004914.
                                                                                                       99WO-US021547.
99WO-US023089.
99WO-US028214.
99WO-US028313.
99WO-US028301.
98WO-US021141.
98WO-US022991.
98WO-US022892.
98WO-US022808.
99WO-US025108.
99WO-US005028.
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2000WO-US000277.
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99WO-US031243,
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02-DEC-1999;
02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
30-DEC-1999;
30-DEC-1999;
30-DEC-1999;
05-JAN-2000;
06-JAN-2000;
06-JAN-2000;
07-OCT-1998,
29-OCT-1998,
20-ONOV-1998,
05-JAN-1998,
05-JAN-1999,
08-MAR-1999,
10-MAR-1999,
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14-MAY-1999,
02-JUN-1999,
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18. SEP-11999
19. NOV-11999
10. NOV-11999
11. DEC-11999
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(GETH ) GENENTECH INC.

3 Gao Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G. Gerritsen MS, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-352836/33. P-PSDB; ABU80980.

New isolated PRO polypeptide useful for treating diabetes, rheumatoid arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or heart attack.

Claim 2; Fig 221; 643pp; English.

The present invention relates to the isolation of novel human PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the treatment of diabetes, bone and/or cartilage disorders (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity, hyper-or hypo-insulineamia, hearing loss, and coagulation disorders (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity burification of PRO from recombinant cell culture or natural sources. ACA66994-AAA6768 represent cDNA sequences encoding the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at segdata.uspto.gov/psipsDIDEntry.html

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

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Human, PRO polypeptide, secreted and transmembrane protein,
tumour necrosis factor-alpha, TNF-alpha, blood, proliferation,
differentiation, chondrocyte, tumour, genetic disorder, cytostatic, gene,
                 Gaps
                 0
                             1129 TITITITITITITITITICAGCIGCACACACAGGCIGGTITITATI 1083
     DB 1; Length 1129;
   Query Match
1.1%; Score 21.4; DB 1; Length 11
Best Local Similarity 66.0%; Pred. No. 45;
Matches 31; Conservative 0; Mismatches 16; Indels
                                                                                                          cDNA encoding human PRO polypeptide #111.
                                                                     ACA03713 standard; cDNA; 1129 BP
                                                                                                                                                                                                                          98WO-US018624
98WO-US019093
98WO-US019094
98WO-US019177
98WO-US019437
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99WO-US020594.
99WO-US020944.
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98WO-US014552.
98WO-US017888.
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98WO-US024855.
98WO-US025108.
99WO-US000106.
99WO-US0005028.
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99WO-US012252.
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99WO-US021547.
99WO-US023089.
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98WO-US022991.
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99WO-US031243.
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99WO-US030999
                                                                                             23-MAY-2003 (first entry)
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                                                                                                                                                    Homo sapiens.
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08-SEP-1999;
13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
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30-DEC-1999;
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06-JAN-2000; 2000WG-USCO0277.

16-JAN-2000; 2000WG-USCO0277.

16-JAN-2000; 2000WG-USCO0277.

18-FEB-2000; 2000WG-USCO0441.

18-FEB-2000; 2000WG-USCO0441.

24-FEB-2000; 2000WG-USCO0441.

24-FEB-2000; 2000WG-USCO0441.

15-WAR-2000; 2000WG-USCO0619.

15-WAR-2000; 2000WG-USCO0619.

15-WAR-2000; 2000WG-USCO0619.

15-WAR-2000; 2000WG-USCO0619.

15-WAR-2000; 2000WG-USCO0619.

16-WAR-2000; 2000WG-USCO0619.

17-WAR-2000; 2000WG-USCO0619.

17-WAR-2000; 2000WG-USCO0619.

17-WAR-2000; 2000WG-USCO0619.

17-WAR-2000; 2000WG-USCO0619.

18-WAR-2000; 2000WG-USCO0619.

18-WAR-2000; 2000WG-USCO0619.

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18-WAR-2000; 2000WG-USCO0619.

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18-WAR-2000; 2000WG-USCO0619.

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18-WAR-2000; 2000WG-USCO0619.

18-WAR-2000; 2000WG-USCO0619.

18-WAR-2000; 2000WG-USCO0619.

18-WAR-2000; 2000WG-USCO0619.

18-WAR-2000; 2000WG-USCO0619.

18-WAR-2000; 2000WG-USCO0619.

18-WAR-2000; 2000WG-USCO0619.
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New secreted and transmembrane PRO nucleic acids, useful for gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification.

Gao W;

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gr Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-332040/31. P-PSDB; ABU66680. 10664775-3.rng

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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking biological activities of cells expressing PRO polypeptides, and for for identifying agonists or antagonists. The PRO polypeptides are useful for the stimulating the release of tumour necrosis factor (TNF)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocytes, and detecting the proliferation or differentiation of chondrocytes, and detecting the presence of tumours. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the generation of antisense RNA and genetic disorders, and in gene therapy. Actobiol ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS ACTOSIOS A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; ative 0; Mismatches 16; Indels 0;
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ABX89251/C
ID ABX89251;
XX
AC ABX89251;
XX
XX
DT 13-MAY-2003 (first entry)
XX
DY Human; PRO; hypertrophy of neonatal cardiac insufficiency disorder; can adrenal cortical capillary endothell who wascular endothelial growth factor of the endothelial call growth factor; wascular endothelial growth factor; wascular endothelial growth inhibitor; wascular endothelial growth inhibitor; wascular endothelial growth inhibitor; wascular endothelial all growth inhibitor; wascular endothelial growth inhibitor; wascular endothelial growth inhibitor; wascular endothelial growth inhibitor; wascular endothelial growth inhibitor; wascular endothelial call growth inhibitor; was retinal disorder; retinitis pigment was chondrocyte redifferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wascularitis; horselferentiation; sport wasculariti
Claim 2; Fig 221; 660pp; English
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Matches 31; Conservative
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ACD41905 standard; cDNA; 1129 BP

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RESULT 60
ACD41905/c
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à ద 2000WO-US004414 2000WO-US004914

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Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis.
                                                                                                                                                   Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                      Claim 2; Fig 221; 659pp; English
                                    2001WO-US019692.
2001US-00887879.
2001WO-US020116.
                                                              2001WO-US021066.
                                                                                        2001US-00924419.
2001US-00927796.
2001US-00931836.
                   2001US-00882636.
2001US-00886342.
  2001WO-US017800
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                                                                                 2001US-00908827
                                                                                                                                                          Banct ..., Goddard Smith V, Stewart TA,
                                                                                                                                   (GETH ) GENENTECH INC.
                                                                                                                                                                                        WPI; 2003-148238/14.
P-PSDB; ABU59761.
                                           21-JUN-2001;
22-JUN-2001;
29-JUN-2001;
                                                                     09-JUL-2001;
18-JUL-2001;
06-AUG-2001;
09-AUG-2001;
16-AUG-2001;
                          19-JUN-2001;
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Gao W;

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO cuseful for treating cardiac insufficiency disorders. PRO184 and PRO186 polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus cardiac insufficiency disorders. PRO1854 and PRO186 cuseful for treating cardiac insufficiency disorders. PRO1856, PRO88

Gaps 1835 TICTIAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881 DB 1; Length 1129; 16; Indels 0; Mismatches Query Match 1.1%; Score 21.4; I Best Local Similarity 66.0%; Pred. No. 45; Matches 31; Conservative 0; Mismatches

1129 ritritritritritritricaderedeacacadederitritari 1083

Human; ss; gene; PRO; secreted protein; transmembrane protein; tumour; cytostatic; gene therapy; tumour necrosis factor-alpha; TNF-alpha; blood; proteoglyan; cartilage; cytokine; peripheral blood mononuclear cell; PBMC; glucose uptake; FFA; skeletal muscle cell; adipocyte cell; chondrocyte cell proliferation; chondrocyte cell differentiation; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell; A-peptide; factor VIIA. Human secreted/transmembrane protein (PRO) cDNA #111. 10-MAY-2002; 2002US-00142431 98WO-US018824 98WO-US019437 98WO-US021141 99WO-US000106 99WO-US008615 99WO-US010733 98WO-US019177 98WO-US019330 98WO-US022991 98WO-US024855 99WO-US020111 99WO-US021090 99WO-US021547 99WO-US023089 99WO-US020944 99WO-US028214 99WO-US028409 99WO-US028313 99WO-US028301 99WO-US028634 99WO-US028565 05-SEP-2003 (first entry) 98WO-US025 99WO-US00 98WO-US0 99WO-US0 SU-OM66 US2003036179-A1 Homo sapiens. 06-JAN-2000; 06-JAN-2000; 11-FEB-2000; 22-DEC-1999; 30-DEC-1999; 30-DEC-1999; 05-JAN-2000; 20-FEB-2003 999 ACD41905; ó

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20-DEC-2000; 2000US-00/10/20
20-DEC-2000; 2000WO-US034956.
28-FEB-2001; 2001US-00796498.
28-FEB-2001; 2001WO-US006520.
                                                                                                                                                             10-MAY-2001, 2001US-00854208.

10-MAY-2001; 2001US-00854280.

18-MAY-2001; 2001US-00860216.

25-MAY-2001; 2001US-00860218.

25-MAY-2001; 2001US-0086034.

25-MAY-2001; 2001WS-0097092.

01-JUN-2001; 2001WS-0087035.
                                                                                                                                  01-MAR-2001, 2001WO-US006666.
09-MAR-2001, 2001US-00802706.
14-MAR-2001, 2001US-00808689.
22-WAR-2001, 2001US-00816744.
05-APR-2001, 2001US-00828366.
                                                                                                 2000WO-US033873.
2000WO-US032678.
2000US-00747259.
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### (GETH ) GENENTECH INC

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W; Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

### WPI; 2003-466355/44. P-PSDB; ABO24951.

New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or PRO4978, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

# Claim 2; Fig 221; 659pp; English.

The invention relates to an isolated nucleic acid comprising at least 80% sequence and transmembrane protein) cDNA comprising a nucleic acid (a) encoding a PRO polypeptide, or its extracellular domain (with or without its associated signal peptide), which comprises any of the 275 120-850 residue amino acid sequences, given in the specification; (b) comprising any of the 275 300-3500 nucleotide sequences, given in the specification; or (c) comprising the

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till-length coding sequence of the nucleotide sequences given in the specification, or of the DNA deposited under any of the American Type Culture Collection (ATCC) Accession Numbers listed in the specification. Also included are a vector comprising the novel nucleic acid, a host cell comprising the vector producing a PRO polypeptide, the isolated PRO polypeptide of timed to a chimeric molecule comprising the PRO polypeptide of timed to a heterologues amino acid sequence, an anti-PRO antibody, detecting a PRO polypeptide in a sample suspected of containing the PRO polypeptide, include a bloactive molecule to a cell expressing a PRO polypeptide, stimulating the release of tumour necrosis factorialpha (TNP-alpha) from human blood, (or proteoglycans from cartilage or cytokine from peripheral blood mononuclear cells (PBMC)), andipocyte cells stimulating the proliferation of differentiation of adipocyte cells stimulating the proliferation of inner ear utricular supporting calls or proliferation of inner ear utricular supporting cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the binding of A-peptide to factor VIA, or differentiation of adipocyte cells (or proliferation for in mammal and an or oligonucleotide probe derived from any of the nucleotide sequences given in the specification. The polynucleotide is useful in molecular biology, including uses as hybridiserion probes, in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy. The propoment and screening of therapeutically useful reagents. The PRO polypeptide or the polympetide or responsive to the polypeptide or antibody, such as tumours, and in cesponsive to the polypeptide or sequence encodes a PRO polypeptide or vergons and in preparing a medicament for treating a condition or vergons and in preparating either transgenic and in cesponsive to the polypeptide or antibody, such as tumours, and in
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Gaps Match 1.1%; Score 21.4; DB 1; Length 1129; Local Similarity 66.0%; Pred. No. 45; es 31; Conservative 0; Mismatches 16; Indels 0; Query Match Matches

## 1835 ITCTTAATTTTTCATTTCCAGATTTCCTTCAGTTTTGGTTTTGTTT 1881 1129 rinirininininininin 1083

ACA04134/c RESULT 61

ACA04134 standard; cDNA; 1129 BP.

ACA04134;

27-MAY-2003 (first entry)

Human cDNA encoding a secreted/transmembrane protein, SEQ ID 221.

Human; ss; gene; secreted protein; transmembrane protein; PRO; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertlity; birth defects; premature aging; AIDS; biosensor; acquired immunodeficiency syndrome; cancer; diabetic complication; bioreactor; tumour.

Homo sapiens.

US2003032155-A1.

13-FEB-2003.

03-MAY-2002; 2002US-00137865

31-MAR-1997;

98WO-US012456. 98WO-US014552. 98WO-US017888. 98WO-US018824. 98WO-US019093. 

28-AUG-1998; 10-SEP-1998; 14-SEP-1998;

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99WO-US028551.
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2000WO-US000376
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15-MAR-2000;
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21-MAR-2000;
30-MAR-2000;
                             29-OCT-1998;
29-OCT-1998;
20-NOV-1998;
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05-JAN-1999;
08-MAR-1999;
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20-DEC-1999;
22-DEC-1999;
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29-NOV-1999;
30-NOV-1999;
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24-FEB-2000;
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25-MAY-2001; 200105-00866034.

25-MAY-2001; 200105-00866034.

10-UUN-2001; 200105-00874503.

01-UUN-2001; 200105-00874503.

14-UUN-2001; 200105-00874503.

14-UUN-2001; 200105-00886342.

20-UUN-2001; 200105-00886342.

20-UUN-2001; 200105-00886342.

22-UUN-2001; 200105-0088779.

23-UUN-2001; 200105-0098827.

06-AUG-2001; 200105-00924419.

09-AUG-2001; 200105-00924419.

09-AUG-2001; 200105-00924419.

09-AUG-2001; 200105-0092419.
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18-MAY-2001;
25-MAY-2001;
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Gao W; Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Matanabe CK, Wood WI, Zhang Z;

#### WPI; 2003-331925/31. P-PSDB; ABU66956.

New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or cancer.

# Claim 2; Fig 221; 659pp; English.

The invention relates to an isolated nucleic acid comprising, or which is at least 80% identical to, or the full-length coding sequence of, any of the 25 nucleotide sequences, encoding the corresponding PRO polypeptide (one of 275 secreted or transmembrane proteins). The nucleic acid further comprises the full-length coding sequence of the DNA deposited under American Type Culture Collection (ATCC) accession number in a list given in the specification. Also included are vectors and host calls for producing PRO proteins, Also included are vectors and host calls for extracellular domains and mature sequences, methods of detecting PRO proteins, methods for stimulating the release of TNF-alpha (tumour concerning PRO proteins, methods for stimulating the release of TNF-alpha (tumour carilage, proliferation of fondrocyte cells, the release or proliferation of carrilage, proliferation of inner ear urticular supporting cells, the carilage, proliferation of T-lymphocyte cells, the release or groteferation of T-lymphocyte cells, the release or grotiferation of conductation of conductating the upcause of glucose or free carrilage, proliferation of the method for modulating the upcake of glucose or free proliferation of T-lymphocyte cells, a method for inhibiting the problem of the differentiation of adipocyte cells, a method for detecting the presence of a tumour in a mammal and oligonucleotide probe derived from any of the nucleotide sequences cited above. The nucleic acids and polypeptides are useful for treating of infammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or diabetic complications. The nucleic acids are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both concert invention and in generating antisense RNA or DNA. The polypeptides are useful in tissue typing. The present sequence encodes a PRO protein.

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; Query Match Best Local Similarity

2001US-00816744 2001US-00828366 2001US-00854208

05-APR-2001;

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Human; secreted and transmembrane protein; PRO; gene; ss;
Tumour necrosis factor alpha release; TNF-alpha release;
Jucose uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell proliferation inhibitor; cytokine release stimulator;
lumg tumour, prostate tumour; prostate tumour;
cervical tumour; inver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
                                                                                                                                                                                                    Novel human secreted and transmembrane protein PRO4327 cDNA
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98WO-US019330.
98WO-US019437.
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98WO-US019093.
98WO-US019094.
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98WO-US025108.
99WO-US000106.
                                                   ADA45740 standard; cDNA; 1129
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16-SEP-1998;
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15-SEP-1999;
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
30-DEC-1999; 99WO-US031274.

05-JAN-2000; 2000WO-US0002719.

06-JAN-2000; 2000WO-US000277.

06-JAN-2000; 2000WO-US0003765.

11-FEB-2000; 2000WO-US003565.

18-FEB-2000; 2000WO-US004341.

18-FEB-2000; 2000WO-US004341.

24-FEB-2000; 2000WO-US004341.

24-FEB-2000; 2000WO-US004341.

24-FEB-2000; 2000WO-US004314.

24-FEB-2000; 2000WO-US006319.

11-MAR-2000; 2000WO-US006319.

15-MAR-2000; 2000WO-US006319.

15-MAR-2000; 2000WO-US006319.

15-MAR-2000; 2000WO-US006319.

21-MAR-2000; 2000WO-US006319.

21-MAR-2000; 2000WO-US006319.

21-MAR-2000; 2000WO-US006319.

22-MAR-2000; 2000WO-US004491.

23-MAR-2000; 2000WO-US014941.

24-MAR-2000; 2000WO-US014941.

25-MAR-2000; 2000WO-US014941.

26-UUL-2000; 2000WO-US014941.
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10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854280.
18-MAY-2001; 2001US-008660216.
25-MAY-2001; 2001US-00866028.
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28-FEB-2001; 2001W3-US005230.
01-MAR-2001; 2001W0-US006520.
09-MAR-2001; 2001W3-US006666.
14-MAR-2001; 2001US-00808689.
22-MAR-2001; 2001US-00808689.
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2001WO-US017800
2001WS-US017800
2001US-00882636
2001US-00882636
2001WS-US019692
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16-AUG-2001; 2001US-00931836.
19-DEC-2001; 2001US-00028072.
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2000WO-US032678.
2000US-00747259.
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2001WO-US021066
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2000WO-US023328.
2000WO-US030952.
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Gerritsen ME, Goddard A,
Smith V, Stewart TA, Tu
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14-JUN-2001; 2
19-JUN-2001; 2
20-JUN-2001; 2
21-JUN-2001; 2
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24-AUG-2000; 2
10-NOV-2000; 2
01-DEC-2000; 2
20-DEC-2000; 2
20-DEC-2000; 2
20-PEC-2000; 2
20-PEC-2000; 2
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Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.

P-PSDB; ADA45741.

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Gao

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05-JAN-2000;
06-JAN-2000;
06-JAN-2000;
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The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the uptake of release of TMP-alpha from human blood, for modulating the uptake of glucose or FPA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating proliferation of endothelial cells, for stimulating the proliferation of endothelial cells, for stimulating the proliferation of endothelial cells, for stimulating proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour. The oligonucleotide probes are useful for isolating genomic and CDNA nucleotide sequences or are useful for isolating genomic and CDNA nucleotide sequences or interaction. A polymuleotide (II) encoding (I) is useful in chromosome mapping, in generation of antisense RNA and DNA, in the preparation of PRO polympeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and corremoning of therapeutically useful reagents, in gene therapy, for chromosome identification, as chromosome marker, and for generating probes. An anti-(I)-antibody is useful in the development and probes. An anti-(I)-antibody is useful in the development and correcting its expression in specific cells, tissues or serum, and for secures (I) and (II) are useful for tissue typing. This sequence encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TWF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; live; microvascular endothelial cell; glucose; FRA; skeletal muscle cell; adipocyte cell; glucose; FRA; endothelial cell tube formation; bone disorder cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteogylvan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a novel human secreted and transmembrane PRO polypeptide.
Claim 2; Fig 221; 659pp; English.
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Best Local Similarity
Matches 31; Conserv
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12-JUN-1998
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RESULT 63 ADA76171,

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2000WO-US000277,
2000WO-US000376,
98WO-US019330
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2001WO-US006666
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22-MAR-2001, 2001US-00816744, 2005-ARR-2001, 2001US-00818386. 10-MAY-2001, 2001US-00818386. 10-MAY-2001, 2001US-00864280. 10-MAY-2001, 2001US-00866216. 25-MAY-2001, 2001US-00866028. 25-MAY-2001, 2001US-00866028. 25-MAY-2001, 2001US-00866028. 25-MAY-2001, 2001US-00872015. 01-JUN-2001, 2001US-00882828. 19-JUN-2001, 2001US-00882838. 25-JUN-2001, 2001US-00887879. 22-JUN-2001, 2001US-01887879. 22-JUN-2001, 2001US-01887879. 22-JUN-2001, 2001US-018679.
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18-JUL-2001; 2001US-00908827.
06-AUG-2001; 2001US-00924419.
09-AUG-2001; 2001US-0092796.
16-AUG-2001; 2001US-0093836.
19-DEC-2001; 2001US-00028072.
2001US-00808689
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Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

XX OS

#### (GETH ) GENENTECH INC.

Gao W; Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G: Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

#### WPI; 2003-687639/65. P-PSDB; ADA76172.

New isolated nucleic acid encoding a secreted and transmembrane polypeptide, designated e.g. PRO1114 or PRO4978, useful in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

## Claim 2; Fig 221; 659pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for simulating the release of tumour necrosis factor-albba (TNR-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for proliferation or differentiation of chondrocyte cells and a method for opporting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The prolymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisenses kNA and DNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of herapeutically useful.

Competing either transgenic animals or knock-out animals which are useful in the development as tumours, for stimulating of proparing a condition responsive to the polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of submer ear utricular supporting cells, for stimulating differentiation of adipocyte cells, for stimulating differation of inner ear utricular supporting cells, for stimulating are useful for treating such a sports injuries and articular cartilage are useful for treating such as sports injuries and articular cartilage are useful for treating sports earlied of signification of supporting thalassemias and carticular parances and articular cartilage are useful for treating various mammalian and articular submaned local immune system cell infiltration. This associated disorders such as various thalassesement and manned for transpressed from uspresented f

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                                                                                                                                                                                               Human, gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; lung; colon; breast; prostate; rectum; cervix; liver; tumour; cancer; glucose uptake, PFA; adipocyte cell; pericyte cell; proteoglycan; cartilage; inner ear utricular supporting cell; cytokine; A-peptide; factor VIIA; endothelial cell.
                       Gaps
Query Match
Best Local Similarity 66.0%; Pred. No. 45;
Matches 31; Conservative 0; Mismatches 16; Indels 0;
                                           1835 ITCTIAATTITICATTITCCAGATTITCCTTCAGTITGGGTTTTGTTT 1881
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                                                                                                                 ADA18821 standard; cDNA; 1129 BP
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14-SEP-1998;
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ADA18821/c
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2000WO-US030873.
2000WO-US032678.
2000US-00747259.
                             99WO-US031274.
2000WO-US000219.
2000WO-US000277.
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2000WO-US004914.
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2000WO-US005601.
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2000WO-US030952,
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2001US-00796498.
2001WO-US006520.
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05-APR-2001; 2001US-00828366.
10-MAY-2001; 2001US-00854208.
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2001US-00886342.
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Filvaroff E, Gao W; Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; WPI; 2003-521854/49. P-PSDB; ADA18822.

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. lung, colon, breast, prostate, rectal, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides are useful in molecular by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the colon polypeptides or antibodies are used in preparing PRO polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies, such as tumours, for modulating the uptake of glucose or FRA by adipocyte cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the release of proteoglycans from pericyte cells, for stimulating the release of cytokines from PBMC cells, for inhibiting the binding of A-peptide to factor VIIA, for inhibiting the binding of A-peptide to factor VIIA, for inhibiting the binding of A-peptide to factor VIIA, for proliferation of endercedies of the invention. One of this sequence capresents a human PRO polymucleotide of the invention. One the sequence capresents a human page of all and and an antibodies.
New PRO nucleic acid, useful for preparing a composition for treating
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                                                                                    Claim 2; Fig 221; 660pp; English.
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                                 e.g., tumors.
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ADA61444 standard; cDNA; 1129 BP 20-NOV-2003 (first entry) Homo sapiens. ADA61444; ADA61444/c

Human; secreted and transmembrane protein, PRO, gene, ss, Tumour necrosis factor alpha release; TNF-alpha release; glucose uptake modulator; glucose uptake modulator; sell proliferation stimulator; cell differentiation stimulator; cell differentiation inhibitor; cytokine release stimulator; tumour; cell differentiation unithibitor; cytokine release stimulator; tumour; cervical tumour; rectal tumour; prostate tumour; rectal tumour; errical tumour; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker. ransmembrane. secreted. protein. PRO4327. cDNA. Novel. human. 

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02 - DEC - 1999; 99W0-USCSES 334.
02 - DEC - 1999; 99W0-USCSES 334.
02 - DEC - 1999; 99W0-USCSES 54.
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02 - DEC - 1999; 99W0-USCSES 55.
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05 - JAN - 2009; 99W0-USCS 105.
06 - JAN - 2009; 99W0-USCS 105.
06 - JAN - 2000; 2000W0-USCS 105.
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### (GETH ) GENENTECH INC.

3 Gao Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G: Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

#### WPI; 2003-695892/66. P-PSDB; ADA61445.

New PRO nucleic acid and encode polypeptides, are useful for manufacturing a medicament for diagnosing or treating cancer

### Claim 2; Fig 221; 660pp; English.

The invention describes 305 mucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the profile from human blood, for modulating the uptake of glucose or FRA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of Tlymphocyte cells, for stimulating the proliferation of Tlymphocyte cells, for stimulating the proliferation of Tlymphocyte cells, for stimulating the proliferation of Tlymphocyte cells, for stimulating the proliferation of Tlymphocyte cells, for stimulating proliferation of Tlymphocyte cells, for stimulating the brinding of A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte cells, for stimulating proliferation of endothelal cells, for stimulating proliferation of endothelal cells, for stimulating proliferation of endothelal cells, for stimulating proliferation of endothelal cells, for stimulating proliferation of endothelal cells, for stimulating proliferation of endothelal cells, for stimulating proliferation of endothelal cells, in dispension of proparation of reviews and consequences or are useful for isolating genomic and coher and endother protein of antisense probes (I) is also useful and endother endother and corremptor of the proparation of antisense RNA and DNA, in the proparation of PRO polypeptide, for generating transgent and correming of therapeutically useful reagents, and for generating probably in generation of antisense probases or serum, and detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from Economic cells, tissue typing. This sequence encodes confined the superior cells, tissue typing. This sequence encodes

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Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ga
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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a novel human secreted and transmembrane PRO polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         07-0CT-1998;
29-0CT-1998;
29-0CT-1998;
20-NOV-1998;
01-DEC-1998;
05-JAN-1999;
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15-SBP-1999;
15-SBP-1999;
05-OCT-1999;
29-NOV-1999;
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10-SEP-1998;
14-SEP-1998;
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                                                                                                                                                          ADB19229;
                                                                                                                      RESULT 66
SXXC
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Gao W;

Novel secreted and transmembrane PRO polypeptides useful for stimulating the release of tumor necrosis factor alpha and detecting the presence of tumor in a mammal.

stimulating the

Claim 2; Fig 221; 660pp; English.

The invention describes 305 nucleic acids encoding PRO (secreted and transmembranes) polypeptides (1). (1) is useful for stimulating the release of TNF-alpha from human blood, for modulating the uptake of glucose or FRA by skeletal muscle cells or adipocyt 

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps Match 1.1%; Score 21.4; DB 1; Length 1129; Local Similarity 66.0%; Pred. No. 45; les 31; Conservative 0; Mismatches 16; Indels 0; Query Match Matches

ö

RESULT 67

ò

ADB27770 standard; cDNA; 1129 BP. ADB27770/c

ADB27770;

20-NOV-2003 (first entry)

cDNA encoding human PRO polypeptide #111.

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; addenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; PPA; skeletal muscle cell; adipocyte cell; perioyte cell; perioyte cell; perioyte cell; perioyte cell; perioyte cell; perion cell; perioy cell; period cell; period cell; period cell; period cell; period cell; period cell; period cell; period cell; period cell; period cell; period cell; period cell; protecglycan; articular cartilage defect; ostecarchritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration. CCCCCXSX TAX BY THE PROPERTY BY THE STANDARD STA

Homo sapiens.

US2003082704-A1.

01-MAY-2003.

24-APR-2002; 2002US-00131819.

99US-0170262P. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072. 09-DEC-1999;

(GETH ) GENENTECH INC.

Deforge L, Desnoyers L, Filvaroff E, Gao W; A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Gerritsen ME, Goddard A, Smith V, Stewart TA, Tu Baker KP, Beresini M,

WPI; 2003-765415/72. P-PSDB; ADB27771. New PRO nucleic acid, useful for preparing a composition for treating e.g., tumor or for tissue typing

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis

cc factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. addrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as a missense RNA and DNA and in gene therapy. The polynucleotides may also consistent in preparing PRO polyopetides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful useful in the development and screening of therapeutically useful useful in the development and screening of therapeutically useful useful in the development and screening of therapeutically useful useful as tumours, for stimulating an inhibiting proliferation of medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of subman miscrovascular endothelial cells, for modulating proliferation of subman of or gene expression in periorte cells, for stimulating the proliferation of inner ear urricular supporting cells, for stimulating the proliferation of inner ear urricular supporting cells, for inducing endothelial cell tube formation and for cartilage defects, osteoarthritis and rheumacoid arthritis. PRO polypeptides which stimulate the release of protogolycans truncitular cartilage are useful for treating various mammalian haemoglobin-may benefit from enhanced local immune system cell infiltration. This sequence encodes a human PRO polypeptide of the invention. Note: The sequence encodes a human PRO polypeptide of the invention. Note: The sequence date for this pasent is also available in electronic format from

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; 

Gaps 1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; ive 0; Mismatches 16; Indels 0; 31; Conservative Similarity Query Match Local Best Loca Matches

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RESULT 68 ADA86249/c

ADA86249 standard; cDNA; 1129 BP.

(first entry) 20-NOV-2003

Novel human secreted and transmembrane protein PRO4327 cDNA.

Human; secreted and transmembrane protein; PRO; gene; ss;

Tumour necrosis factor alpha release; TNR-alpha release;

Jucose uptake modulator;

cell proliferation stimulator; cell differentiation stimulator;

cell differentiation inhibitor; cytokine release stimulator; tumour;

liver tumour; breast tumour; prosette tumour; rectal tumour;

cervical tumour; liver tumour; chromosome mapping; gene mapping;

gene therapy; chromosome identification; chromosome marker. 

Homo sapiens.

US2003082711-A1.

01-MAY-2003.

16-MAY-2002; 2002US-00147508.

98US-0091519P. 99WO-US012252. 99US-0143048P. 99US-00380137. 02-JUN-1999;

07~JUL-1999; 25-AUG-1999; 30-MAR-2000;

27

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The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (1). (1) is useful for stimulating the upcake of release of TYD-alpha from human blood, for modulating the upcake of gone expression in peake of stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of endotherial cells, for stimulating the proliferation of endotherial cells, for stimulating the proliferation of endotherial cells, for stimulating the proliferation of endotherial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour. The oligonucleotide probes are useful for isolating genomic and cells esequences or antisense probes. (1) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding in assays to identify other proteins or molecules involved in binding and gene mapping, in generation of antisense RNA and RNA, in the preparation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, in gene therapy, for chromosome identification, as chromosome marker, and for generating probes. An anti-(1)-antibody is useful in diagnostic assays for RNO, engo probes. An anti-(1)-antibody is useful in diagnostic assays for RNO, as an over a sources on in specific cells, tissue sor serum, and for a source an overed whimen servers of the proper properties of the properties and recombinant cell culture or natural and recome and the properties of the properties and recombined to the properties and recombined to the properties and re
                                                                                                                                                                                                                                                                                        Gao W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New PRO nucleic acid, useful for preparing a composition for treating
                                                                                                                                                                                                                                                                       Deforge L, Desnoyers L, Filvaroff E, G. A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2, Fig 221; 637pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e.g., tumor or for tissue typing.
01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
                                                                                                                                                                                                                                                                                                                                      Goddard A,
                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                             Beresini M,
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                                                                                                                                                                                                                                                                             Baker KP,
                                                                                                                                                                                                                                                                                                                                      Gerritsen
Smith V,
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; 0 Gaps .; 0 1.1%; Score 21.4; DB 1; Length 1129; 1835 TICTTAATITITICATITICCAGATITICCTTCAGTITIGGGTTTTGTTT 1881 1129 TTTTTTTTTTTTTTTTTCAGCTGGCACACAGGCTGGGTTTTTATT 1083 66.0%; Pred. No. 45; ive 0; Mismatches 31; Conservative Local Similarity Query Match Best Loca Matches a

Human, gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell: quicose: FFb. ADB15813 standard; cDNA; 1129 BP Human PRO polynucleotide #111. 20-NOV-2003 (first entry) ADB15813/ ID ADB1 XX AC ADB1 XX ADE XX ADE XX HUMB XX HUMB XW HUMB XW TUMP XW TUMP XW TUMP

endothelial cell tube formation, bone disorder, cartilage disorder, sports injury, protecylycan, articular cartilage defect, osteoarthritis, rheumatoid arthritis, haemoglobin-associated disorder thalassaemia; immine system cell infiltration.

Homo sapiens.

US2003087350-A1.

08-MAY-2003.

22-APR-2002; 2002US-00127821.

99WO-US012252. 04-AUG-1998; 02-JUN-1999; 25-AUG-1999;

98US-0095301P

30-MAR-2000; 2000WO-US008439. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC.

Gao W; Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ga ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; Gerritsen N Smith V, Baker KP,

2003-786941/74. P-PSDB; ADB15814 New PRO nucleic acid, useful for preparing a recombinant PRO polypeptide, and for manufacturing a medicament for diagnosing or treating tumor.

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polypucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the prelease of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymicalecides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymical cities may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful section as tumours, for stimulating and inhibiting proliferation antibodies, such as tumours, for stimulating and inhibiting proliferation of reagents. The PRO polypeptides or antibodies are used in presparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation glucose or FFA by skeletal muscle cells or adipocyte cells, for stimulating the moliferation of for gene expression in perioyte cells, for stimulating the proliferation of progression in perioyte cells, for stimulating the proliferation of adipocyte cells, for stimulating the proliferation of or gene expression in perioyte cells, for stimulating the proliferation of an appropriate and an analyses. the proliferation of inner car utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatofid arthritis. PRO polypeptides are also useful for treating various mammalian hemoglobin-associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polymucleotide of the invention. Note: The sequence data for this parent is also available in electronic format from USPIO at segdata.uspto.gov/sequence.html.

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

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Human, gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; artilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
TICTIAATITITICATITICCAGATITICCTTCAGITITGGGTTTTGTTT 1881
            1129 TITITITITITITITITITITITITITITITI
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98WO-US012456.
98WO-US017888.
98WO-US018024.
98WO-US019093.
98WO-US019094.
98WO-US019330.
98WO-US0193177.
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99WO-US020111.
99WO-US020594.
                                                               599/c
ADA47599 standard; cDNA; 1129
                                                                                                                                  Human PRO polynucleotide #111.
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99WO-US030095
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99WO-US030999
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                                                                                                               20-NOV-2003 (first entry)
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14.4UL-1998,
10.SEP-1998,
14.SEP-1998,
14.SEP-1998,
14.SEP-1998,
16.SEP-1998,
16.SEP-1998,
17.SEP-1998,
29.OCT-1998,
29.OCT-1998,
29.OCT-1998,
01.DEC-1998,
01.DEC-1998,
01.DEC-1998,
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15-SEP-1999;
05-OCT-1999;
29-NOV-1999;
30-NOV-1999;
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20-APR-1999;
14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                 17-APR-2003
 1835
                                                                                           ADA47599;
                                                    RESULT 70
ADA47599/
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New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, detecting the presence of tumor in a mammal, or
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        30-DEC-1999; 99W0-US031274.
30-DEC-1999; 99W0-US031274.
30-DEC-1999; 99W0-US031274.
30-DEC-1999; 99W0-US031274.
30-DEC-1990; 2000W0-US000277.
66-JAN-2000; 2000W0-US000277.
11-FEB-2000; 2000W0-US0003441.
24-FEB-2000; 2000W0-US004341.
24-FEB-2000; 2000W0-US004341.
24-FEB-2000; 2000W0-US004414.
24-FEB-2000; 2000W0-US004914.
24-FEB-2000; 2000W0-US006501.
10-MAR-2000; 2000W0-US005746.
02-MAR-2000; 2000W0-US005841.
10-MAR-2000; 2000W0-US005841.
11-MAR-2000; 2000W0-US005841.
11-MAR-2000; 2000W0-US005841.
11-MAR-2000; 2000W0-US005841.
11-MAR-2000; 2000W0-US005841.
11-MAR-2000; 2000W0-US005841.
11-MAR-2000; 2000W0-US005841.
11-MAR-2000; 2000W0-US005841.
11-MAR-2000; 2000W0-US005841.
11-MAR-2000; 2000W0-US005841.
11-MAR-2000; 2000W0-US005841.
11-MAR-2000; 2000W0-US005841.
11-MAR-2000; 2000W0-US005841.
11-MAR-2000; 2000W0-US005841.
11-MAR-2000; 2000W0-US005841.
11-MAR-2000; 2000W0-US005841.
11-MAR-2000; 2000W0-US005841.
11-MAR-2000; 2000W0-US005841.
11-MAR-2001; 2001WS-US00586622.
22-MAY-2001; 2001WS-US086622.
25-MAY-2001; 2001WS-US086622.
25-MAY-2001; 2001WS-US086623.
25-MAY-2001; 2001WS-US086623.
25-MAY-2001; 2001WS-US086623.
25-MAY-2001; 2001WS-US086633.
21-UNN-2001; 2001WS-US088633.
21-UNN-2001; 2001WS-US088633.
21-UNN-2001; 2001WS-US088633.
21-UNN-2001; 2001WS-US088633.
21-UNN-2001; 2001WS-US088633.
22-UNN-2001; 2001WS-US088633.
23-UNN-2001; 2001WS-US088633.
24-UNN-2001; 2001WS-US088633.
25-UNN-2001; 2001WS-US088633.
25-UNN-2001; 2001WS-US088633.
25-UNN-2001; 2001WS-US088633.
25-UNN-2001; 2001WS-US088633.
26-UNN-2001; 2001WS-US088633.
27-UNN-2001; 2001WS-US088633.
27-UNN-2001; 2001WS-US088633.
27-UNN-2001; 2001WS-US088633.
27-UNN-2001; 2001WS-US088633.
27-UNN-2001; 2001WS-US088633.
27-UNN-2001; 2001WS-US088633.
27-UNN-2001; 2001WS-US088633.
27-UNN-2001; 2001WS-US088827.
27-UNN-2001; 2001WS-US088633.
27-UNN-2001; 2001WS-US088633.
27-UNN-2001; 2001WS-US088633.
27-UNN-2001; 2001WS-US088633.
27-UNN-2001; 2001WS-US088633.
27-UNN-2001; 2001WS-US088633.
27-UNN-2001; 2001WS-US088633.
27-UNN-2001; 2001WS-US088633.
27-UNN-2001
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P-PSDB; ADA47600.
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22-DEC-1999;

CT:/#:/T C Sny uon

장원

modulating the uptake of glucose or free fatty acid by skeletal muscle cells or adipocyte cells.

US2003068795-A1

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TMF-alpha) from human blood, a method for stimulating the prospected, a method for stimulating the release of tumour necrosis factor-alpha (TMF-alpha) from human blood, a method for stimulating the prospected of a tumour in a mammal (e.g. adrema). In the prospection of a tumour in a mammal (e.g. adrema) in the constant prospection of a tumour in a mammal (e.g. adrema). The colymucleotides are useful in molecular biology, including uses as a second in proparing PRO MA and in gene therapy. The polymucleotides may also be used in proparing PRO Polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapoutically useful reagents. The PRO Polypeptides by recombinant techniques and in medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating of human microvascular endothelial cells, for modulating the uptake of stimulating differentiation of adipocyte cells, for stimulating proliferation of inner are articular supporting cells or T-lymphocyte cells, for inducing endothelial cells or adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating are useful for treating sports injuries and release of proteoglycans from cartilage are useful for treating sports injuries and arthritis and rheumatoid arthritis and rheumatoid arthritis and rheumatoid activities and second may benefit from enhanced local immune system cells and rheumatoid submand of second immune system cells in electronic format may benefit be may benefit be a training spatent is also various beneful sor treating second for the prolemation of the prolemance of the prolemance of the prole
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                                                                                     Claim 2; Fig 221; 659pp; English.
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Gaps Query Match
1.1%; Score 21.4; DB 1; Length 1129;
Best Local Similarity 66.0%; Pred. No. 45;
Matches 31; Conservative 0; Mismatches 16; Indels 0; Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

1835 TICTIAATITITICATITICAGATITICCTICAGTITIGGGTTTTGTTT 1881 ઠ g

ADA67394 standard; cDNA; 1129 BP Human PRO polynucleotide #111. 20-NOV-2003 (first entry) ADA67394; RESULT 71 ADA67394/c 

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; Thralpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; PRA; skeletal muscle cell; adipcoyte cell; glucose; PRA; inner ear utricular supporting cell; pericyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; endothelial cell tube formation; bone disorder; cartilage disorder; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Homo sapiens

98WO-US021141 99WO-US000106 99WO-US008615 99WO-US010733 99WO-US021090 99WO-US021547 99WO-US028214 98WO-US022991 98WO-US025108 99WO-US005190 99WO-US012252 99WO-US020944 99WO-US023089 99WO-US028634 000WO-US000376 2000WO-US004342 2000WO-US004414 2000WO-US004914 99WO-US028301 99WO-US031243 2000WO-US003565 000WO-US000277 000WO-US004341 24-AUG-2000; 2000WO-US023328 08-NOV-2000; 2000WO-US030952 SU-OW66 -0M66 99WO-15-APR-2002; 20-DEC-1999; 22-DEC-1999; 30-DEC-1999; 06-JAN-2000; 10-APR-2003 

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10-NOV-2000, 2000WO-US030873.
20-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000WO-US034956.
28-FEB-2011; 2001WS-00796498.
28-FEB-2011; 2001WS-00796498.
28-FEB-2011; 2001WS-US006520.
01-MAR-2001; 2001WS-0081649.
22-MAR-2001; 2001WS-0081649.
10-MAY-2001; 2001WS-0081649.
10-MAY-2001; 2001WS-0081649.
10-MAY-2001; 2001WS-0081649.
10-MAY-2001; 2001WS-0081649.
25-MAY-2001; 2001WS-00816638.
25-MAY-2001; 2001WS-00816638.
25-MAY-2001; 2001WS-00816638.
25-MAY-2001; 2001WS-00816638.
25-MAY-2001; 2001WS-00816638.
25-MAY-2001; 2001WS-00816638.
25-MAY-2001; 2001WS-0081638.
25-MAY-2001; 2001WS-00816938.
25-MUN-2001; 2001WS-0088187.
25-MUN-2001; 2001WS-0088187.
25-MUN-2001; 2001WS-0088187.
25-MUN-2001; 2001WS-0088187.
25-MUN-2001; 2001WS-0088187.
25-MUN-2001; 2001WS-0088187.
25-MUN-2001; 2001WS-0088187.
25-MUN-2001; 2001WS-0088187.
25-MUN-2001; 2001WS-0088187.
25-MUN-2001; 2001WS-0088187.
25-MUN-2001; 2001WS-00891887.
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#### (GETH ) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gr Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

#### WPI; 2003-695926/66. P-PSDB; ADA67395.

Novel isolated PRO secreted and transmembrane polypeptides useful for stimulating the release of tumor necrosis factor-alpha from human blood and detecting the presence of a tumor in a mammal.

# Claim 2; Fig 221; 660pp; English

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide a method for stimulating the release of tumour necrosis according the presence of a tumour in a mammal (e.g. adrenal, necrosis of actor-alpha (TNF-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. adrenal, lung, certification or differentiation of condrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating of these transgenic animals or knock-out animals which are hybridisation propering PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are used in preparing a condition responsive to the polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours. for stimulating of therapeutically useful readents and screening of incore or PRA by skeletal muscle cells, for modulating the uptake of stimulating differentiation of adipocyte cells, for stimulating proliferation of or gene expression in periotyte cells, for stimulating proliferation of or gene expression in periotyte cells, for stimulating proliferation of an expression in periotyte cells, for stimulating the public stimulating differentiation of adipocyte cells, for stimulating cells or stimulating and and for traating various bone and/or cartilage disconcers such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans

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from cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian hasmoglobin-associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polymucleotide of the invention. Note: The sequence data for this patent is also available in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrend; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FRA; skeleral muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; pericyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage disorder; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
                                                                                                                                                                                                             Gaps
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                                                                                                                                                                           1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; tive 0; Mismatches 16; Indels 0;
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                                                                                                                                              Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
                                                                                                                 from USPTO at sequata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA encoding human PRO polypeptide #111.
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ADB30401 standard; cDNA; 1129 BP.
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98WO-US022992.
98WO-US024855.
98WO-US025108.
99WO-US000106.
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98WO-US019177.
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98WO-US019093
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                                                                                                                                                                                              Best Local Similarity 66.0
Matches 31; Conservative
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2001US-00927796
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18-FEB-2000;
22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
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08-NOV-2000;
10-NOV-2000;
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06-AUG-2001;
09-AUG-2001;
                                01-DEC-1999;
01-DEC-1999;
02-DEC-1999;
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15-MAR-2000;
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02-MAR-2000;
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                29-NOV-1999
30-NOV-1999
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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for proliferation presence of a tumour in a mammal (e.g. adremal, lung, colon, breast, prosetate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology in generating to polymorleotides are useful in molecular biology, in generating a turissense RNA and BNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of theoryptides may also generating either transgenic animals or knock-out animals which are useful in the development and screening of the properties or antibodies are used in preparing a condition responsive to the polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies are used in preparing of interaction of adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating the uptake of stimulating differentiation of adipocyte cells, for stimulating the proliferation of or gene expression in periory cells, for stimulating the proliferation of or gene expression in periory cells, for stimulating and cells. For stimulating the proliferation of or gene expression in periory cells, for stimulating and arthritis. PRO polypeptides which stimulate such as various medicans or training each useful for treating various medicated disorders such as various thalassasemias and carting are useful for treating v
                                                                                                                                                                                                                                                                                         New isolated PRO polypeptides e.g. PRO1801 and PRO1114, useful in the preparation of a medicament for treating a condition responsive to PRO polypeptide, and as therapeutic agents e.g. vaccines.
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                                                                                                                   Deforge L, Desnoyers L, Filvaroff E, G:
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 221; 660pp; English.
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16-AUG-2001; 2001US-00931836.
19-DEC-2001; 2001US-00028072.
                                                                                                                     Baker KP, Beresini M, De
Gerritsen ME, Goddard A,
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                                                                                                                                                Gerritsen ME, Goddard
Smith V, Stewart TA,
                                                                     (GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO4327 cDNA.

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Human; secreted and transmembrane protein; PRO; gene; ss;
Tumour necrosis factor alpha release; TNF-alpha release;
glucose uptake modulator;
glucose uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inhibitor; cytokine release stimulator;
lung tumoue; colon tumour; breast tumour; prostate tumour; rectal tumour;
cervical tumour; liver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
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Homo sapiens.

US2003082693~A1.

01-MAY-2003.

22-APR-2002; 2002US-00127843.

05-JUN-2000; 2000US-0209832P. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G? Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-786907/74. P-PSDB; ADA85698. New PRO nucleic acid, useful for preparing a composition for treating e.g., tumor or for tissue typing.

Claim 2; Fig 221; 637pp; English.

The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the upcake of glucose or FFA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of endothelial cost stimulating the proliferation of endothelial cost estimulating proliferation of endothelial colls, for stimulating the proliferation of endothelial colls, for stimulating the binding the presence of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour. The oligonucleotide probes are useful for seleting groupliferation of endothelial cells, for defecting the proteins or molecules involved in binding in assays to identify other proteins or molecules involved in binding interaction. A polymulectide (II) endothed (II) succells involved in binding in generation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development, and screening of therapeutically useful reagents, in gene therapy, for chromosome identification, as chromosome marker, and for generating the structing for probes. An anti-(I) -antibody is useful in disponent assays for PRO, e.g. Chromosome identification, as chromosome marker, and for generating and for a propertion of the propertion of screening of the propertion of screening of the propertion of screening of second or screening of the propertion of screening of second or screening of second or screening of second or screening of second or screening of second or screening of second or screening of s detecting its expression in specific cells, tissues or serum, and for adfinity purification of RNO from recombinant cell culture or natural sources. (I) and (II) are useful for tissue typing. This sequence encodes a novel human secreted and transmembrane PRO polypeptide. 

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps 0; Query Match
1.1%; Score 21.4; DB 1; Length 1129;
Best Local Similarity 66.0%; Pred. No. 45;
Matches 31; Conservative 0; Mismatches 16; Indels 0.

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ADA96909 standard; cDNA; 1129 BP

20-NOV-2003 (first entry)

Human PRO polynucleotide #111.

ostecarthritis; Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; INF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteogytean; articular cartilage defect; osteoarthritis, rheumatoid arthritis, haemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Homo sapiens.

JS2003082705-A1.

01-MAY-2003.

24-APR-2002; 2002US-00131829.

09-DEC-1999; 99US-0170262P. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC.

3 Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G. Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-755112/71. P-PSDB; ADA96910.

New PRO nucleic acid, useful for preparing a composition for treating e.g., tumor or for tissue typing.

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNP-alpha) from human blood, a method for stimulating the proliferation of indended of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as phytidisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also antisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in penerating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful andicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for modulating definer expression in periorte cells, for stimulating proliferation of of inner ear utricular supporting cells, for stimulating proliferation of of inner ear utricular supporting cells, for stimulating cells, for induding endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and ADA96909/
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11-FEB-2000;
        $\frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{\pi} & \frac{\pi}{
arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian hemoglobin-associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polynucleotide of the invention. Note: The sequence data for this patent is also available in electronic format from USPIO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FRA; skeletal muscle cell; adipocyte cell; geriotre cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rhewmatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
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                                                                                                                                                                                                                                                      DB 1; Length 1129;
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                                                                                                                                                                                                                Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
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66.0%; Pred. No. 45;
htive 0; Mismatches 16; Indels
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98WO-US019093.
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98WO-US017888
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98WO-US022991.
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99WO-US012252
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99WO-US020594
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                                                                                                                                                                                                                                                                     Best Local Similarity
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ADA79213/c
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2001US-00854280
2001US-00866216.
2001US-00866028.
2001US-00866034.
2001US-00866034.
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2001US-00874503,
2001US-00882636,
2001US-00886342,
2001WO-US019692,
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2001US-00828366.
2001US-00854208.
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99WO-US030095
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2000WO-US005004.
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2001US-00908827.
2001US-00924419.
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99WO-US021547
                                        99WO-US028313
                                                      99WO-US028409
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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNR-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. adrenal, lung, or proliferation or differentiation of chondrocyte cells and a method for proliferation presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prosetate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating a natisanse RNA and BNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening or knock-out animals which are useful in the development and screening or knock-out animals which are useful in the development as tumours, for antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or studential cells, for modulating the uptake of glucose or FRA by skeletal muscle cells, for stimulating differentiation of adipocyte cells, for stimulating the proliferation of inner ar utricular supporting cells, for stimulating the proliferation of inner ar utricular supporting cells, for reating various mentaling and cells. For inducing endothelial cells is entitled to retain a supporting cells, for meating sortes related joint problems, articular cartilage are useful for treating sortes related joint problems, articular as valouse thal sessence and articular submaned local immune system cell infiltration. This may benefit from enhanced local immune system cell infil
                                                                                                                                                                                                     New secreted and transmembrane PRO polypeptides and nucleic acids, useful in detection and treatment of cancer and in modulating the uptake of glucose or free fatty acid by skeletal muscle cells or adipocyte cells.
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                                                                                          Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gr
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z,
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ADA87352/c
ID ADA87352 standard; cDNA; 1129
09-AUG-2001; 2001US-00927796.
16-AUG-2001; 2001US-00931836.
19-DEC-2001; 2001US-00028072.
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                                                             (GETH ) GENENTECH INC
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P-PSDB; ADA79214.
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Human; secreted and transmembrane protein; PRO; gene; ss;
furmour necrosis factor alpha release; TMF-alpha release;
glucose uptake modulator; FFA uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inhibitor; cytokine release stimulator;
lung tumoue; colon tumour; breast tumour; prostate tumour; rectal tumour;
cervical tumour; liver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
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2000WO-US0063197
99WO-US008615.
99WO-US010733.
99WO-US012252.
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99WO-US020944.
99WO-US021090.
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99WO-US030095.
99WO-US030911.
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98WO-US019093
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06-JAN-2000; 2
06-JAN-2000; 2
11-FEB-2000; 3
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14-SEP-1998;
16-SEP-1998;
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15-SEP-1999;
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The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the release of FNF-alpha from human blood, for modulating the uptake of glucose or FFA by skeletal muscle cells or adjoovte cells, for stimulating the proliferation of differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in periove cells, for stimulating the release of proteoglycans from cartilage, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating can be provided to factor VIIA, for inhibiting the differentiation of adjoocyte cells, for stimulating proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour. The oligonucleotide probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beresini M, Deforge L, Desnoyers L, Filvaroff E, G
NE, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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2001US-00802706
2001US-00808689
2001US-0081866744
2001US-00884208
2001US-00884208
2001US-00860216
2001US-008660216
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2001US-00874503.
2001US-00882636.
2001US-00886342.
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2001US-00887879
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Smith V, Stewart TA,
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20-DEC-2000;
20-DEC-2000;
                                                                30-MAY-2000;
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Gao W;

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are useful for isolating genomic and cDNA nucleotide sequences or antisense probes. (I) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding interaction. A polymucleotide (II) encoding (I) is useful in chromosome and gene mapping, in generation of antisense RNA and DNA, in the preparation of ERO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful in the development and chromosome identification, as chromosome marker, and for generating probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g. detecting at its agression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. (I) and (II) are useful for tissue typing. This sequence encodes a novel human secreted and transmembrane PRO polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tummour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FPA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
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0; Mismatches 16; Indels
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25-AUG-1999; 99US-00380137.
02-MAR-2000; 2000WO-US005841.
01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
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                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                         Matches
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New PRO nucleic acid, useful for preparing a recombinant PRO polypeptide, and for manufacturing a medicament for diagnosing or treating tumor.

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Gao

Deforge L, Desnoyers L, Filvaroff E, Ga A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z;

Baker KP, Beresini M, De Gerritsen ME, Goddard A,

Stewart TA,

Gerritsen ME, Smith V, Stewe

WPI; 2003-786940/74. P-PSDB; ADB16555.

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Mon Aug

from USPTO at segdata.uspto.gov/sequence.html. Fig 221; 637pp; English 5 

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps · 0 Score 21.4; DB 1; Length 1129; Pred. No. 45; 0; Mismatches 16; Indels 0. Query Match Best Local Similarity 66.0%; Matches 31; Conservative ઠ

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1129 trritritritritritritrageracacacacacacacacacacararrara 1083 1835 ITCITAATITITCATITCCAGATITCCTTCAGITTGGGTTTTGTTT 셤

ADA91646; RESULT 78

(first entry) 20-NOV-2003 Novel human secreted and transmembrane protein PRO4327 cDNA.

Human; secreted and transmembrane protein; PRO; gene; ss;
Tumour necrosis factor alpha release; TNF-alpha release;
Jucose uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inhibitor; cytokine release stimulator; tumour;
lung tumoue; colon tumour; breast tumour; prostate tumour; rectal tumour;
cervical tumour; liver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker. 

Homo sapiens

US2003082694-A1

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNR-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating attribution probes, in chromosome and gene mapping, in generating attribution probes, in chromosome and gene mapping, in generating attribution that the number of the stay. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in Companion of the stay glucose or FFA by Sketered imustre cells, for stimulating proliferation of or gene expression in pericyte cells, for stimulating proliferation of or gene expression in pericyte cells, for stimulating proliferation of inner ear utricular supporting cells, for stimulating cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage are cell tube formation and for treating various bone and/or cartilage which stimulate the release of proteoglycans arthcular cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. Proplypeptides are also useful for treating various mammalian haemoglobinmay benefit from enhanced local immune system cell infiltration. Note: The sequence represents a human PRO polymclectide of the invention. Note:

ADA91646 standard; cDNA; 1129 BP.

01-MAY-2003

22-APR-2002; 2002US-00127845.

03-MAR-2000; 2000US-0187202P. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC.

Gao W; Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ga Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-786908/74. P-PSDB; ADA91647 New PRO nucleic acid, useful for preparing a recombinant PRO polypeptide, or a composition for treating e.g., tumor or for tissue typing.

Claim 2; Fig 221; 637pp; English

The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (1). (1) is useful for stimulating the creates of TNN-alpha from human blood, for modulating the uptake of glucose or FRA by skeletal muscle cells or adipocyte cells, for grimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of the capression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating cells, corrected the presence of tumour in a mammal. The tumour is lung, colon, breast, cells, for stimulating proliferation of endochelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, corrected isolating genomic and cDNA nucleotide sequences or antisense probes. (1) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding in gene mapping, in generation of antisense study in the companies of therapeutically useful reagents, in gene therapy, for chromosome identification, as chromosome marker, and for generating correcting its expression in specific cells, tissues or serum, and for animals or animal servet of probes. (1) are useful in this sequence encodes sourced and transmentation. novel human secreted and transmembrane PRO polypeptide.

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps / Match 1.1%; Score 21.4; DB 1; Length 1129; Local Similarity 66.0%; Pred. No. 45; nes 31; Conservative 0; Mismatches 16; Indels 0; Ouery Match Best Loca Matches

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1835 TICTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881 

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ADB14709 standard; cDNA; 1129 (first entry) 20-NOV-2003 ADB14709; ADB14709/c RESULT 79 UX XX BX BX BX BX BX

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;

Human PRO polynucleotide #111.

liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; anner ear utricular supporting cell; practicyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; sports injury; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Homo sapiens.

US2003087351-A1.

08-MAY-2003.

22-APR-2002; 2002US-00127822.

17-UUN-1999; 99US-0089532F.

02-UW-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0380137.

30-NOV-1999; 99US-0

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W; Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; WPI; 2003-786942/74.
P-PSDB; ADB14710.
New PRO nucleic acid, useful for manufacturing a medicament for

diagnosing or treating tumor.

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the prositeration or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The projuncleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating colon, breast, prostated and mementar biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating a chical manuals or knock-out animals which are setul in the development and screening of knock-out animals which are useful in the development and screening or knock-out animals which are useful in the development and screening or antibodies are used in preparing a condition responsive to the polypeptides or antibodies are used in preparing a muticovascular andothelal cells, for modilating the uptake of thuman microvascular andothelal cells, for modilating the uptake of stimulating differation of inner ar utricular supporting cells, for stimulating the proliferation of inner ar utricular supporting cells, for stimulating cells, for modilating the uptake of stimulating differation of inner ar utricular supporting cells, for stimulating cells, for modilating cells, for modilating cells, for modilating and continues and carthritis. PRO polypeptides which stimulates as ports injuries and articular cartilage are useful for treating sports-related joint problems, also useful for treating sports-related joint problems, associated disorders such as various thalassaemias and andore cartilage defects, osteoarthritis and rhemmatoid at heared local immune system cell infilteration. This sequence repres

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

ó Gaps Human, secreted and transmembrane protein; PRO; gene; ss;
Tumour necrosis factor alpha release, TNF-alpha release;
glucose uptake modulator; FFA uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inhibitor; cytokin. ö 1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; ive. 0; Mismatches 16; Indels 0; 1835 TICITAATITITICATITICCAGATITICCTICAGITITGGGTTITGTTT 1881 Novel human secreted and transmembrane protein PRO4327 cDNA. ADB18670 standard; cDNA; 1129 BP. 15-APR-2002; 2002US-00123292. 98WO-US025108 99WO-US000106 99WO-US020594 99WO-US028214 99WO-US030720 99WO-US031243 98WO-US014552 98WO-US017888 98WO-US019094 98WO-US022992 98WO-US024855 99WO-US005028 99WO-US005190 99WO-US008615 99WO-US010733 99WO-US020111 99WO-US021090 99WO-US021547 99WO-US023089 98WO-US019177 98WO-US019437 98WO-US021141 99WO-US020944 99WO-US028313 99WO-US028409 99WO-US028301 99WO-US028634 99WO-US028564 99WO-US030095 99WO-US028551 99WO-US030911 (first entry) Ouery Match Best Local Similarity 66.08 Matches 31, Conservative 99WO-US0 US2003073211-A1. 20-DEC-1999; 22-DEC-1999; 30-DEC-1999; Homo sapiens. , 666 :666 666 20-NOV-2003 , 998; 666 6666 17-APR-2003 ADB18670; 16-SEP-19 17-SEP-19 -SEP-08-SEP-ADB18670/c RESULT 80 ò qq

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21. PAR. 2000; 2000MO-US01919.

22. MAY - 2000; 2000MO-US01919.

23. MAY - 2000; 2000MO-US01941.

24. MAG - 2000; 2000MO-US01941.

26. JUL - 2000; 2000MO-US01952.

21. AUG - 2000; 2000MO-US01952.

23. AUG - 2000; 2000MO-US02031.

24. AUG - 2000; 2000MO-US02352.

24. AUG - 2000; 2000MO-US03952.

25. AUG - 2000; 2000MO-US03952.

26. DEC - 2000; 2000MO-US03952.

26. DEC - 2000; 2000MO-US03952.

26. DEC - 2000; 2000MO-US03952.

27. DEC - 2000; 2000MO-US03952.

28. FEB - 2001; 2000MO-US03952.

20. DEC - 2000; 2000MO-US03952.

20. DEC - 2000; 2000MO-US03952.

20. DEC - 2000; 2000MO-US03952.

20. DEC - 2000; 2000MO-US03952.

20. MAR - 2001; 2001WS-00866.

25. MAR - 2001; 2001WS-00866.

25. MAY - 2001; 2001WS-00866.

25. MAY - 2001; 2001WS-00866.

26. MAY - 2001; 2001WS-00866.

27. UNN - 2001; 2001WS-00866.

29. JUN - 2001; 2001WS-00866.

29. JUN - 2001; 2001WS-00866.

29. JUN - 2001; 2001WS-0086.

29. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

20. JUN - 2001; 2001WS-0086.

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                                                  06-JAN-2000; 2000WO-US000376:
11-PEB-2000; 2000WO-US000376:
11-PEB-2000; 2000WO-US000341:
12-PEB-2000; 2000WO-US00441:
24-PEB-2000; 2000WO-US004414:
24-PEB-2000; 2000WO-US006414:
24-PEB-2000; 2000WO-US005004
10-MAR-2000; 2000WO-US00581:
10-MAR-2000; 2000WO-US00581:
11-MAR-2000; 2000WO-US00581:
11-MAR-2000; 2000WO-US00581:
11-MAR-2000; 2000WO-US00581:
11-MAR-2000; 2000WO-US00581:
11-MAR-2000; 2000WO-US00581:
11-MAR-2000; 2000WO-US00581:
11-MAR-2000; 2000WO-US00581:
11-MAR-2000; 2000WO-US00753:
11-MAR-2000; 2000WO-US00753:
11-MAR-2000; 2000WO-US00753:
11-MAR-2000; 2000WO-US00753:
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Gao W; Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gr Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Matanabe CK, Wood WI, Zhang Z;

2003-695954/66. P-PSDB; ADB18671. New isolated nucleic acid and encoded PRO polypeptide, are useful in the diagnosis and treatment of cancer.

Claim 2; Fig 221; 638pp; English.

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                The invention describes 305 nucleic acids encoding PRO (secreted and transmembranes) polypeptides (1). (1) as useful for stimulating the release of TNF-alpha from human blood, for modulating the uptake of glucose or PFA by skeletal muscle cells or adipocyt
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                                                                                                                                                                 1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; ative 0; Mismatches 16; Indels 0
                                                                                                                                                                                                                                                           1835 ITCTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881
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                                                                                                                           Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
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ID ADA93885 standard; cDNA; 1129 BP.
                                                                                                                                                                                           al Similarity 66.0
31; Conservative
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                                                                                                                                                                        Query Match
Best Local &
                                                                                                                                                                                                                  Matches
X88888X8
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Human; gene, ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; PFA; seeletal muscle cell; adipocyte cell; perfocyte cell; perfocyte cell; perfocyte cell; perfocyte cell; perfocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; shound alphay; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration. 

Human PRO polynucleotide #111.

20-NOV-2003 (first entry)

US2003077722-A1. Homo sapiens.

24-APR-2003.

03-MAY-2002; 2002US-00137872.

03-MAR-2000; 2000US-0187202P. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ge Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; WPI; 2003-755077/71.

P-PSDB; ADA93886.

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Gao

for the New isolated, secreted and transmembrane PRO nucleic acid, useful for tdiagnosis, prevention and/or treatment of tumors, such as lung, colon, breast, prostate, rectal, cervical and/or liver tumors.

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNP-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The

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polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating anticense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and soreening of therapeutically useful cagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of adipocyte cells, for stimulating proliferation of adipocyte cells, for stimulating proliferation of adipocyte cells, for stimulating proliferation of inner ear utricular supporting cells or T-lymphocyte proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothedial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and articular cartilage are useful for treating sports-related joint problems, for mon cartilage are also useful for treating various mammalian haemoglobinent associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human RRO polymcleotide of the invention. Note:

The sequence represents a human RRO polymcleotide of the invention format from repon at account an appendix also are also useful for the also are also the immune and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human RRO polymcleotide of the invention. Note:

The sequence represents a human RRO polymcleotide of the invention of the formation of the formation of the formation of the formation of the formation of the formation o
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Tumour necrosis factor alpha release; TNF-alpha release;
glucose uptake modulator;
cell proliferation stimulator; tel differentiation stimulator;
lung tumous; colon tumour; breast tumour; prostate tumour; rectal tumour; und tumous; colon tumour; breast tumour; prostate tumour; rectal tumour; oervical tumour; inver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
1.1%; Score 21.4; DB 1; Length 1:
Best Local Similarity 66.0%; Pred. No. 45;
Matches 31; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from USPTO at segdata.uspto.gov/sequence.html.
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99WO-US020111.
99US-00403297.
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02-UUN-2000; 2000WO-US015264.
23-AUG-2000; 2000WO-US023522.
01-DEC-2000; 2000WO-US033678.
19-DEC-2001; 2001US-00028072.
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01-SEP-1999;
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The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (1). (1) is useful for stimulating the uptake of release of TNF-alpha from human blood, for modulating the uptake of glucose or FPA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells, cor stimulating the proliferation of inner ear utricular supporting cells, tor stimulating the proliferation of Inner ear utricular supporting cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the brobiteration of T-lymphocyte cells, for stimulating the proliferation of F-lymphocyte cells, for stimulating the brobiteration of F-lymphocyte cells, for stimulating proliferation of E-long the beptide to factor VIIA, for inhibiting the differentiation of adipocyte cells, for stimulating proliferation of endothelial cells, for stimulating proliferation of endothelial cells, for detecting choracted and colon, breast, prostate, rectal, cervical or liver tumour. The oligonucleotide probes or are useful for isolating genomic and cDNA nucleotide sequences or antisense probes. (1) is also useful as therapeutic agent. PRO in useful in assays to identify other proteins or molecules involved in binding in separation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and correction, as chromosome identification, as chromosome marker, and for generating correction of probes. An anti-(1) antibody is useful in diagence or screening of therapeutically useful in diagense in a derivative process. An anti-(1) antibody is useful in diagense in anti-(1) and process or an anti-(1) antibody is useful in diagense in a dentification, as chromosome agence or and gene therapy, for the probes, An anti-(1) antibody is useful in diagense or an anti-order and anti-order and acceptance or an acceptance or an acceptance or an acceptance
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                                                                                                                                                                                                                                                                      PRO nucleic acid, useful for preparing a composition for treating e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. (I) and (II) are useful for tissue typing. This sequence enco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                       Beresini M, Deforge L, Desnoyers L, Filvaroff E, G.
ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1835 TICTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a novel human secreted and transmembrane PRO polypeptide.
                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Fig 221; 637pp; English.
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                                                                                                                                                                                                                                                                                                          tumor or for tissue typing.
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(GETH ) GENENTECH INC.
                                                                                                                      Stewart TA,
                                                                                                                                                                                 WPI; 2003-755108/71.
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                                                           Baker KP,
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                                                                                                                      Smith V,
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Homo sapiens.

01-MAY-2003

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Novel human secreted and transmembrane protein PRO4327 cDNA.
                                              ACD98534 standard; cDNA; 1129 BP.
                                                                                                                                26-SEP-2003 (first entry)
                                                                                                                                                                                                                                                                                        Homo sapiens.
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14-SEP-1998;
14-SEP-1998;
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08-SEP-1999;
13-SEP-1999;
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05-JAN-2000;
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01-DEC-1999
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                                                                                        ACD98534;
    RESULT 84
                            ACD98534/
                                                                      The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNR-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and amethod for detecting the presence of a tumour in a mammal (e.g. adremal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The prolynucleotides are useful in melecular biology, in generating a riseases KNA and bin gene therapy. The polynucleotides may also a riseases KNA and bin gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening or knock-out animals which are useful in the development and screening or knock-out animals which are useful in the development as tumours, for stimulating and inhibiting proliferation of antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for medilating the uptake of stimulating differantiation of antipocyte cells, for stimulating the proliferation of inner ear utrivilar such as sports injuries and arthritis. PRO polypeptides which stimulate cells, for stimulating and continue ear utrivilar such as sports injuries and arthritis. PRO polypeptides which stimulates and the machine are useful for treating various marmalian are cartilage are useful for treating various marmalian and arthritis. PRO polypeptides which stimulassaemias and arthritis and cartilage are useful for treating various marmalian and eaguence tase useful for treating various and may benefit from enhanced local immune system cell infilleration. This sequence tare or this patent is also event in the may benefit from temperation and when the may benefit from te
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New PRO nucleic acid, useful for preparing a recombinant PRO polypeptide, preparing a composition for treating e.g., tumor, or for tissue typing.
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66.0%; Pred. No. 45;
tive 0; Mismatches 16; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                 Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gz
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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immune system cell infiltration.
                                                                                                                                                                                                                  09-DEC-1999; 99US-0170262P.
01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
                                                                                                                                                                             16-MAY-2002; 2002US-00147484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.0°
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
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P-PSDB; ADB13094.
                                                                                    US2003082710-A1.
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Human, secreted and transmembrane protein; PRO; gene therapy; chromosome identification; tissue typing; gene; ss.
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99WO-US028565
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The invention describes an isolated nucleic acid encoding a PRO (secreted and transmembrane) polypeptide. Nucleic acids which encode PRO can be used to generate either transgenic animals or Knock-out animals useful in developing and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy, in chromosome identification, as chromosome markers, or in generating probes. The PRO polypeptides are useful as molecular markers protein electrophoresis, and the isolated PRO polypeptides and nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO, and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, or in generating probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G.
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                                                                                                                                           2001US-00802706.
2001US-00806689.
2001US-00816744.
2001US-00854208.
2001US-00854280.
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2001US-00866028.
2001US-00866034.
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2001WO-US006520.
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2001US-00882636.
2001US-00886342.
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2001US-00908827.
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02-MAR-2000;
10-MAR-2000;
15-MAR-2000;
20-MAR-2000;
21-MAR-2000;
30-MAR-2000;
17-MAY-2000;
22-MAY-2000;
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14-MAR-2001;
22-MAR-2001;
05-APR-2001;
10-MAY-2001;
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28-FEB-2001;
01-MAR-2001;
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20-DEC-2000;
20-DEC-2000;
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25-MAY-2001;
                                                                                                                      02-JUN-2000;
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Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FPA; skeletal muscle cell; adipocyte cell; perioyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
affinity purification of PRO from recombinant cell culture or natural sources. This sequence encodes a novel human secreted and transmembrane PRO polypeptide
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                                                                                                                                                                                                                   DB 1; Length 1129;
                                                                                                                                             Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
                                                                                                                                                                                                                Query Match
1.1%; Score 21.4; DB 1; Length 1
Best Local Similarity 66.0%; Pred. No. 45;
Matches 31; Conservative 0; Mismatches 16; Indels
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98WO-US024855.
98WO-US025108.
99WO-US000106.
99WO-US005028.
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ADA74347/C
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23-MAY-2000; 2000WO-US014941.
02-UTN-2000; 2000WO-US014941.
13-AUG-2000; 2000WO-US015264.
23-AUG-2000; 2000WO-US022031.
23-AUG-2000; 2000WO-US02328.
08-NOV-2000; 2000WO-US023328.
08-NOV-2000; 2000WO-US03328.
09-DEC-2000; 2000WO-US03673.
10-NOV-2000; 2000WO-US03678.
20-DEC-2000; 2000WO-US0366498.
28-FEB-2001; 2001WG-US06666.
01-MAR-2001; 2001WG-US06666.
01-MAR-2001; 2001US-00808689.
22-MAR-2001; 2001US-00808689.
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2000WO-US000377-
2000WO-US000376-
2000WO-US004441.
2000WO-US004412-
2000WO-US004414-
2000WO-US004414-
2000WO-US004414-
2000WO-US0050501-
2000WO-US0050501-
2000WO-US005546-
2000WO-US005546-
2000WO-US005546-
2000WO-US005546-
2000WO-US005546-
2000WO-US005546-
2000WO-US005546-
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99WO-US03095.
99WO-US03099.
99WO-US030720.
99WO-US031243.
99WO-US028634.
99WO-US028634.
99WO-US028551.
99WO-US028564.
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09-AUG-2001; 2001US-00927796
16-AUG-2001; 2001US-00931796
19-DEC-2001; 2001US-00028072.
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(GETH ) GENENTECH INC

3 Gao Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gr E, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; Stewart TA, Baker KP, Beres Gerritsen ME, ( Smith V, Steway

WPI; 2003-625490/59.

P-PSDB; ADA74348. 

Novel secreted and transmembrane PRO polypeptides and polynucleotides enceding them, useful for treating bone disorders, arthritis, heart attack, injuries, tumors, and stimulating release of Tumor Necrosis Pactor-alpha from human blood.

Claim 2; Fig 221; 659pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO invention also relates to an antibody which specifically binds to a PRO invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the proferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adremal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The prolynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides may also a release that and some mapping, in generating colon probe by the polymore of the proparating properties by recombinant techniques and in gene therapy. The polymore of the ast the development and screening of knock-out animals which are useful in the development and screening of the proparating as tumours, for stimulating of interaction as tumours, for stimulating and inhibiting proliferation of inner and condition and inhibiting proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for stimulating differentiation of adipocyte cells, for stimulating of the proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cells, for madinating the uproblems, brone and/or cartilage disorders such as sports injuries and articular cartilage are useful for treating sports engage of the proliferation of inner ear utricular sports of the proliferation of inner ear utricular sports injuries and articular cartilage are useful for treating sports-related joint problems, articular cartilage are useful for treating sports-related joint problems, associated disorders such as various thalassaemas and conditions. This sequence represents

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps ; 0 Query Match 1.1%; Score 21.4; DB 1; Length 1129; Best Local Similarity 66.0%; Pred. No. 45; Matches 31; Conservative 0; Mismatches 16; Indels 0;

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1835 ITCTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881 1129 TITTITITITITITITICAGCTGGCACACAGCCTGGGTTTTATT 1083 ð

ADB24580 standard; cDNA; 1129 BP ADB24580/

ADB24580;

20-NOV-2003 (first entry)

Human PRO polynucleotide SEQ ID NO 221.

Human, gene, ss, PRO; secreted polypeptide, transmembrane polypeptide, tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer, adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endochelial cell; glucose; FRA; MARKE KEKEKEKE

skeletal muscle cell, adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheunatoid arthritis; hemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Homo sapiens.

US2003077713-A1.

24-APR-2003.

22-APR-2002; 2002US-00127839.

05-JUN-2000; 2000US-0209832P. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC.

Gao W; Baker XP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ge Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

2003-755068/71. P-PSDB; ADB24581 New isolated, secreted and transmembrane PRO polypeptides and nucleic acids, useful for the diagnosis, prevention and/or treatment of tumors, such as lung, colon, breast, prostate, rectal, cervical and/or liver

Claim 2; Fig 221; 637pp; English.

%XCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCX

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynuclectides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, color, breast, prostate, rectal, kidney, cervical and liver tumours). The colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymuclectides are useful in molecular biology, including uses as a nicker transpends by recombinant techniques and also the used in preparing PRO polypeptides by recombinant techniques my also consistent in the development and screening of therapeutically useful especial to the PRO polypeptides or antibodies are useful in the development and screening of therapeutically useful resignating the transpends of the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of the proliferation of situal englocyte cells, for stimulating the uptake of glucose or FRA by skeletal muscle cells, for modulating the uptake of stimulating differentiation of almost ecells, for stimulating cells, for stimulating or relymphocyte cells, for inducing endothelial cell tube formation and for treating constitutions and onditions which stimulate the release of prolegolycans arthritis. PRO polypeptides which stimulate the release of proteoglycan arthritis. PRO polypeptides which stimulate the release of proteoglycan artialage are useful for treating sports-related joint problems, arthritis. PRO polypeptides which stimulate the release of proteoglycans artialage are also useful for treating various mammalian haemoglobin-consequence and and/or cartilage are hand as various thalassaemias and conditions which may benefit from enhanced local immune system cells infile for media from USPTO at segdata.uspto.gov/sequence.html

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Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
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1.1%; Score 21.4; 66.0%; Pred. No. 45;

Query Match Best Local Similarity

DB 1; Length 1129;

; 0 Human, gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FRA; skeletal muscle cell; adipocyte cell; glucose; FRA; inner ear utricular supporting cell; practoyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteogylvan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration. Gaps . 0 1835 ITCTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881 1129 ritririririririririricaecieecacacaecieeririrari 1083 16; Indels 0; Mismatches BP. Human PRO polynucleotide #111. ADA82104 standard; cDNA; 1129 20-NOV-2003 (first entry) 31; Conservative ADA82104; Matches 4DA82104/c RESULT 87 à

Homo sapiens.

US2003082701-A1.

01-MAY-2003.

23-APR-2002; 2002US-00128686.

25-dun-1999; 98US-0100634P. 02-dun-1999; 99WO-US012252. 25-AUG-1999; 99US-00380137. 30-MAR-2000; 2000WO-US008439. 02-dun-2000; 2000WO-TS008439. 98US-0098525P. 31-AUG-1998;

02-JUN-2000; 2000WO-US015264. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC.

Gao Deforge L, Desnoyers L, Filvaroff E, G. A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Gerritsen ME, Goddard A, Baker KP, Beresini M, Stewart TA, Smith V,

WPI; 2003-755110/71. P-PSDB; ADA82105. PRO nucleic acid, useful for preparing a composition for treating e.g., tumor or for tissue typing.

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynuclectides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the approximant and annother animals which are

reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for modulating the uptake of glucose or FPA by skeletal muscle cells or adipocyte cells, for stimulating to stimulating the uptake of stimulating of or stimulating in periotyte cells, for stimulating to proliferation of or gene expression in periotyte cells, for stimulating to proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating cells, for inducing endothelial cell tube formation and for treating a sports injuries and arthritis. PRO polypeptides which stimulate the release of proceoglycans from cartilage are useful for treating sports-related joint problems, continuar cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin-associated disorders such as various thalassaemias and conditions which asystem cartering represents a human PRO polymucleotide of the invention. This sequence cata for this patent is also available in electronic format from USPTO at segdata.uspto.gov/sequence.html. 

99WO-US008615. 99WO-US010733. 99WO-US012252.

99WO-US005028

20-NOV-1998; 01-DEC-1998; 05-JAN-1999; 08-MAR-1999; 10-MAR-1999; 14-MAY-1999; 02-JUN-1999; 01-SED-1999; 08-SEP-1999;

99WO-US020944. 99WO-US021090. 99WO-US021547.

13-SEP-1999; 15-SEP-1999; 15-SEP-1999;

99WO-US023089 99WO-US028214

99WO-US020111 99WO-US020594

99WO-US028313. 99WO-US028409. 99WO-US028301. 99WO-US028634.

05-OCT-1999; 29-NOV-1999; 30-NOV-1999; 30-NOV-1999; 01-DEC-1999;

99WO-US028551. 99WO-US028564. 99WO-US028565.

99WO-US030095. 99WO-US030911. 99WO-US030999.

02-DEC-1999; 02-DEC-1999; 02-DEC-1999; 16-DEC-1999; 20-DEC-1999; 22-DEC-1999;

99WO-US030720

2000WO-US004341 2000WO-US004342 2000WO-US004414

18-FEB-2000;

2000WO-US000376

2000WO-US003565

2000WO-US000219

30-DEC-1999; 30-DEC-1999; 05-JAN-2000; 06-JAN-2000; 06-JAN-2000; 11-FEB-2000;

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps 1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; rative 0; Mismatches 16; Indels 0; 1835 TTCTTAATTTTTTCATTTCCAGATTTCCTTCAGTTTTGGGTTTTGTTT 1881 DB 1; Length 1129; Query Match Best Local Similarity 66.03 Matches 31; Conservative ò g

067/c ADA75067 standard; cDNA; 1129 BP. RESULT 88 ADA75067/c

20-NOV-2003 (first entry)

ADA75067;

Human PRO polynucleotide #111.

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; artilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarchritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Homo sapiens

US2003073216-A1.

17-APR-2003

30-MAY-2002; 2002US-00160498

98WO-US012456. 98WO-US014552. 98WO-US017888. 98WO-US019094 98WO-US019177 98WO-US019330 98WO-US019437 98WO-US018824 98WO-US019093 98WO-US021141 98WO-US022991 28-AUG-1998; 10-SEP-1998; 14-SEP-1998; 14-SEP-1998; 14-SEP-1998; 16-SEP-1998; 31-MAR-1997; 12-JUN-1998 17-SEP-1998 07-OCT-1998 29-OCT-1998 29-OCT-1998 

98WO-US022992

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2000WO-US02352 2000WO-US023328 2000WO-US030873 2000WO-US030873 2000WO-US032678 2000WO-US034956 2000WO-US034956 2000WO-US034956 2000WO-US034956 2000WO-US034956 2000WO-US034956 2000WO-US034956 2000WO-US034956 2000WO-US0349656 2000WO-US0349656 2000WO-US0349656 2000WO-US0349656 2000WO-US004914. 2000WO-US005004. 2000WO-US005601. 2000WO-US005746. 2001US-00828366. 2001US-00854208. 2001US-00854280. 2000WO-US015264. 2000WO-US020710. 2000WO-US022031. 2001US-00872035. 2001WO-US017800 2000WO-US014042 2000WO-US014941 18-FEB-2000; 22-FEB-2000; 24-FEB-2000; 10-NOV-2000; 01-DEC-2000; 20-DEC-2000; 10-MAR-2000; 15-MAR-2000; 

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2001US-00887879.
2001WO-US020116.
2001WO-US021066.
     2001US-00882636.
2001US-00886342.
2001WO-US019692.
                                  2001US-00908827.
2001US-00924419.
                              2001WO-US021735.
                                          2001US-00927796.
2001US-00931836.
                                              16-AUG-2001; 2001US-00931836
19-DEC-2001; 2001US-00028072
                                                            (GETH ) GENENTECH INC
                                                                                          P-PSDB; ADA75068
                 21-JUN-2001;
22-JUN-2001;
29-JUN-2001;
             20-JUN-2001;
                                  18-JUL-2001;
                                      06-AUG-2001;
                                           09-AUG-2001;
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New secreted and transmembrane PRO polypeptides useful for stimulating the release of tumor necrosis factor alpha in human blood and detecting the presence of tumor in a mammal. Gao W; Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G. Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; rom USPTO at segdata.uspto.gov/seguence.html Claim 2; Fig 221; 638pp; English. 2003-765392/72.

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

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Query Match
1.1%; Score 21.4; DB 1; Length 1129;
Best Local Similarity 66.0%; Pred. No. 45;
Matches 31; Conservative 0; Mismatches 16; Indels 0.
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Human; secreted and transmembrane protein; PRO; gene; ss; Tumour necrosis factor alpha release; TNF-alpha release; glucose uptake modulator; PFA uptake modulator; cell proliferation stimulator; cell differentiation stimulator; cell differentiation inhibitor; cytokine release stimulator; tumour; lung tumoue; colon tumour; breast tumour; prostate tumour; rectal tumour; attumour; cervical tumour; inver tumour; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker. Novel human secreted and transmembrane protein PRO4327 cDNA. ADA85145 standard; cDNA; 1129 BP. 22-APR-2002; 2002US-00127846. 20-NOV-2003 (first entry) US2003082695-A1. Homo sapiens. 01-MAY-2003. ADA85145; ADA85145/ 

03-MAR-2000; 2000US-0187202P. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC.

Deforge L, Desnoyers L, Filvaroff E, Gr A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Baker KP, Beresini M, De Gerritsen ME, Goddard A, Smith V, Stewart TA, WPI; 2003-786909/74.

P-PSDB; ADA85146.

New nucleic acid encoding a PRO polypeptide, useful for preparing a composition for treating e.g. tumor by gene therapy, or for tissue typing.

Claim 2; Fig 221; 637pp; English.

Transmembrane) polypeptides (1). (1) is useful for stimulating the release of TNR-alpha from human blood, for modulating the uptake of release of TNR-alpha from human blood, for modulating the uptake of stimulating the proliferation of differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in pericyte for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of Inner ear utricular supporting cells, for stimulating the proliferation of Inner ear utricular supporting cells, to stimulating the proliferation of Fordynche (2) or stimulating proliferation of Endowhelm (2) for stimulating of he release of a cytokine from PRMC cells, for stimulating of A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte cells, for stimulating proliferation of Endowhelm (2) colon, breast, cells, for stimulating proliferation of Endowhelm (2) colon, breast, to stimulating proliferation of Man uncolotide sequences or antisense probes. (1) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding in generation of antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, in gene therapy, for chromosome marker, and for generating cor serum, and for grobes. An anti-(1)-antibody is useful in diagnostic assays for RNO, e.g. probes. An anti-(1)-antibody is useful in diagnostic assays for RNO, e.g. probes. An anti-(1)-antibody is useful in diagnostic assays for RNO, e.g. The invention describes 305 nucleic acids encoding PRO (secreted and

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The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the release of TNR-alpha from human blood, for modulating the uptake of glucose or FFA by skeletal muscle calls or adipocyte calls, for stimulating the proliferation of or gene expression in pericyte calls, for stimulating the proliferation of or gene expression in pericyte calls, for stimulating the release of proteoglycans from cartilage, for stimulating the proliferation of inner ear utricular supporting calls, the release of a cytokine from pRMC calls, for inhibiting the binding of A-peptide to factor VIIA, for inhibiting the binding of A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte chils, for stimulating proliferation of endothelial calls, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour. The oligonucleotide probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted and transmembrane protein; PRO; gene; ss;
Tumour necrosis factor alpha release; TWF-alpha release;
Jucose uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inhibitor; cytokine release stimulator; tumour;
cell differentiation inhibitor; cytokine release stimulator; tumour;
cervical tumour; breast tumour; prostate tumour; rectal tumour;
gene therapy; chromosome identification; chromosome mapping;
sources. (I) and (II) are useful for tissue typing. This sequence encodes a novel human secreted and transmembrane PRO polypeptide.
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                       DB 1; Length 1129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human secreted and transmembrane protein PRO4327 cDNA
                                                                                              Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
                                                                                                                                                                          Score 21.4; DB 1; Length 1
Pred. No. 45;
0; Mismatches 16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA84593 standard; cDNA; 1129 BP
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01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
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                                                                                                                                                                              1.18;
                                                                                                                                                                                                           66.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                   Conservative
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Gerritsen ME, Goddard
Smith V, Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
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P-PSDB; ADA84594.
                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                   31;
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ADAB453/C
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Gaps

0; Mismatches 16; Indels 0; Score 21.4; DB 1; Length 1129; Pred. No. 45;

Local Similarity 66.0%;

Query Match Best Local &

Matches

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31; Conservative

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; a novel human secreted and transmembrane PRO polypeptide.

are useful for isolating genomic and cDNA nucleotide sequences or antisense probes. (I) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding interaction. A polynucleotide (II) encoding (I) is useful in chromosome and gene mapping, in generation of antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, in gene therapy, for chromosome identification, as chromosome marker, and for generating probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g. detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. (I) and (II) are useful in the interaction of the

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Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; perioyte cell; inner ear utricular supporting cell; T-lymphocyte cell; sports injury; proteoglycan; articular cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; hemoglobin-associated disorder thalassaemia; immune system cell infiltration. cDNA encoding human PRO polypeptide #111. ADB29849 standard; cDNA; 1129 BP. 98WO-US014552. 98WO-US017888. 98WO-US018824. 98WO-US019093. 98WO-US019177. 98WO-US022991. 98WO-US022992. 98WO-US024855. 98WO-US019437. 98WO-US021141. 98WO-US025108. 99WO-US000106. 99WO-US005190 2002US-00124822 (first entry) US2003073214-A1. Homo sapiens. 17-APR-2002; 20-NOV-2003 17-APR-2003. 28-AUG-1998; 14-SEP-1998; 14-SEP-1998; 14-SEP-1998; 16-SEP-1998; 07-0CT-1998, 29-0CT-1998 29-OCT-1998 ADB29849; ADB29849/c  10664775-3.rng

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99WO-US020944.
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99WO-US031243.
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2000WO-US004914.
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05-OCT-1999;
29-NOV-1999;
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24-AUG-2000;
08-NOV-2000;
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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. adrena), ung, colon, breast, prostate, rectal, kidney, cervical and invertumours). The prolynucleotides are useful in molecular biology, including uses a hybridisation probes, in chromosome and gene mapping, in generating antiennes RNA and brook polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO Polypeptides or antibodies are used in preparing a mediament for treating a condition responsive to the polypeptides or antibodies such as tumours, for stimulating and inhibiting proliferation of thuman microvascular endothelial cells, for modulating the uptake of slumman microvascular endothelial cells, for stimulating the proliferation of antibodies, such as tumours, for stimulating and inhibiting proliferation of or gene expression in pericyte cells, for stimulating the proliferation of adipocyte cells, for stimulating edication of adipocyte cells, for stimulating cells, for inducing endothelial cell to mediame to a sports injuries and cells, for articulas edicock as such as sports injuries and returnities and prepared and propaptides which stimulate the release of proteoglycans from carticular cartilage defects, osteoarthritis and rhemmatoid atthrities and prepared contained specific from annowed local immune system cell infilteration. This associated disorders such as various braiassaemias and conditions which sequence encodes a human RRO polypeptide of the invention. Note: The sequence encodes a human RRO polypeptide of the invention. Note: The sequence encodes a human encodes a huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel secreted and transmembrane PRO polypeptides useful for stimulating the release of tumor necrosis factor alpha and detecting the presence of
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Goddard A, Godowski PJ, Gurney AL, Sherwood S;
art TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Fig 221; 638pp; English.
                29-JUN-2001, 2001W0-US021066.

09-JUL-2001, 2001W0-US02135.

18-JUL-2001, 2001US-00908827.

06-AUG-2001, 2001US-00924419.

09-AUG-2001, 2001US-00921836.

16-AUG-2001, 2001US-00931836.
2001WO-US020116
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Smith V, Stewart TA,
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P-PSDB; ADB29850.
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RESULT 92 ADA80377/c ID ADA80377 standard; cDNA; 1129 BP

ADA80377;

20-NOV-2003 (first entry)

Human PRO polynucleotide #111.

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FRA; skelectal muscle cell; adipocyte cell; gericyte cell; inner ear utricular supporting cell; promotyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports nijury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Homo sapiens.

US2003082761-A1.

01-MAY-2003

12-APR-2002;

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97WO-US005230. 98WO-US012456. 98WO-US0174552. 98WO-US019093. 98WO-US019094. 98WO-US019074. 98WO-US019177. 98WO-US01947. 12 - CMAR - 1997 12 - CMN - 1998 12 - SABC - 1998 14 - SEP - 1998 14 - SEP - 1998 14 - SEP - 1998 16 - SEP - 1998 17 - SEP - 1998 17 - SEP - 1998 17 - SEP - 1998 18 - SEP - 1998 19 - SEP - 1998 19 - SEP - 1998 19 - SEP - 1999

98WO-US024855. 98WO-US025108. 99WO-US000106. 99WO-US005028. 98WO-US022991. 98WO-US022992.

99WO-US005190. 99WO-US008615. 99WO-US010733. 99WO-US012252.

99WO-US020111 99WO-US020111 99WO-US021094 99WO-US021090 99WO-US02147 99WO-US02814 99WO-US028113 99WO-US028113 99WO-US028611 99WO-US028611 99WO-US028611 99WO-US028611 15-SEP-1999 15-SEP-1999 28-NOV-1999 30-NOV-1999 30-NOV-1999 01-DEC-1999 02-DEC-1999 02-DEC-1999 02-DEC-1999 02-DEC-1999 03-DEC-1999 03-DEC-1999 03-DEC-1999 03-DEC-1999 03-DEC-1999 03-DEC-1999 03-DEC-1999 03-DEC-1999 03-DEC-1999 03-DEC-1999 03-DEC-1999 04-DEC-1999 06-JAN-2000 06-JAN

99WO-US030911.

99WO-US031243 99WO-US031274. 2000WO-US000219. 2000WO-US000277. 030720

2000WO-US004341. 2000WO-US004342. 2000WO-US004414.

24-FEB-2000; 2000WO-US004914.

21-MAR-2000; 2000WO-US0050604.

22-MAR-2000; 2000WO-US005546.

10-MAR-2000; 2000WO-US005546.

11-MAR-2000; 2000WO-US005641.

12-MAR-2000; 2000WO-US005641.

12-MAR-2000; 2000WO-US005919.

13-MAR-2000; 2000WO-US006819.

13-MAR-2000; 2000WO-US001439.

13-MAR-2000; 2000WO-US001439.

11-ANG-2000; 2000WO-US014941.

22-MAY-2000; 2000WO-US014941.

23-MAY-2000; 2000WO-US014941.

24-MG-2000; 2000WO-US014941.

24-MG-2000; 2000WO-US014941.

24-MG-2000; 2000WO-US014941.

24-MG-2000; 2000WO-US01952.

24-MG-2000; 2000WO-US01952.

24-MG-2000; 2000WO-US01952.

24-MG-2000; 2000WO-US019666.

25-MAR-2001; 2001WG-US01849.

26-MAR-2001; 2001WG-US01666.

27-MAR-2001; 2001WG-US01666.

28-FEB-2001; 2001WG-US01666.

28-FEB-2001; 2001WG-US01669.

21-MAY-2001; 2001WG-US01669.

22-MAY-2001; 2001WG-US01799.

20-JUN-2001; 2001WG-US01799.

21-JUN-2001; 2001WG-US011969.

22-JUN-2001; 2001WG-US011969.

22-JUN-2001; 2001WG-US011969.

22-JUN-2001; 2001WG-US011969.

23-JUN-2001; 2001WG-US011969.

23-JUN-2001; 2001WG-US011969.

23-JUN-2001; 2001WG-US011969.

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23-JUN-2001; 2001WG-US011969.

23-JUN-2001; 2001WG-US011969.

23-JUN-2001; 2001

(GETH ) GENENTECH INC.

3 Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; , S; Z;

WPI; 2003-755115/71. P-PSDB; ADA80378.

New PRO polypeptides useful for treating diabetes, hyper- or hypo-insulinemia, sports injuries, arthritis, obesity, stroke, heart attack, various coagulation disorders and tumors.

Claim 2; Fig 221; 638pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for

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Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ge Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zharg Z;

WPI; 2003-765414/72.

P-PSDB; ADA75620

detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymucleotides may also be used in preparing PRO polymeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful caseful in the development and screening of therapeutically useful and polymeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polymeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of medicament for treating a condition responsive to the polymeptides or antibodies, such as tumours, for stimulating the uptake of glucose or FPA by skeletal muscle cells, for adipocyte cells, for stimulating the uptake of glucose or FPA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation of or gene expression in periove cells, for stimulating the proliferation of cartilage disorders such as sports injuries and arthritis. PRO polypeptides which estimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, arthritis. PRO polypeptides are useful for treating sports-related disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polymucleotide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at sequence. The sequence of the invention.

New PRO nucleic acid, useful for preparing a composition for treating

Claim 2, Fig 221; 637pp; English. e.g., tumor or for tissue typing.

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps . 0 1835 TICTTAATTTTTTCATTTCCAGATTTCCTTCAGTTTTGGGTTTTGTTT 1881 DB 1; Length 1129; 0; Mismatches 16; Indels Pred. No. 45; Score 21.4; 1.1%; 66.08; 31; Conservative Best Local Similarity Query Match Matches ð

ADA75619 standard, cDNA; 1129 BP. Human PRO polynucleotide #111. 20-NOV-2003 (first entry) ADA75619; 

Human, gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adread; prostate; rectum, kidney; cervix; liver; microvascular endothalial cell; glucose; FRA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; Prymphocyte cell; inner ear utricular supporting cell; T-lymphocyte cell; sports injury; protecoglycan; atticular cartilage defect; osteoarthitis; sports injury; protecoglycan; atticular cartilage defect; osteoarthitis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Homo sapiens.

US2003082703-A1.

01-MAY-2003.

23-APR-2002; 2002US-00128691. 99US-0170262P. 09-DEC-1999;

01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072. (GETH ) GENENTECH INC.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. adrenal, lung, corolification or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, collon, breast, prostate, rectal, kidney, cervical and liver tumours). The colymucleotides are useful in molecular biology, including uses as hyridisation probes, in chromosome and gene mapping in generating a strissnes RAM and bn gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals and in generating either transgenic animals or knock-out animals and in second section in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of thuman microvascular endothelial cells, for stimulating proliferation of sumer each endipocyte cells, for stimulating proliferation of inner ear utricular supporting cells, for stimulating are useful for treating sports-related joint problems arthitis. PRO polypeptides which stimulate the release of proteoglycans tricular cartilage are useful for treating sports-related joint problems arthitis. PRO polypeptides which stimulate the release of proteoglycans arthitis. PRO polypeptides which stimulate the release of proteoglycans arthitis. PRO polypeptides which stimulate the release of proteoglycans arthitis and insenting sports-related joint problems engletices are also useful for treating various mammalian headened disorder Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; from USPTO at segdata.uspto.gov/seguence.html Conservative Local Similarity nes 31; Conserv Query Match Matches ઠે ò

Gaps 0 1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; tive 0; Mismatches 16; Indels 0; 1835 TICTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881 1129 TITTITITITITITICAGCIGGCACACACAGGCTGGGTTTTATT 1083

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ADA46844 standard; cDNA; 1129 BP Human PRO polynucleotide #111. 20-NOV-2003 (first entry) ADA46844/c 

Human, gene, ss, PRO; secreted polypeptide, transmembrane polypeptide, tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate, rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; ekpleral muscle cell; adhomice and

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inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rhewmatoid arthritis; haemolobin-associated disorder thalassaemia; immune system cell infiltration.
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30 DEC-1999; 99WO-US031243.
31 DEC-1999; 99WO-US031243.
32 DEC-1999; 99WO-US031243.
33 DEC-1999; 99WO-US031243.
34 DEC-1999; 99WO-US031243.
35 DEC-1999; 99WO-US031243.
36 DEC-1999; 99WO-US031243.
37 DEC-1999; 99WO-US00219.
37 DEC-1999; 99WO-US00219.
38 PEB-2000; 2000WO-US004341.
39 PEB-2000; 2000WO-US004341.
39 PEB-2000; 2000WO-US004914.
30 PEB-2000; 2000WO-US004914.
31 DEC-1999; 99WO-US005004.
31 DEC-1999; 99WO-US005004.
32 DEC-1999; 99WO-US005004.
33 DEC-1999; 99WO-US005004.
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30-MAR-2000;
17-MAY-2000;
                                                                  Homo sapiens.
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29-OCT-1998;
20-NOV-1998;
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30. MAY - 2000, 2000MO - 05014941.
28 - JUL - 2000, 2000MO - 05014941.
28 - JUL - 2000, 2000MO - 05015264.
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24 - AUG - 2000, 2000MO - US02352.
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21 - MAX - 2001, 2001MO - US06668.
22 - MAX - 2001, 2001MS - 00866218.
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26 - JUN - 2001, 2001MS - US01780.
27 - JUN - 2001, 2001MS - US01786.
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#### (GETH ) GENENTECH INC.

Gao W; Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G. Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

#### WPI; 2003-644800/61. P-PSDB; ADA46845

New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or PRO4978, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

### Claim 2; Fig 221; 638pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymuclectides encoding them. The invention also relates to an antibody which specifically binds them. The propagatide, a method for stimulating the release of tumour necrosis factor-alpha (TWP-alpha) from human blood, a method for stimulating the proliferation or differentiation of fondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, Kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating on tisense RNA and DNA and in gene therapy. The polymucleotides may also antisense RNA and DNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a-condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation

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Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G. Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Matanabe CK, Wood WI, Zhang Z; Human PRO polynucleotide SEQ ID NO 221. ADB25140 standard; cDNA; 1129 BP. 99WO-US012252. 99US-00380137. 2000WO-US008439. 02-JUN-2000; 2000WO-US015264. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072. 98US-0098525P. 98US-0100634P. 23-APR-2002; 2002US-00128693 20-NOV-2003 (first entry) Conservative (GETH ) GENENTECH INC. Local Similarity US2003077715-A1. 31-AUG-1998; 16-SEP-1998; 02-JUN-1999; Homo sapiens. 25-AUG-1999; 30-MAR-2000; 31; 24-APR-2003, ADB25140; Query Match Matches qq

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of human microvascular endothelial cells, for modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating proliferation of or gene expression in periote cells, for stimulating the proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and articular cartilage are useful for treating sports injuries and articular cartilage defects, oscoarthritis and rheumatoid arthritis. PRO polypeptides which stimulas store are useful for treating various mammalian haemoglobin-associated disorders such as various thalassaemia and conditions which may benefit from enhanced local immune system cell infiltration. This csquence data for this patent is also available in electronic format from USPTO at segdata.uspto.gov/sequence.html.
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Gao W;

WPI; 2003-755070/71.

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) From human blood, a method for stimulating the presence of a tumour in a mammal (e.g. adrenal, und, for proliferation or differentiation of chondcrocyte cells and a method for proliferation probes, in chromosome and gene mapping in generating a ratesense RM and bn gene therapy. The polymucleotides may also be used in preparing PRO POLYPEPTION of the polypeptides or antibodies are useful in molecular biology, including uses and in generating either transgent animals or knock-out animals and in generating a the propospection of the polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies are used in preparing of human microvascular endothelial cells, for modulating the uptake of glucose or FRA by skeletal muscle cells, for simulating differentiation of adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating and preparing expression in pericyte cells, for stimulating and condition stimulating and individual endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injunities and cells, for artitulage defected. Setecathritis and rheumatoid arthritis and propules which stimulate the release of proteglycans arthritis. PRO polypeptides which stimulate the release of proteglycans arthritis and rheuman pRO polypeptides are also useful for treating sports called disorders such as various bone and/or setals for minimal sequence represents a human PRO polypeptides are also useful for treating serions of the invention. T
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                                              New isolated, secreted and transmembrane PRO nucleic acids, useful for
the diagnosis, prevention and/or treatment of tumors, such as lung,
colon, breast, prostate, rectal, cervical and/or liver tumors.
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Best Local Similarity 66.0%; Pred. No. 45;

Conservative 0; Mismatches 16; Indels
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                                                                                                                                                              Claim 2; Fig 221; 637pp; English.
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P-PSDB; ADB25141.
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Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; inner ear utricular supporting cell; perioyte cell; endothelial cell tube formation; Done disorder; artilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
                                                                                                                                                                          cDNA encoding human PRO polypeptide #111
                                             BP.
                                          ADB26666 standard; cDNA; 1129
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10-SEP-1998;
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                                                                                          ADB26666;
RESULT 97
                          ADB26666,
                                                                                       The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, amethod for stimulating the release of tumour necrosis factor-alpha (TMF-alpha) from human blood, a method for stimulating the polyneptide, amethod for chondrooty-cells and amethod for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as plynucleotides are useful in molecular biology, including uses as colon, breast man probas, in chromosome and gene mapping, in generating enter transgenic antimals or knock-out animals which are useful in the development and screening of therapeutically useful cuseful in the development and screening of therapeutically useful are useful in the development and screening of therapeutically useful cuseful in the development and screening of therapeutically useful readicament for treating a condition responsive to the pulpeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of conference or FRA by skeleral muscle cells, for modulating the uptake of stimulating differentiation of adipocyte cells, for stimulating proliferation of inner ear utricular supporting cells, for stimulating proliferation of inner ear utricular supporting cells, for stimulating cells, for inducing endethelial cell tube formation and for treating carting sports induced disorders such as sports injuries and contilions are useful for treating sports related joint problems. FRO polypeptides which stimulate the release of proteoglycans from cartilage are also useful for treating sorts-related joint problems. Con any benefit from enhanced local immune system cell infilteration. This sequence represents a human PRO polymucleotide of the invention. This consequence in the proliferation of inner ear useful as a
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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from USPTO at segdata.uspto.gov/sequence.html.
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01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
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Query Match

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2001MO-US006666
2001US-00802706
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2001US-00860216
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2001US-00908827
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19-DEC-2001; 2001US-00028072
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18-MAY-2001;
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01-DEC-2000
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28-FEB-2001
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### (GETH ) GENENTECH INC.

3 Gao Beresini M, Deforge L, Desnoyers L, Filvaroff E, Game, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; Baker KP, Gerritsen Smith V,

WPI; 2003-777249/73. P-PSDB; ADB26667 Novel isolated PRO polypeptide useful for treating diabetes, hyper- or hypo-insulinemia, sports injuries, arthritis, obesity, stroke, heart attack, various coagulation disorders, tumors.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The Claim 2; Fig 221; 660pp; English.

Compeptide, a method for simulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the factor-alpha (TNF-alpha) from human blood, a method for stimulating the prosleder of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polyuncleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and bnX and in gene therapy. The polyuncleotides may also consistent by preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are consecunt in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells of adipocyte cells, for stimulating the uptake of stimulating differentiation of adipocyte cells, for stimulating the proliferation of or gene expression in percept cells, for individual cells or T-lymphocyte cells, for individual endothelial cells to the proliferation of siner ear utricular supporting cells, for individual endothelial cells to cells, for individual endothelial cells to sports injuries and cells, for individual endothelial cells to some and/or cartilage disorders such as various bone and/or cartilage disorders such as various benefit for treating various mammalian haemodlobin-cells, for individual endothelial for treating various mammalian haemodlobin-cells, may benefit from enhanced local immune system cell infiltration. This sequence encodes a human PRO polypeptide of the invention. The sequence encodes a human proper various benefit for treating encodes a hu invention also relates to an antibody which specifically binds to the USPTO website at segdata.uspto.gov. 

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps ., 1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; ative 0; Mismatches 16; Indels 0 1129 fritiriririririririricadciascacacacacacacacacacitrirari 1083 1835 ITCTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881 Local Similarity 66.0 nes 31; Conservative Query Match Matches à Dp

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ADB30953/c RESULT 98

ADB30953 standard; cDNA; 1129 BP.

ADB30953;

20-NOV-2003 (first entry)

cDNA encoding human PRO polypeptide #111.

Human, gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletel muscle cell; adipocyte cell; glucose; FFA; inner ear utricular supporting cell; pricyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; endothelial cell tube formation; bone disorder; cartilage disorder; rheumatoid arthritis; hemosplobin-associated disorder thalassaemia; immune system cell infiltration. 

Homo sapiens

US2003096386-A1.

22-MAY-2003.

11-APR-2002; 2002US-00121042;

97WO-US005230. 31-MAR-1997;

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Mon Aug
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12-JUN-1998; 98WO-US014556.

18-JUG-1998; 98WO-US014552.

16-SEP-1998; 98WO-US018024.

14-SEP-1998; 98WO-US01903.

14-SEP-1998; 98WO-US01903.

14-SEP-1998; 98WO-US01903.

14-SEP-1998; 98WO-US01903.

16-SEP-1998; 98WO-US019177.

16-SEP-1998; 98WO-US019330.

17-SEP-1998; 98WO-US019330.

18-SEP-1998; 98WO-US019330.

19-WAR-1999; 98WO-US022991.

29-OCT-1998; 98WO-US022991.

29-OCT-1998; 98WO-US019177.

11-SEP-1999; 98WO-US019177.

12-SEP-1999; 98WO-US019177.

13-SEP-1999; 99WO-US01919.

14-MAY-1999; 99WO-US01919.

15-SEP-1999; 99WO-US01919.

16-SEP-1999; 99WO-US01919.

16-SEP-1999; 99WO-US01919.

16-SEP-1999; 99WO-US01919.

16-SEP-1999; 99WO-US01911.

16-SEP-1999; 99WO-US01911.

16-SEP-1999; 99WO-US01911.

16-SEP-1999; 99WO-US01911.

16-SEP-1999; 99WO-US01911.

16-SEP-1999; 99WO-US01911.

16-SEP-1999; 99WO-US01911.

16-SEP-1999; 99WO-US01911.

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16-SEP-1999; 99WO-US01911.

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16-SEP-1999; 99WO-US01911.

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16-SEP-1999; 99WO-US01911.

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16-SEP-1999; 99WO-US01911.

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16-SEP-1999; 99WO-US01911.

16-SEP-1999; 99WO-US01911.

16-SEP-1999; 99WO-US01911.

16-SEP-1999; 99WO-US0191.

16-SEP-1999; 99WO-US0191.

16-SEP-1999; 99WO-US0191.

16-SEP-1999; 99WO-US0191.

16-SEP-1999; 99WO-US0191.

16-SEP-1999; 99WO-US0191.

17-MAR-2000; 2000WO-US0196.

17-WAR-2000; 200WO-US0196.

17-WAR-2000; 200WO-US0196.

17-WAR-2000; 200WO-US01
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09-MAR-2001, 2001US-00802706.
22-MAR-2001, 2001US-00808689.
22-MAR-2001, 2001US-00816744.
05-APR-2001, 2001US-00854208.
10-MAY-2001, 2001US-00854208.
10-MAY-2001, 2001US-00866218.
25-MAY-2001, 2001US-00866218.
25-MAY-2001, 2001US-00866218.
25-MAY-2001, 2001US-00866218.
25-MAY-2001, 2001US-00866218.
01-JUN-2001, 2001US-00882342.
19-JUN-2001, 2001US-00882636.
19-JUN-2001, 2001US-00882618.
22-JUN-2001, 2001US-00882618.
22-JUN-2001, 2001US-008827166.
09-JUL-2001, 2001US-00882713.
18-JUL-2001, 2001US-00908827.
16-AUG-2001, 2001US-00908827.
16-AUG-2001, 2001US-00908837. 

### (GETH ) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao ' Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-786990/74. P-PSDB; ADB30954.

Novel isolated PRO polypeptide useful for treating diabetes, hyper- or hypo-insulinemia, sports injuries, arthritis, obesity, stroke, heart attack, various coagulation disorders, tumors.

Claim 2; Fig 221; 638pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. adream). Indice to polypeptide, a method for stimulating the presence of a tumour in a mammal (e.g. adream). Indice to polynucleotides are useful in molecular biology, including uses as polynucleotides are useful in molecular biology, including uses as polynucleotides are useful in molecular biology, including uses as the polymolectides may also a present of the properties by recombinant techniques and in generating either transgenic animals or knock-out animals which are setul in the development and screening of therapeutically useful cagents. The PRO polypeptides or antibodies are used in preparing a temporary for stimulating and inhibiting proliferation of human microvascular endothelial cells, for modulating the uptake of glucose or FPA by skeletal muscle cells, for stimulating differentiation of adipocyte cells, for stimulating confideration of adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating confideration of adipocyte cells, for stimulating confideration of adipocyte cells, for stimulating and condition cartilage disorders such as sports injuries and remained arthrities propolypeptides which stimulate the release of proteoglycans cartilage defects, osteoarthritis and rheumatoid anthrities propolypeptides which stimulate the release of proteoglycans articular cartilage defects, osteoarthritis and rheumatoid anthrities mannanced coll immune system cell infilteration. Note: The sequence encodes a human PRO polypeptide of the invention. Note: The sequence data for this patent is also available in electronic format format formation.

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99WO-US030095.
99WO-US030911.
99WO-US030999.
99WO-US031243.
99WO-US031244.
                                99WO-US028409.
99WO-US028301.
99WO-US028634.
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99WO-US028564.
99WO-US028565.
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2001US-0081689.
2001US-0081644.
2001US-00854208.
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2001US-00860216.
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2000WO-US005841.
2000WO-US006884.
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2001US-00872035.
2001WS-US017800.
2001US-00874503.
2001US-0082636.
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2000WO-US004414
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2001WO-US006520.
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14-WAR-2001; 2
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11-MAY-2001; 2
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25-MAY-2001; 2
25-MAY-2001; 2
25-MAY-2001; 2
10-JUN-2001; 2
01-JUN-2001; 2
01-JUN-2001; 2
14-JUN-2001; 2
14-JUN-2001; 2
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06-JAN-2000)

11-FEB-2000)

11-FEB-2000)

18-FEB-2000)

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24-FEB-2000)

24-FEB-2000)

24-FEB-2000)

25-FEB-2000)

21-MAR-2000)

15-MAR-2000)

15-MAR-2000)

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16-DEC-1999;
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24-AUG-2000)
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01-BC-2000)
20-BC-2000)
20-BC-2000)
28-FBB-2001)
28-FBB-2001)
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                                                                                                                                                                                                                Human; secreted and transmembrane protein; PRO; gene; ss;
fumour necrosis factor alpha release; TNF-alpha release;
glucose uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inhibitor; cytokine release stimulator;
lung tumoue; colon tumour; breast tumour; prostate tumour; rectal
cervical tumour; liver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
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                                                                       1835 TTCTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881
                                                                                         DB 1; Length 1129;
                Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
                                                        16; Indels
                                   Query Match
1.1%; Score 21.4; DE
Best Local Similarity 66.0%; Pred. No. 45;
Matches 31; Conservative 0; Mismatches
the USPTO website at segdata.uspto.gov.
                                                                                                                   RESULT 99
ADA60881/c
ID ADA60881 standard; cDNA; 1129 BP.
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98WO-US022991.
98WO-US022992.
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98WO-US019093.
98WO-US019094.
98WO-US019177.
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99WO-US005190.
99WO-US008615.
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98WO-US025108.
99WO-US000106.
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99WO-US012252.
99WO-US020111.
99WO-US020944.
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98WO-US017888.
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                                                                                                                                                                             20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                      US2003049817-A1.
                                                                                                                                                                                                                                                                                                                                          transmembrane.
                                                                                                                                                                                                Homo sapiens.
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10-SEP-1998;
14-SEP-1998;
14-SEP-1998;
14-SEP-1998;
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20-APR-1999
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secreted.
and.
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PRO4327.
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(GETH ) GENENTECH INC. 

The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypoptides (1). (1) is useful for stimulating the crease of TNF-alpha from human blood, for modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating proliferation of endothelial cells, for stimulating the proliferation of endothelial cells, for detecting the release of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour. The oligonucleotide probes cells, for stimulating genomic and CDNA nucleotide sequences or artisense probes. (1) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding interaction. A polynucleotide (II) encoding (I) is useful in chromosome concenting of therapeutically useful reagents, in gene therapy, for probes. An anti-(I)-antibody is useful in the development and sorchered in sexpression in specific cells, tissues or servan, and for generating concess. An anti-(I)-antibody is useful in diagnostic assays for PRO, eggenores. (I) and (II) are useful for tissue typing. This sequence encodes a novel human secreted and transmembrane PRO polypeptide. New secreted and transmembrane PRO polypeptide and nucleic acid, useful for manufacturing a medicament for diagnosing or treating tumor. Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ga Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; Claim 2; Fig 221; 658pp; English 2003-695893/66. P-PSDB; ADA60882.

Query Match
Best Local Similarity 66.0%; Pred. No. 45;
Matches 31; Conservative 0; Mismatches 16; Indels 0; Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

1835 TICTTAATTTTTCATTTCCAGATTTCCTTCAGTTTTGGTTTTT 1881

Gaps

1129 TTTTTTTTTTTTTTTTTCAGCTGGCACAGGCTGGGTTTTTATT 1083 ADB24028 standard; cDNA; 1129 BP ADB24028; ద

20-NOV-2003 (first entry)

Human, gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer, adrend; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; PRA; skeletal muscle cell; adipocyte cell; perioyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; Human PRO polynucleotide SEQ ID NO 221. 

rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Homo sapiens.

Gao W;

JS2003077714-A1.

24-APR-2003

22-APR-2002; 2002US-00127901

17-JUN-1998; 98US-0089599P. 02-JUN-1999; 99WO-US012252. 25-AUG-1999; 99US-00380137. 30-NOV-1999; 99WG-US028313. 30-MRR-2000; 2000WG-US008439. 01-DEC-2000; 2000WG-US008439.

(GETH ) GENENTECH INC.

Gao W; Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ga Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-755069/71. P-PSDB; ADB24029 New isolated, secreted and transmembrane PRO polypeptides and nucleic acids, useful for the diagnosis, prevention and/or treatment of tumors, such as lung, colon, breast, prostate, rectal, cervical and/or liver

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis (actor-alpha (TMF-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. adrenal, lung, cervicial and a method for colon, breast, prostate, rettal, kidney, cervical and liver tumours). The polyuncleotides are useful in molecular biology, including uses as thy byridisation probes, in chromosome and gene mapping, in generating colon, breast, prostately proplypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of knock-out animals which are useful in the development and screening of knock-out animals which are useful in the development and screening of knock-out animals which are useful in the development and screening of knock-out animals which are useful in the development and screening or knock-out animals which are useful mindicals, such as tumours, for stimulating of inpreprides or antibodies are used in preparing a condition responsive to the polypeptides of thuman microvascular endothelial cells, for modulating the uptake of stimulating differentiation of inner ear utricular supporting cells, for stimulating proliferation of or gene expression in pericyte cells, for stimulating cells or 1 lymphocyte cells, for stimulating architics propreptides which stimulates and rheumatoid architics and structiles are useful for treating various mammalian hemoglobing architics are useful for treating various mammalian hemoglobing equence represents a human PRO polymoredes cells of the invention. One sequence represents a human PRO polymoredes control to the equence data for this patent is also available in electronic formation. 

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45;

Query Match Best Local Similarity

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   16; Indels
   0; Mismatches
31; Conservative
Matches
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ADA96357 standard; cDNA; 1129 BP

ADA96357;

(first entry) 20-NOV-2003

Human PRO polynucleotide #111.

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; PRA; inner ear utricular supporting cell; priorte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sporte infury; proteoglycan; articular cartilage defect; osteoarthritis; theumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Homo sapiens.

US2003082690-A1

22-APR-2002; 2002US-00127837

99WO-US020111. 99US-00403297. 2000WO-US004342. 18-FEE-2000; 2000WO-USO04342. 08-NOV-2000; 2000WO-USO30955. 01-DEC-2000; 2000WO-USO32678. 19-DEC-2001; 2001US-00028072. 01-SEP-1998; 01-SEP-1999; 18-OCT-1999;

(GETH ) GENENTECH INC.

Deforge L, Desnoyers L, Filvaroff E, Gr A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Zhang Beresini M, 1E, Goddard Stewart TA, Gerritsen ME, Smith V, Stew Baker KP,

Gao W;

2003-755107/71. WPI; 2003-755107/ P-PSDB; ADA96358. PRO nucleic acid, useful for preparing a composition for treating e.g. tumor or for tissue typing.

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, clon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful cagents. The PRO polypeptides or antibodies are used in preparing a 

medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of the human microvascular endothelial cells, for modulating the uptake of glucose or FFA by skeletal muscle cells of adipocyte cells, for stimulating the uptake of stimulating differentiation of adipocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans continular cartilage defects, osteoarthritis and rheumandid arthritis. PRO polypeptides are also useful for treating sports-related joint problems, atticular cartilage defects, osteoarthritis and rheumandid nemoglobin-collypeptides are also useful for treating various mammalian haemoglobin-collypeptides are also useful for treating various mammalian haemoglobin-collypeptides are also useful for treating various mammalian haemoglobin-collypeptides are also useful for treating various mammalian carthritis and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polypudicolide of the invention. Note: Gaps ; 0 DB 1; Length 1129; Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; 16; Indels from USPTO at segdata.uspto.gov/sequence.html. Pred. No. 45; 0; Mismatches 1.1%; Score 21.4; 66.08; Conservative Local Similarity 31; Query Match Best Loca Matches 8X8888888888888888888888888888888 ò

TICITAATITITICATITICCAGAITITICCTICAGITITIGGGTTTTGTTT 1881 1835

1129 TITTTTTTTTTTTTTCAGCTGGCACACAGGCTGGGTTTTTATT 1083

В

RESULT 102 ADA80929,

1929/c ADA80929 standard; cDNA; 1129

ВВ

ADA80929;

(first entry) 20-NOV-2003

Human PRO polynucleotide #111.

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FPA; skeletal muscle cell; adipocyte cell; glucose; FPA; inner ear utricular supporting cell; J-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports alphury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Homo sapiens.

US2003082702-A1. 

01-MAY-2003

23-APR-2002; 2002US-00128690.

02-MAR-2000; 2000WO-US005841. 30-MAY-2000; 2000WO-US014941. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC.

Gao W; Deforge L, Desnoyers L, Filvaroff E, Ga A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Baker KP, Beresini M, Deforge Gerritsen ME, Goddard A, Godow. Smith V, Stewart TA, Tumas D, Gerritsen ME, Smith V, Stew

WPI; 2003-755111/71. P-PSDB; ADA80930.

US2003082759-A1

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polypucleotides encoding them. The invention also relates to an antibody which spedifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TWF-alpha) from human blood, a method for stimulating the release of tumour necrosis of proliferation or differentiation of chondrocyte cells and amended for detecting the presence of a tumour in a mammal (e.g. adremal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The prolymucleotides are useful in molecular biology, in generating to polymucleotides are useful in molecular biology, in generating this statements. The PRO Polypeptides by recombinant techniques and in this sense in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of knock-out animals which are useful in the development and screening of knock-out animals which are useful in the development and screening of knock-out animals which are useful in the development and screening or knock-out animals which are useful in the development and screening or knock-out animals which are useful set undouted as tumours, for stimulating and inhibiting proliferation of matumours, for stimulating and inhibiting proliferation of submore are useful set modulating the uptake of glucose or FPA by skeletal muscle cells, for stimulating differentiation of submore are useful for streating sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans of from cartilage are useful for treating various mammalian hamoglablems, articular cartilage are useful for treating various mammalian hamoglablems, articular cartilage are useful for treating various mammalian made for this patent is also sequence represents a whoman PRO polymorectide of the invention. This sequence represents a whoman PRO polymorectide of t
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New PRO nucleic acid, useful for preparing a composition for treating e.g., tumor or for tissue typing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.1%; Score 21.4; DB 1; Length 1129; Best Local Similarity 66.0%; Pred. No. 45; Matches 31; Conservative 0; Mismatches 16; Indels 0
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                                                                       Claim 2; Fig 221; 637pp; English.
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ADA95805/c
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11-APR-2002;
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14-SEP-1998;
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28-FEB-2001; 2001US-00796498.
28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US006666.
09-MAR-2001; 2001US-00802706...
                                                        14-MAR-2001; 2001US-00808689.
22-MAR-2001; 2001US-00816744.
05-APR-2001; 2001US-00828366.
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25-MAY-2001; 2001US-00866028.
25-MAY-2001; 2001US-00866034.
25-MAY-2001; 2001WO-US017092.
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2001US-00872035.
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2001US-00886342.
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21-JUN-2001; 2001US-00887879.
22-JUN-2001; 2001WO-US020116.
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09-AUG-2001; 2001US-00927796.
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P-PSDB; ADA95806.
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14-JUN-2001; 2
19-JUN-2001; 2
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Gao W; Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

New isolated PRO polypeptides, useful for treating diabetes, hyper- c hypo-insulinemia, sports injuries, arthritis, obesity, stroke, heart attack, various coagulation disorders and tumors.

# Claim 2; Fig 221; 638pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. adrenal, lung, orlynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antiparation probes, in dromosome and gene mapping, in generating antiparation properides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for modulating the uptake of stimulating differentiation of adipocyte cells, for stimulating to proliferation of or gene expression in pericyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of an endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans

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PRO
from cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRC polypeptides are also useful for treating various mammalian haemolobin-associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polyuucleotide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeleral muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; sports injury; proteoglycan; articular cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis, haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
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                                                                                                                                                                         1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; tive 0; Mismatches 16; Indels 0
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                                                                                                                                            Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding human PRO polypeptide #111.
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es 31; Conservative
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14-SEP-1998;
16-SEP-1998;
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Matches
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2001US-00808689. 2001US-00816744. 2001US-00828366. 2001WO-US006666. 2001US-00802706. 2001US-00866028 2001US-00872035 001US-00882636 19-JUN-2001; 2001US-00886342 001US-00860216 001US-00866034 2001US-00927796 99WO-US030720 99WO-US031243 2000WO-US000277 2000WO-US003565 2000WO-US004341 2000WO-US004342 2000WO-US004914 20-DEC-2000; 2000US-00747259 99WO-US021547. 99WO-US028214 99WO-US028313 99WO-US028634 99WO-US028564 99WO-US030911 99WO-US028301 99WO-US030095 99WO-US028409 99WO-US03 99WO-US0 2000WO-US 22-DEC-1999; 30-DEC-1999; 30-DEC-1999; 05-JAN-2000; 06-JAN-2000; 111-AUG-2000; 23-AUG-2000; 24-AUG-2000; 28-FEB-2001; 01-MAR-2001; 09-MAR-2001; 20-JUN-2001; 22-JUN-2001; 06-JAN-2000; 10-NOV-2000; 01-DEC-2000; 02-DEC-1999, 20-DEC-1999; 21-MAR-2000 .7-MAY-2000 22-MAY-2000 02-JUN-2000 28-JUL-2000 01-JUN-2001 29-NOV-1999 01-DEC-1999 20-MAR-2000 

16-AUG-2001; 2001US-00931836. 19-DEC-2001; 2001US-00028072. (GETH ) GENENTECH INC. 

Gao W;

New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, detecting the presence of tumor in a mammal, or modulating the uptake of glucose or free fatty acid by skeletal muscle cells or adipocyte cells. Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gr Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; WPI; 2003-777204/73. P-PSDB; ADB26115. Smith V,

Claim 2; Fig 221; 659pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the prostering the presence of a tumour in a memmal (e.g. adrenal, lung, certorical and invention and method for opportunities are useful in molecular blooky, including uses as polymucleotides are useful in molecular blooky, including uses as polymucleotides are useful in molecular blooky, including uses as polymucleotides are useful in molecular blooky, including uses as polymucleotides are useful in gene therapy. The polymucleotides may also arisanse RNA and BNA and in gene therapy. The polymucleotides may also be used in preparing RNA polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapputically useful transpenses. The RRO polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies are used in preparing of human microvascular endothelial cells, for modulating the uptake of glucese or FRA by skeletal muscle cells, for stimulating differentiation of adipocyte cells, for stimulating differentiation of alphocyte cells, for stimulating and condition screens of inner ear utricular supporting cells or T-lymphocyte cells, for stimulating and condition and cells or adipocyte cells, for stimulating and cells or the proliferation of anothalial cell tube formation and for treating cartings are useful for treating various mammalian hammed conditions which proliferates are useful for treating various mammalian hamped condition associated disorders such as various thalasseamias and condition. Note: The sequence data for this patent is also available in electronic format from the patent of the useful for treating various mamm

Sequence 1129 BP, 231 A, 369 C, 335 G; 194 T, 0 U, 0 Other;

Gaps 0; Query Match
1.1%; Score 21.4; DB 1; Length 1129;
Best Local Similarity 66.0%; Pred. No. 45;
Matches 31; Conservative 0; Mismatches 16; Indels 0;

0

ADB21599 standard; cDNA; 1129 ADB21599; ADB21599/ ID ADB2 XX AC ADB2 XX DT 20-N XX DE Nove

RESULT 105

BP.

20-NOV-2003

Novel human secreted and transmembrane protein PRO4327 cDNA.

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Human; secreted and transmembrane protein; PRO; gene; ss; Tumour necrosis factor alpha release; TNP-alpha release; Towner necrosis factor alpha release; TNP-alpha release; glucose uptake modulator; FPA uptake modulator; cell proliferation stimulator; cell differentiation stimulator; cell differentiation stimulator; cytokine release stimulator; tumour; cell differentiation inhibitor; cytokine release stimulator; tumour; cervical tumour; liver tumour; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker.
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11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004342.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US004414.
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10-MAR-2000; 2
15-MAR-2000; 2
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02-JUN-1999;
01-SEP-1999;
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05-OCT-1999;
29-NOV-1999;
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New secreted and transmembrane PRO polypeptide useful for detecting the presence of tumor in a mammal, or modulating the uptake of glucose or free fatty acid by skeletal muscle cells or adipocyte cells.
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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2000WO-US0332678
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09-AUG-2001; 2001US-00927796.
16-AUG-2001; 2001US-009218072.
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                                                                                                                                                                                                                                                      28-FEB-2001;
28-FEB-2001;
01-MAR-2001;
09-MAR-2001;
14-MAR-2001;
22-MAR-2001;
30-MAR-2000;
17-MAY-2000;
22-MAY-2000;
30-MAY-2000;
02-JUN-2000;
28-JUL-2000;
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08-hug-2000;
10-NOV-2000;
01-DEC-2000;
20-DEC-2000;
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21-JUN-2001;
22-JUN-2001;
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25-MAY-2001;
25-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                     05-APR-2001;
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Gao W;

The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the release of TNF alpha from human blood, for modulating the uptake of glucose or FNA by skeletal muscle cells or adjocyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the release of proteoglycans from cartilage, for stimulating the proliferation of inner ear utifular supporting cells, for stimulating the proliferation of Inner ear utifular supporting cells, for stimulating the release of a cytokine from PBMC cells, for inhibiting the binding of peptide to factor VIIA, for inhibiting the differentiation of adipocyte cells, for stimulating the proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast,

2000WO-US006319 2000WO-US006884

prostate, rectal, cervical or liver tumour. The oligonucleotide probes are useful for isolating genomic and cDMA nucleotide sequences or antisense probes. (I) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding interaction. A polymucleotide (II) encoding (I) is useful in chromosome and gene mapping, in generation of antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and sor chromosome identification, as chromosome marker, and for generating probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g. detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. (I) and (II) are useful for tissue typing. This sequence encodes a novel human secreted and transmembrane PRO polypeptide. ö 0; Gaps TICTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881 DB 1; Length 1129; Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; Query Match 1.1%; Score 21.4; DB 1; Length 1 Best Local Similarity 66.0%; Pred. No. 45; Matches 31; Conservative 0; Mismatches 16; Indels 1835 δ g

10-MAR-1999; 99W0-US005190.
20-ARY-1999; 99W0-US008615.
14-MAY-1999; 99W0-US012052.
02-JUN-1999; 99W0-US012053.
02-JUN-1999; 99W0-US012054.
13-SEP-1999; 99W0-US020544.
13-SEP-1999; 99W0-US020544.
15-SEP-1999; 99W0-US020544.
15-SEP-1999; 99W0-US020544.
15-SEP-1999; 99W0-US020544.
15-SEP-1999; 99W0-US020544.
16-SEC-1999; 99W0-US020565.
16-DEC-1999; 99W0-US020565.
16-DEC-1999; 99W0-US020565.
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16-DEC-1999; 99W0-US020505.
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16-DEC-1999; 99W0-US020565.
16-DEC-1999; 99W0-US020506.
16-DEC-1999; 99W0-US02056.
16-DEC-1999; 99W0-US02056.
16-D

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration. 378/c ADA77378 standard; cDNA; 1129 BP. Human PRO polynucleotide #111. 20-NOV-2003 (first entry) ADA77378;

US2003068797-A1 Homo sapiens. 10-APR-2003

2002US-00140921 07-MAY-2002;

97WO-USOD5230. 98WO-USO12456. 98WO-USO114552. 98WO-USO11903. 98WO-USO19093. 98WO-USO19094. 98WO-USO19094. 98WO-USO19177. 98WO-USO19177. 98WO-USO19147. 98WO-USO2141. 98WO-USO2263. 12 - UUN - 1998 14 - UUL - 1998 10 - SEP - 1998 14 - SEP - 1998 14 - SEP - 1998 14 - SEP - 1998 16 - SEP - 1998 17 - SEP - 1998 17 - CEP - 1998 17 - CEP - 1998 29 - CCT - 1998 29-00T-1998; 20-NOV-1998; 01-DEC-1998; 05-JAN-1999; 08-MAR-1999; A 1757 A

18 FEB - 2000; 2000WO-USO04414.
24 - FEB - 2000; 2000WO-USO04414.
24 - FEB - 2000; 2000WO-USO06414.
24 - FEB - 2000; 2000WO-USO05014.
24 - FEB - 2000; 2000WO-USO05014.
25 - MAR - 2000; 2000WO-USO05019.
15 - MAR - 2000; 2000WO-USO05819.
15 - MAR - 2000; 2000WO-USO05819.
15 - MAR - 2000; 2000WO-USO05819.
15 - MAR - 2000; 2000WO-USO05819.
17 - MAR - 2000; 2000WO-USO17377.
21 - MAR - 2000; 2000WO-USO17377.
22 - MAY - 2000; 2000WO-USO1747.
23 - MAY - 2000; 2000WO-USO1747.
24 - AUG - 2000; 2000WO-USO174.
25 - MAY - 2000; 2000WO-USO174.
26 - MAR - 2000; 2000WO-USO174.
26 - AUG - 2000; 2000WO-USO174.
27 - AUG - 2000; 2000WO-USO174.
28 - FEB - 2001; 2000WO-USO174.
29 - AUG - 2000; 2000WO-USO174.
20 - DEC - 2000; 2000WO-USO174.
20 - DEC - 2000; 2000WO-USO174.
21 - AUG - 2000; 2000WO-USO174.
22 - MAR - 2001; 2001US - 0074.
25 - MAR - 2001; 2001US - 0086.
25 - MAR - 2001; 2001US - 0086.
25 - MAR - 2001; 2001US - 0086.
25 - MAR - 2001; 2001US - 0086.
26 - MAR - 2001; 2001US - 0086.
26 - MAR - 2001; 2001US - 0086.
27 - MAY - 2001; 2001US - 0086.
28 - MAY - 2001; 2001US - 0086.
29 - MAR - 2001; 2001US - 0086.
20 - 100 - 2001US - 2001US - 0086.
21 - 100 - 2001; 2001US - 0086.
22 - MAY - 2001; 2001US - 0086.
23 - MAY - 2001; 2001US - 0086.
24 - 100 - 2001; 2001US - 0086.
25 - MAY - 2001; 2001US - 0086.
26 - 100 - 2001US -

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TWF-alpha) from human blood, a method for stimulating the poliferation or differentiation of chondrocyte cells and a method for proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adremal, lung, collon, breast, prostate, rectal, kidney, cervical and liver tumours). The colymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and in gene therapy. The polymucleotides may also cantisense RNA and propositides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the Gevelopment and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of inner endothelial cells, for simulating differentiation of adipocyte cells, for stimulating proliferation of inner ear unicular supporting cells. for inducing endothelial cell tube formation and for treating proliferation of adipocyte cells, for stimulating and prelamination and adipocyte cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage defects, escenathatics and rheamatoid attrities PRO polypeptides which stimulate the release of proteoglycans arthities. PRO polypeptides which stimulate the release of proteoglycans arthities are also useful for treating sports-related joint problems, arthities are also useful for treating various manmallan hamoglobin-may benefit from enhanced local immune system cells in the propertion of the manned
                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated, secreted and transmembrane PRO polypeptides e.g. PRO1801 and PRO1114, useful in the preparation of a medicament for treating a condition responsive to PRO polypeptide, and as therapeutic agents e.g.
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                  2001WG-US020116.
2001WG-US0210135.
2001WG-US021735.
2001US-00924419.
2001US-00924419.
2001US-0092796.
    2001US-00887879
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Stewart TA,
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                                                                                                                                                                                                                (GETH ) GENENTECH INC.
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P-PSDB; ADA77379.
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19-DEC-2001;
                                        29-JUN-2001;
                                                               09-JUL-2001;
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Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
irom USPTO at segdata.uspto.gov/sequence.html.
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; 0 Gaps ô 1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; 1835 TICTIAATTITICATTICCAGAITTCCTICAGITTIGGGTTTIGTTI 1881 0; Mismatches 16; Indels 31; Conservative Query Match Best Local Similarity Matches

1129 TITITITITITITITITITITICAGCIGGCACACACACGCIGGCTITITATI 1083

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; PFA; skeletal muscle cell; adipocyte cell; gericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteogylycan; articular cartilage disorder; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration. cDNA encoding human PRO polypeptide #111. ADB18118 standard; cDNA; 1129 BP. 99WO-US020111, 99US-00403297, 30-NOV-1999; 99WO-USO28313. 18-FEB-2000; 2000WO-USO04342. 01-DEC-2000; 2000WO-USO32678. 19-DEC-2001; 2001US-00028072. 22-APR-2002; 2002US-00127825 (first entry) JS2003077710-A1 22-OCT-1998; 01-SEP-1999; 18-OCT-1999; Homo sapiens. 20-NOV-2003 24-APR-2003 ADB18118; 

Gao W;

Deforge L, Desnoyers L, Filvaroff E, Ga A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z;

Gao W; Beresini M, Deforge L, Desnoyers L, Filvaroff E, G ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; (GETH ) GENENTECH INC. Stewart TA, Baker KP, Ber Gerritsen ME, Smith V,

WPI; 2003-755065/71. P-PSDB; ADB18119 New secreted and transmembrane PRO polypeptides and nucleic acids, usef in gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in identifying chromosomes.

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polypucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. adrenal, lung, cloif prast, prostate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful medicament for treating a condition responsive to the polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies. Such as tumours, for stimulating and inhibiting proliferation of plucose or FRA by skeletal muscle cells, for stimulating che uptake of glucose or FRA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation of or gene exporting cells or T-lymphocyte cells, for stimulating the proliferation of inner ear uniticular supporting cells or T-lymphocyte cells, for stimulating the proliferation and inner ear uniticular supporting cells or T-lymphocyte cells, for stimulating the cells, for stimulating the proliferation of inner ear uniticular supporting cells or T-lymphocyte cells, for stimulating the cells, for stimulating the medicament cells in the proliferation of inner ear uniticular supporting cells or T-lymphocyte cells, for stimulating the cells, for stimulating cells or medicament cells, for stimulating cells or medicament cells, for stimulating cells or cells, cells, cells, cells, cells, cells, cells, cells, cells, cells, cells,

RESULT 107 ADB18118/c

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Tumour necrosis factor alpha release; TNF-alpha release;
Jucose uptake modulator;
cell proliferation stimulator; FRA uptake modulator;
cell differentiation stimulator; cell differentiation stimulator;
cell differentiation inhibitor; cytokine release stimulator; tumour;
cell differentiation inhibitor; cytokine release stimulator; tumour;
cervical tumour; breast tumour; prostate tumour; rectal tumour;
gene therapy; chromosome identification; chromosome marker.
                     arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems. Atticular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian heemoglobin-associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence encodes a human PRO polypeptide of the invention. Note: The sequence data for this patent is also available in electronic format from the USPTO website at segdata.uspto.gov.
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for tissue
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bone and/or cartilage disorders such as sports injuries and
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                                                                                                                                                                                                                                                                                                                                                                    Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 1.1%; Score 21.4; DB 1; Length 1 larity 66.0%; Pred. No. 45; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1835 TICTIAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT
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02-JUN-1999; 99WG-US012252.
25-AUG-1999; 99US-00380137.
30-MAR-2000; 2000WG-US002678.
01-DEC-2001; 2001US-00028072.
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Gerritsen ME, Goddard
Smith V, Stewart TA,
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P-PSDB; ADA86802.
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nes 31; Conserv
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release of TNP-alpha from human blood, for modulating the uptake of glucose or FPA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating proliferation of T-lymphocyte cells, for stimulating proliferation of For inhibiting the binding of A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte cells, for stimulating proliferation of module is lung, colon, breast, the presence of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour. The oligomucleotide probes care useful for isolating genomic and cDNA nucleotide sequences or antisense probes. (I) is also useful as therapeutic agent. PRO is useful in therapeutic and promosome and adminible or properation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, in gene therapy, for chromosome identification, as chromosome marker, and for generating probes. An anti-(I)-antibody is useful in diagnostic assays. for PRO, esgreecting type sexpression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. (I) and (II) are useful for tissue typing. This sequence encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted and transmembrane protein; PRO; gene; ss;
fumour necrosis factor alpha release; TNF-alpha release;
glucose uptake modulator; FFA uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inhibitor; cytokine release stimulator; tumour;
lung tumoue; colon tumour; breast tumour; prostate tumour; rectal tumour;
cervical tumour; liver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 21.4; DB 1; Length 1129;
Pred. No. 45;
0; Mismatches 16; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1835 TICTIAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human secreted and transmembrane protein PRO4327 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a novel human secreted and transmembrane PRO polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA87904 standard; cDNA; 1129 BP
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01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.0
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2003082700-A1.
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ADA87904/c
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20-MAR-2003

Tumas D, Watanabe CK, Wood WI, Zhang Z;

Smith V,

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The invention describes 30b nucleic acids encoding PRO (secreted and transmembrane) polypeptides (1). (1) is useful for stimulating the uptake of release of TNF-alpha from human blood, for modulating the uptake of glucose or FRA by skeletal muscle cells or adjocyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in periorte cells, for stimulating the proliferation of or gene expression in periorte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating of C A-peptide to factor VIIA, for inhibiting the binding of C A-peptide to factor VIIA, for inhibiting the binding of the presence of tumour in a mammal. The tumour is lung, colon, breast, cells, for stimulating genomic and cDNA nucleotide sequences or prostate, rectal, cervical or liver tumour. The oligonucleotide probes are useful for isolating genomic and cDNA nucleotide sequences or antisense probes. (1) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding in assays to identify other proteins or molecules involved in binding in assays to identify other proteins or generating transgenic animals or screening of therapeutically useful reagents, in gene therapy, for knockout animals which in turn are useful in diagnostic assays for pRO, ergorbes. An anti-(1)-antibody is useful in diagnostic assays for pRO, ergorbes. The antibody is useful in diagnostic assays for pRO, ergorbes. The antibody is useful in diagnostic assays for pRO, ergorbes. The and (II) are useful for tissue typing. This sequence encodes a novel human secreted and transmembrane PRO polypeptide.
                                                                                                                                                                                                                                                                                   invention describes 305 nucleic acids encoding PRO (secreted and
                                                                                                                                      New PRO nucleic acid, useful for e.g., tumor or for tissue typing.
                                                                                                                                                                                                                          Claim 2; Fig 221; 637pp; English.
  Stewart TA,
                                                        WPI; 2003-786910/74.
                                                                                      P-PSDB; ADA87905
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0 1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; tive 0; Mismatches 16; Indels 0; Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; Query Match
Best Local Similarity 66.04
Matches 31, Conservative ò

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RESULT 110 ADA46292/c ID ADA46292 standard; cDNA; 1129 BP. ADA46292; 

20-NOV-2003 (first entry)

Novel human secreted and transmembrane protein PRO4327 cDNA.

Human; secreted and transmembrane protein; PRO; gene; ss; Yumour necrosis factor alpha release; TNF-alpha release; glucose uptake modulator; PFA uptake modulator; cell proliferation stimulator; cell differentiation stimulator; cytokine release stimulator; tumour; cell differentiation inhibitor; cytokine release stimulator; tumour; lung tumour colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker.

Homo sapiens.

JS2003054516-A1

12-APR-2002; 2002US-00121050. 98WO-US017888 98WO-US018824 99WO-US000106 38WO-US019177 99WO-US028409 99WO-US028564 99WO-US030095 98WO-US022991 99WO-US020594 99WO-US020944 99WO-US023089 99WO-US028214 99WO-US028301 99WO-US030720 2000WO-US000219 000WO-US000277 99WO-US028551 000WO-US004341 000WO-US004342 000WO-US005004 000WO-US004414 000WO-US004914 000WO-US005746 000WO-US006B84 98WO-US021 98WO-US024 99WO-US02 000WO-US0 SU-OM66 -0M66 24-FEB-2000; .4-SEP-1998; 30-MAY-2000; 14-JUL-1998 28-AUG-1998 -SEP-1998 30-MAR-2000; 10-SEP-1998 15-JAN-2000; 0-DEC-1999 2-DEC-1999 ; 0 useful for preparing a composition for treating Gaps

(GETH ) GENENTECH INC

2001US-00924419. 2001US-00927796. 2001US-00931836. 2001US-00028072.

3 Gao Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ge Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-521853/49. P-PSDB; ADA46293.

New PRO nucleic acid, useful for preparing a composition for treating e.g., tumor

Claim 2; Fig 221; 200pp; English.

The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the transmembrane of TNT-alpha from human blood, for modulating the uptake of glucose or FPA by skeletal muscle cells or adipocyte cells, for glucose or FPA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of proteoglycans from cartilage, for stimulating the proliferation of Tlymphocyte cells, for stimulating the proliferation of for 1 proportion of adipocyte cells, for stimulating the proliferation of Flymphocyte cells, for stimulating the proliferation of Flymphocyte cells, for stimulating of the release of a cytokine from PBMC cells, for inhibiting the binding of the release of two function in a mammal. The differentiation of adipocyte cells, for stimulating proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, cells, for solating genomic and cDNA nucleotide sequences or are useful for isolating genomic and cDNA nucleotide sequences or contisense probes. (I) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding in assays to identify other proteins or molecules involved in binding conditions of proparation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and conforming of therapeutically useful reagents, in gene therapy, for chromosome identification, as chromosome marker, and for generating conforming its expression in as chromosome marker, and for generating conforming its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural confinition and transmembrane PRO polypeptide. 

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; shelver; microvascular endothelial cell; glucose; FP; inner ear utricular supporting cell; pericyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration. Gaps . 0 TICTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881 1129 thritritritritritritriadciacacacacacacidecitritrit 1083 DB 1; Length 1129; Sequence 1129 BP; 231 A; 369 C; 335,G; 194 T; 0 U; 0 Other; Score 21.4; DE Pred. No. 45; 0; Mismatches cDNA encoding human PRO polypeptide #111. ADB28322/c ID ADB28322 standard; cDNA; 1129 1.1%; 20-NOV-2003 (first entry) 1.1 Best Local Similarity 66.0 Matches 31, Conservative 1835 ADB28322; RESULT X S ò 원

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17-JUN-1998; 98US-0089599P. 02-JUN-1999; 99WS-US012252. 25-AUG-1999; 99WS-US028313. 30-MOV-1999; 99WO-US028313. 30-MAR-Z000; 2000WO-US032678. 01-DEC-2000; 2001US-00028072. 22-APR-2002; 2002US-00127851. 01-MAY-2003.

US2003082699-A1 Homo sapiens.

3 Gao Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

(GETH ) GENENTECH INC.

WPI; 2003-777202/73. P-PSDB; ADB28323 New PRO nucleic acid, useful for preparing a composition for treating e.g., tumor or for tissue typing.

claim 2, Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TMF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating

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cc antisense RNA and DNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in cgenerating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or conditions. For stimulating and inhibiting proliferation of antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for modularing the uptake of glucose or FFA by skeletal muscle cells, for stimulating colliferation of or gene expression in pericyte cells, for stimulating proliferation of or gene expression in pericyte cells, for stimulating colliferation of or gene expression in pericyte cells, for stimulating colliferation of or gene expression in pericyte cells, for stimulating colliferation of or gene expression in pericyte cells, for treating cells, for stimulating cells, for stimulating cells, for stimulating cells, for stimulating cells, for treating endothelial cell tube formation and for treating cells, for arthritis and for treating sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans creativals are also useful for treating various mammalian haemoglobin—associated discorders such as various thalasseamias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence encodes a human PRO polypeptide of the invention. Note: The condition wheels at seadars and conditions was from the strong format from the form wheels a service is also available in electronic format from the form wheels and the propertions of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of th ô Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tummour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tummour; cancer; aderanl; hung; colon; break; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; glucose; FFA; endothelial cell; adipocyte cell; pericyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; hemoglobin-associated disorder thalassaemia; immune system cell infiltration. Gaps Score 21.4; DB 1; Length 1129; Pred. No. 45; 0; Mismatches 16; Indels 0; 1835 TICTIAAIITTICAITTICCAGAITTICCTICAGTITGGGTTITGTIT 1881 1129 hiriririririririririchieciescacacadascrideririrair 1083 Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; cDNA encoding human PRO polypeptide #111. the USPTO website at segdata.uspto.gov. ADB28874 standard; cDNA; 1129 BP. 1.1%; (first entry) Best Local Similarity 66.0 Matches 31; Conservative 20-NOV-2003 ADB28874; Query Match ADB28874/c ઠે

US2003082706-A1. Homo sapiens. 

10-NOV-2000; 2000WO-US030873. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072. 24-APR-2002; 2002US-00131836. 99US-0170262P ', Beresini M, Gerritsen ME, (GETH ) GENENTECH INC 09-DEC-1999; 01-MAY-2003, Baker KP, Gao W,

Deforgre L, Desnoyers L, Filvaroff E; Goddard A, Godowski PJ, Gurney AL, Sherwood S;

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO colypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the polypeptide, a method for stimulating the release of tumour necrosis of proliferation or differentiation of chondrocyte cells and a method for proliferation or differentiation of chondrocyte cells and a method for coll, breast, prostate, rectal, kidney, cervical and liver tumours). The colymucleotides are useful in molecular biology, including uses a polymucleotide may also a secretaring sthe proparing PRO polypeptides by recombinant techniques and in gene therapy. The polymucleotides may also generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for traating a condition responsive to the polypeptides or antibodies are used in preparing of human microvascular endothelial cells, for modulating the uptake of glucose or FRA by skeletal muscle cells, for stimulating differentiation of adipocyte cells, for stimulating cells or to group expression in periotyte cells, for stimulating the proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cells or adipocyte cells, for stimulating and relating the problems, articular cartilage disorders such as sports injuries and cells or adipocyte cells, for stimulating and seful for treating sports injuries and a stochasting cells or articular cartilage are useful for treating various mammalian haemoglobin-may benefit from enhanced local immune system cell and reformed encodes a human PRO polypeptide of the inspection of the properties are also useful for treating various may benefit in sequence encodes a human PRO polypeptide o ö Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FRA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; Trymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; useful for preparing a composition for treating Gaps .; Z Zhang · 0 1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; iive 0; Mismatches 16; Indels 0; 1835 TICTIAATITITICATITICCAGAITTICCTICAGTTIGGGTTTTGTTT 1881 1129 TITITITITITITITITICAGCIGGCACACAGGCIGGGITITITATI 1083 Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; Wood WI, Watanabe CK, the USPTO website at segdata.uspto.gov. New PRO nucleic acid, useful for e.g., tumor or for tissue typing. Claim 2; Fig 221; 637pp; English. Ď, ADA76826 standard; cDNA; 1129 BP. Human PRO polynucleotide #111. Tumas (first entry) Query Match
Best Local Similarity 66.0°
Matches 31, Conservative Smith V, Stewart TA, WPI; 2003-777203/73. P-PSDB; ADB28875. 20-NOV-2003 ADA76826; RESULT 113 ADA76826/c Op ð MARKA MARKA MARKA DA KAKA DA K

rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Homo sapiens,

US2003059909-A1.

27-MAR-2003

2002US-00143032 10-MAY-2002;

97WO-USODS230. 98WO-USO12456. 98WO-USO17888. 98WO-USO17888. 98WO-USO19093. 98WO-USO19093. 98WO-US019437. 98WO-US021141. 14-SEP-1998; 14-SEP-1998; 14-SEP-1998; 17.5EP-1998; 07-0CT-1998; 29-0CT-1998; 29-0CT-1998; 20-NOV-1998; 16-SEP-1998 10-SEP-1998

98WO-US022992. 98WO-US024855. 98WO-US025108. 99WO-US000106. 99WO-US005190. 99WO-US008615. 99WO-US010733. 99WO-US012252. 99WO-US0201111. 05-JAN-1999; 08-MAR-1999; 01-DEC-1998; 20-APR-1999 14-MAY-1999

99WO-US021094. 99WO-US021090. 99WO-US021547. 08-SEP-1999

99WC-US023089. 99WC-US028114. 99WC-US028413. 99WC-US028311. 99WC-US028634. 99WC-US028654. 99WC-US028654. 99WC-US028654. 01-DEC-1999 02-DEC-1999 02-DEC-1999 02-DEC-1999 02-DEC-1999 20-DEC-1999 20-DEC-1999 20-DEC-1999 30-DEC-1999

99WO-US030999.

99WO-US031274 2000WO-US000219 2000WO-US000277

2000WO-US000376

2000WO-US004341. 2000WO-US004342. 2000WO-US004314. 2000WO-US004914. 2000WO-US005601. 2000WO-US005601. 2000WO-US003565

05-0787-11999)
05-0787-2000)
06-0787-2000)
11-FEB-2000)
22-FEB-2000)
24-FEB-2000)
24-FEB-2000)
24-FEB-2000)
20-MAR-2000)
20-MAR-2000)
210-MAR-2000)
210-MAR-2000)
215-MAR-2000)

2000WO-US005841. 2000WO-US006319. 2000WO-US006884.

28-JUL-2000; 2000WO-US022011.
23-AUG-2000; 2000WO-US022011.
23-AUG-2000; 2000WO-US022011.
24-AUG-2000; 2000WO-US023328.
26-NOV-2000; 2000WO-US033282.
10-NOV-2000; 2000WO-US0332873.
10-NOV-2000; 2000WO-US033673.
20-DEC-2000; 2000WO-US032673.
20-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000WO-US032678.
20-PEC-2000; 2000WO-US032678.
20-PEC-2000; 2000WO-US032678.
20-PEC-2000; 2000WO-US032678.
20-PEC-2000; 2000WO-US032678.
20-PEC-2000; 2000WO-US032836.
20-MAR-2001; 2001WS-0086228.
25-MAY-2001; 2001WS-0086028.
25-MAY-2001; 2001WS-0086028.
25-MAY-2001; 2001WS-0086028.
25-MAY-2001; 2001WS-0086028.
25-MAY-2001; 2001WS-0086028.
25-MAY-2001; 2001WS-00874503.
20-JUN-2001; 2001WS-0081268.
20-JUN-2001; 2001WS-0081268.
20-JUN-2001; 2001WS-0081268.
20-JUN-2001; 2001WS-0081283.
21-JUN-2001; 2001WS-0081283.
21-JUN-2001; 2001WS-0081283.
21-JUN-2001; 2001WS-0081283.
21-JUN-2001; 2001WS-0081283.
21-JUN-2001; 2001WS-0081283.
21-JUN-2001; 2001WS-0081283. 

Gao Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G: Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

(GETH ) GENENTECH INC.

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WPI; 2003-540684/51. P-PSDB; ADA76827.

New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or cancer.

Claim 2; Fig 221; 660pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymuclectides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for a timulating the release of tumour necrosis factor-alpha (TNR-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostent, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for modulating the uptake of glucose or FRA by skeletal muscle cells or addipocyte cells, for

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2001WO-US020116
2001WO-US021066
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06-JAN-2000;
11-FEB-2000;
18-FEB-2000;
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11-AUG-2000;
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stimulating differentiation of adipocyte cells, for stimulating proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, polypeptides are also useful for treating various mammalian hamoglobin-polypeptides are also useful for treating various mammalian hamoglobin-associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polymucleotide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted and transmembrane protein; PRO; gene; ss; Tumour necrosis factor alpha release; TNF-alpha release; glucose uptake modulator; prA uptake modulator; cell proliferation stimulator; cell differentiation stimulator; cell differentiation stimulator; cytokine release stimulator; tumour; lung tumoue; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; ilver tumour; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker.
                                                                                                                                                                                                                                                                                                                                                 1.1%; Score 21.4; DB 1; Length 1129;
66.0%; Pred. No. 45;
ative 0; Mismatche9 16; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                            Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
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98WO-US014552.
98WO-US017888.
98WO-US018824.
98WO-US019093.
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98WO-US022992.
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98WO-US025108.
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Best Local Similarity 66.0
Matches 31; Conservative
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2001US-00854208.
2001US-00860216.
2001US-0086028.
2001US-00866034.
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2001WS-0086034.
2001WS-0086034.
2001WS-0087035.
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2000WO-US003565.
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2000WO-US005601.
2000WO-US005746.
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2001US-00808689.
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18-JUL-2001; 2001US-00908827.
06-AUG-2001; 2001US-0092419.
09-AUG-2001; 2001US-00927796.
16-AUG-2001; 2001US-00931836.
19-DEC-2001; 2001US-00028072.
                      (GETH ) GENENTECH INC.
                                         WPI; 2003-743816/70.
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Gao Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ge Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

.. Z

P-PSDB; ADA88457.

New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, detecting the presence of tumor in a mammal, or modulating the uptake of glucose or free fatty acid by skeletal muscle cells or adipocyte cells.

Claim 2; Fig 221; 659pp; English.

transmembrane) polypeptides (1). (1) is useful for stimulating the transmembrane) polypeptides (1). (1) is useful for stimulating the grake of graducose or FFRA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation of or game expression in pericyte cells, for stimulating the proliferation of or game expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of -lymphocyte cells, for stimulating the binding of A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte cells, for stimulating graducon of endothelial cells, for detecting the presence of tumour in amamal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour is lung, colon, breast, prostate, colon, breast, prostate, or identify other proteins or molecules involved in binding in theraction of PRO polypeptide, for generating transgent and consone administration, as dhromosome ladentification, as chromosome marker, and for generating probastically undered and generating probes. An anti-(1)-antibody is useful in diagnostic assays for PRO, ergoneres. (1) and (11) are useful in diagnostic assays for prodessing probes. An anti-(1)-antibody is useful in diagnostic assays for matural sources. (1) and (11) are useful for tissue typing replaced encodes (I) and (II) are useful for tissue typing. This sequence encodes novel human secreted and transmembrane PRO polypeptide.

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps ò Match 1129; Score 21.4; DB 1; Length 1129; Local Similarity 66.0%; Pred. No. 45; es 31; Conservative 0; Mismatches 16; Indels 0; Query Match Matches

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ADA97461 standard; cDNA; 1129 BP ADA97461; RESULT 115 ADA97461/6 ID ADA97 XX AC ADA97 XX XX DT 20-NC XX XX XX XX

Human PRO polynucleotide #111. 20-NOV-2003 (first entry)

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tummour necrosis factor-alpha; TNP-alpha; Chondrocyte cell; tummour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endochelial cell; glucose; PFA; skeletal muscle cell; adipocyte cell; perioyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; esports injury; proteogylycan; atticular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Homo sapiens.

US2003082686-A1. 

01-MAY-2003.

19-APR-2002; 2002US-00125926.

05-JUN-2000; 2000US-0209832P. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC.

Gao W; Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ga Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

2003-755106/71. P-PSDB; ADA97462. Isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or PRO4978, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

Claim 2; Fig 221; 666pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an attibody which specifically binds to a PRO polypeptide, a method for stimulating the invention also relates to an attibody which specifically binds to a PRO polypeptide, a method for stimulating the presence of a tumour in a memmal (e.g. adremal, lung, corol, breast, prostate, rectal, kidney, cervical and liver tumours). The prolynucleotides are useful in mclecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and BNA and in Gene therapy. The polyuncleotides may also constrained the transgenic animals or knock-out animals which are useful in the development and screening of knock-out animals which are useful in the development and screening of knock-out animals which are useful in the development and screening of knock-out animals which are useful in the development and screening of knock-out animals which are useful in the development and screening of knock-out animals which are useful in the development and screening of knock-out animals which are useful in the development of condition are proposition of the proliferation of or stimulating and inhibiting proliferation of human microvascular endothelial cells, for mediating the uptake of stimulating differentiation of adipocyte cells, for stimulating the proliferation of or gene expression in periore cells, for stimulating and carting endothelial cells or adipocyte cells, for stimulating the proliferation of since are utridual responsive or like proliferation of or gene expression in periore cells, for stimulating are useful for treating sports injuries and articular cartilage are useful for treating sports related joint problems, articular cartilage are useful for treating sports. related joint problems, articular cartilage are useful for treating sports. related joint problems, articular as busness of propertice or sequence repr

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

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24-APR-1998;
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29-APR-1998;
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15-APR-1998;
                                                                                                                                                                                                                                                                                                                                                       Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; PRA; skeletal muscle cell; adipocyte cell; perioyte cell; inner ear utricular supporting cell; perioyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
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    DB 1; Length 1129;
  Query Match 1.1%; Score 21.4; DB 1; Length 1 Best Local Similarity 66.0%; Pred. No. 45; Matches 31; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                            cDNA encoding human PRO polypeptide #111.
                                                                                                                                                                                                            ADB27218 standard; cDNA; 1129 BP.
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97US-0066364P.
97US-0066453P.
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21-NOV-1997;
24-NOV-1997;
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17-SEP-1997;
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19-SEP-1997;
19-SEP-1997;
24-SEP-1997;
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29-OCT-1997;
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98US - 0097986P.
98WG - US017888
98US - 0098755P.
98US - 0099536P.
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31-AUG-1998; 01-SEP-1998; 09-SEP-1998; 09-SEP-1998; 10-SEP-1998;

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Human; secreted and transmembrane protein; PRO; gene; ss;
Tumour necrosis factor alpha release; TNF-alpha release;
Jucose uptake modulator;
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cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inihibitor; cytokine release stimulator; tumour;
liver tumour; breast tumour; prostate tumour; rectal tumour;
cervical tumour; liver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
                                                           Novel human secreted and transmembrane protein PRO4327 cDNA
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970S-005617B.
970S-0059113P.
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970S-0059112P.
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970S-0059128P.
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970S-0063818P.
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24-0CT-1997;
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14-SEP-1998

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10-NOV-1998; 17-NOV-1998; 17-NOV-1998;

03-NOV-1998 03-NOV-1998

29-OCT-1998

ö Gaps . 0 Length 1129; 16; Indels 1.1%; Score 21.4; DB 1; ilarity 66.0%; Pred. No. 45; Conservative 0; Mismatches 16; Query Match Best Local Similarity Matches 31; Conservat

97US-0064248P-97US-0064809P-97US-00658146P-97US-0066364P-97US-0066312P-97US-0066710P-97US-0069212P-97US-0069212P-97US-0069218P-97US-0069218P-97US-0069218P-97US-0069218P-97US-0069218P-97US-0069218P-98US-0073612P-98US-0073612P-

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98US-0113315P

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99US-0115557P.
99US-0115562P.
99US-0115564P.
99US-0115733P.

27-OCT-1997 28-OCT-1997 29-OCT-1997 28-OCT-1997

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98US-0099601P. 98US-0099792P. 98US-0099803P.

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Gaps
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1129 TITTITITITITITITITITAGCTGGCACACACAGGCTGGGTTTTATT 1083
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98US-0100263P.

98WO-USO19037.

98WO-USO19177.

98WO-USO19177.

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98WS-010034P.

98WS-010034P.

98WS-01003182P.

98WS-010114P.

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Best Local Similarity 66.0
Matches 31; Conservative
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RESULT 118 ADA66842/c ID ADA66842 standard; CDNA; 1129 BP. xx

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Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; heemoglobin-associated disorder; rheumatoid arthritis; heemoglobin-associated disorder thalassaemia; immune system cell infiltration.
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                    (first entry)
                                                                                                                                                                                       JS2003068793-A1
                                                                                                                                                                      Homo sapiens.
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16-DEC-1999;
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 ADA66842
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24-FEB-2000) 2000WO-USOGSOG10-US-WAR-2000) 2000WO-USOGSOG10-US-WAR-2000) 2000WO-USOGSOG10-US-WAR-2000) 2000WO-USOGSOG110-WAR-2000) 2000WO-USOGSOG119-US-WAR-2000) 2000WO-USOGSOG119-US-WAR-2000) 2000WO-USOGSOG119-US-WAR-2000) 2000WO-USOG11705-UN-AX-2000) 2000WO-USOG11705-US-MAY-2000) 2000WO-USOG11705-US-MAY-2000) 2000WO-USOG11705-US-WAY-2000) 2000WO-USOG11705-US-WAY-2000) 2000WO-USOG11705-US-WAR-2000) 2000WO-USOG11705-US-WAR-2000) 2000WO-USOG11705-US-WAR-2000) 2000WO-USOG11705-US-WAR-2001) 2000WO-USOG11705-US-WAR-2001) 2000WO-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG11705-US-WAR-2001) 2000WS-USOG11705-US-WAR-2001) 2000WS-USOG11705-US-WAR-2001) 2000WS-USOG11705-US-WAR-2001) 2000WS-USOG11705-US-WAR-2001) 2000WS-USOG11705-US-WAR-2001) 2000WS-USOG11705-US-WAR-2001) 2000WS-USOG11705-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2001) 2000WS-USOG116-US-WAR-2
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Gerritsen ME, Goddard
Smith V, Stewart TA,
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P-PSDB; ADA66843.
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Gao Deforge L, Desnoyers L, Filvaroff E, G. A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z;

3

Novel secreted and transmembrane PRO polypeptides useful for stimulating release of tumor necrosis factor-alpha from human blood and detecting the presence of a tumor in a mammal.

Claim 2; Fig 221; 660pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNR-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for

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cclon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymuclectides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymucleotides may also be used in preparing PRO polympeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PDO Polympeptides or antibodies are used in preparing a condition responsive to the polympeptides or antibodies such as tumours, for stimulating and inhibiting proliferation of midocament for treating a condition responsive to the polympeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for stimulating proliferation of or gene expression in periorte cells, for stimulating proliferation of or gene expression in periorte cells, for stimulating the proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating architis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports injuries and onditions which architis and rheumatoid architise. PRO polypeptides such as various thalassaemias and conditions which as sociated disorders such as various thalassaemias and conditions which carbined represents a human PRO polymorlocoide of the invention. This sequence data for this patent is also evaluable in electronic format cor from uspro are sequence contrible of the invention. Onte:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB22703 standard; cDNA; 1129 BP.
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99WO-US020111.
99US-00403297.
99WO-US028313.
2000WO-US004342.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.19
Best Local Similarity 66.09
Matches 31; Conservative
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18-OCT-1999;
30-NOV-1999;
18-FEB-2000;
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ADB22703/c
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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. adrenal, lung, or proliferation or differentiation of chondrocyte cells and a method for proliferation or differentiation of chondrocyte cells and a method for proliferation probes, in chromosome and gene mapping, in generating at this sense RNA and bin gene therapy. The polypuncleotides may also a used in preparing PRO polypeptides by recombinant techniques and in generating either transgenc animals or knock-out animals which are useful in the development and screening of therapeutically useful cuseful in the development and screening of therapeutically useful captains at the PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides of antibodies, such as tumours, for stimulating and inhibiting proliferation of inner expensive to the polypeptides of thuman microvascular endothelial cells, for modulating the uptake of glucose or FRA by skeletal muscle cells, for stimulating differentiation of adipocyte cells, for stimulating cells or Tlymphocyte cells, for inducing endothelial cells or as sports cells, for stimulating are useful for treating sports release of proteoglycans trougs bene and/or cartilage disorders such as sports injunities and cells, arthuities PRO polypeptides which stimulate the release of proteoglycans articular cartilage are useful for treating sports-related joint problems, articular cartilage are useful for treating sports-related joint problems, articular cartilage are useful for treating sports-related solve the proteoglycans are also useful for treating sports-related solve the propertion of the may propose the sequence represents a human 
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                                                                                                                                                                                                                                                                           New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, as diagnostic markers for the presence of a disease condition, or as therapeutic targets for treating tumors, diabetes, obesity or arthritis.
                                                                                                                   Gao W;
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                                                                                                              Deforge L, Desnoyers L, Filvaroff E, G. A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z;
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66.0%; Pred. No. 45;
iive 0; Mismatches 16; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Fig 221; 637pp; English.
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01-DEC-2000; 2000WO-US032678
19-DEC-2001; 2001US-00028072.
                                                                                                              Beresini M, De. ME, Goddard A, Stewart TA, Tum
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Best Local Similarity 66.0%
                                                                    (GETH ) GENENTECH INC
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P-PSDB; ADB22704.
                                                                                                                                       Gerritsen
Smith V,
                                                                                                                   Baker KP,
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ADB23476/c
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Human PRO polynucleotide SEQ ID NO 221.

The sequence data for this patent is also available in electronic format

from USPTO at segdata.uspto.gov/sequence.html.

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthitis; rheumatoid arthritis; heemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Homo sapiens.

US2003077712-A1

24-APR-2003

22-APR-2002; 2002US-00127835 98US-0104987P

01-SEP-1999; 99WO-US020111. 18-CCT-1999; 99US-00403297. 18-FEB-2000; 2000WO-US0A342. 01-DEC-2000; 2000WO-US038678. 20-OCT-1998;

(GETH ) GENENTECH INC.

3 Deforge L, Desnoyers L, Filvaroff E, Gao A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Baker KP, Beresini M, Gerritsen ME, Goddard Smith V, Stewart TA,

WPI; 2003-755067/71. P-PSDB; ADB23477. New isolated, secreted and transmembrane PRO nucleic acid, useful for the diagnosis, prevention and/or treatment of tumors, such as lung, colon, breast, prostate, rectal, cervical and/or liver tumors.

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynuclectides encoding them. The transmembrane polypeptides and the polynuclectides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNR-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyce cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynuclectides are useful in molecular biology, including uses as the nutsense RNA and DNA and in gene therapy. The polynuclectides may also antisense RNA and DNA and in gene therapy. The polynuclectides may also continue the development and screening of therapeutically useful generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful casement for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of convascular endothelial cells, for stimulating differentiation of adipocyte cells, for stimulating confideration of or gene expression in pericyte cells, for stimulating confideration of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating arbane and/or cartillage disorders such as sports injunies and variant endothelial cell tube formation and for treating arbane which are well an expression in pericyte cells, for reating cartillage disorders such as sports injunies and endor cartillage disorders such as sports injunies and endor cartillage disorders such as sports injunies. arthritis. PRO polypeptides which simulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin-associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polynucleotide of the invention. Note:

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The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (1). (1) is useful for stimulating the release of TNF-alpha from human blood, for modulating the uptake of glucose or FRA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation of differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the release of proteoglycans from carcilage, stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the release of a cytokine from PBMC cells, for inhibiting the binding of A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte cells, for stimulating proliferation of endothelial cells, for detecting cells, for stimulating proliferation of endothelial cells, for detecting
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Tumour necrosis factor alpha release; TNF-alpha release;

Jucose uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inihibitor; cytokine release stimulator; tumour;
lung tumous; colo tumour; breast tumour; prostate tumour; rectal tumour;
cervical tumour; liver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
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                                                                                   Length 1129;
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                                                                                                                                                                                                                                                                                                                                                                                                           Novel human secreted and transmembrane protein PRO4327 cDNA.
                                             Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
                                                                                                                         16;
                                                                                     DB 1;
                                                                           1.1%; Scc. No. 45, 66.0%; Pred. No. 45, ...
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99US-00380138.
; 2000WO-US032678.
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25-AUG-1999; 99US-0380138.
01-DEG-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
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                                                                                       Query Match
Best Local Similarity 66.0
Matches 31; Conservative
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                                                                                                                                                                                                                                                         RESULT 121
ADA92198/c
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the presence of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour. The oligonucleotide probes are useful for isolating genomic and cDNA nucleotide sequences or antisense probes. (1) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding in encation of merapeutic agent, pro is useful in chromosome and gene mapping, in generation of antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, in gene therapy, for chromosome identification, as chromosome marker, and for generating concerning its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. (1) and (11) are useful for tissue typing. This sequence encodes a novel human secreted and transmembrane PRO polypeptide.
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Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

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                              Gaps
                              o,
 Score 21.4; DB 1; Length 1129;
Pred. No. 45;
0; Mismatches 16; Indels 0
                                                    1835 TICTIAAITTITICAITICCAGAITICCTICAGAITIGGGTTIGIT 1881
                                                                                1129 Tririririririririririri 1083
1.1%;
ilarity 66.0%;
Conservative (
              Local Similarity
                          31;
                       Matches
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Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FRA; selectal muscle cell; adipocyte cell; glucose; FRA; inner ear utricular supporting cell; pricyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports alphy; proteodly/can; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration. ADB15261/c ID ADB15261 standard; cDNA; 1129 Human PRO polynucleotide #111. (first entry) 20-NOV-2003 ADB15261; RESULT 122 

Homo sapiens.

US2003087352-A1

08-MAY-2003

22-APR-2002; 2002US-00127824.

02-UJV-1999; 99WO-US012252. 25-AUG-1999; 99US-00380137. 30-MAX-2000; 2000WG-US018439. 30-MAX-2000; 2000WG-US014941. 01-DEC-2000; 2000WG-US032678. 19-DEC-2001; 2001US-00028072. 98US-0096891P 17-AUG-1998;

(GETH ) GENENTECH INC.

3 Gao Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ga Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-786943/74. P-PSDB; ADB15262.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis of polypeptide, a method for stimulating the release of tumour necrosis of factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chodioroyte cells and a method for consistent or differentiation of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prosetate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridsation probes, in chromosome and gene mapping, in generating a thypridsation probe, in chromosome and gene mapping, in generating a thissense RNA and DNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by knock-out animals which are custulint the development and screening of knock-out animals which are useful in the development and screening or knock-out animals which are useful in the development and screening or the polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or of thuman microvascular endothelial cells, for midlating the uptake of gruinlating differentiation of adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating are expression in periore cells, for stimulating calls the proliferation of finner ear utricular supporting cells, for stimulating are useful for treating sports inducing and challed are useful for treating such as sports inducing and conditions which stimulate the release of proteoglycans arthorias are also useful for treating sports-related joint problems, articular cartilage are useful for treating sports-related disorders such as various human endomental is also sequence represents a human . 0 New PRO nucleic acid, useful for producing a recombiannt PRO polypeptide and for manufacturing a medicament for diagnosing or treating tumor. Gaps Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; Claim 2; Fig 221; 637pp; English. Query Match Matches 

ô Match 1.1%; Score 21.4; DB 1; Length 1129; Local Similarity 66.0%; Pred. No. 45; es 31; Conservative 0; Mismatches 16; Indels 0. 1835 ITCTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881 ð

ADB38513 standard; cDNA; 1129 BP (first entry) 04-DEC-2003 ADB38513; RESULT 123 g 

Human; secreted and transmembrane protein; PRO; gene; ss; Tumour necrosis factor alpha release; TNF-alpha release; glucose uptake modulator; PFA uptake modulator; cell proliferation stimulator; cell differentiation stimulator; cell differentiation inhibitor; cytokine release stimulator; tumour; lung tumoue; colon tumour; breast tumour; prostett tumour; rectal tumour; attumour; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker.

Novel human secreted and transmembrane protein PRO4327 cDNA.

Homo sapiens.

US2003082766-A1.

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12-70N-1998; 98W0-US012525

14-5EP-1998; 98W0-US014552.

14-5EP-1998; 98W0-US018824;

14-5EP-1998; 98W0-US018824;

14-5EP-1998; 98W0-US019093.

14-5EP-1998; 98W0-US019094.

14-5EP-1998; 98W0-US019094.

14-5EP-1998; 98W0-US01930.

17-5EP-1998; 98W0-US01933.

17-5EP-1998; 98W0-US01933.

17-5EP-1998; 98W0-US01933.

17-5EP-1998; 98W0-US01933.

17-5EP-1998; 98W0-US01933.

18-5EP-1999; 99W0-US01933.

19-5EP-1999; 99W0-US01933.

19-5EP-1999; 99W0-US0193.

19-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

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11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

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11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

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11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

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11-5EP-1999; 99W0-US01944.

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11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

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11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

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11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944.

11-5EP-1999; 99W0-US01944
                                                                   97WO-US005230.
98WO-US012456.
98WO-US0174852.
98WO-US018824.
98WO-US019093.
98WO-US019094.
98WO-US019177.
98WO-US0191370.
                                        30-MAY-2002; 2002US-00158782
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01-DEC-2000, 2000WO-US032678.
20-DEC-2000; 2000US-00747259.
20-DEC-2000; 2000US-00747259.
20-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WS-00796498.
01-MAR-2001; 2001WS-00806520.
01-MAR-2001; 2001WS-008066689.
22-MAR-2001; 2001US-00866210.
10-MAY-2001; 2001US-00866210.
10-MAY-2001; 2001US-00866210.
10-MAY-2001; 2001US-00866210.
10-MAY-2001; 2001US-00866210.
25-MAY-2001; 2001US-00866210.
25-MAY-2001; 2001US-00866210.
25-MAY-2001; 2001US-00866210.
25-MAY-2001; 2001US-00866210.
25-MAY-2001; 2001US-00866210.
25-MAY-2001; 2001US-00866210.
25-MAY-2001; 2001US-0088263.
19-JUN-2001; 2001US-00881879.
22-JUN-2001; 2001US-00881879.
22-JUN-2001; 2001US-00881879.
22-JUN-2001; 2001US-00881879.
22-JUN-2001; 2001US-00998827.
16-JUL-2001; 2001US-00998827.
16-JUL-2001; 2001US-00991836.
16-JUC-2001; 2001US-00921796. 

### (GETH ) GENENTECH INC

3 Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

### WPI; 2003-786921/74. P-PSDB; ADB38514.

New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, detecting the presence of tumor in a mammal, or modulating the uptake of glucose or free fatty acid by skeletal muscle cells or adipocyte cells.

## Claim 2; Fig 221; 660pp; English

The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (1). (1) is useful for stimulating the cransmembrane) polypeptides (1). (1) is useful for stimulating the uptake of glucose or FFA by skeletal muscle cells adipocyte cells, for calease of FFA by skeletal muscle cells adipocyte cells, for stimulating the proliferation of for gene expression in pericyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of Inner ear utilicular supporting cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating proliferation of T-lymphocyte cells, for stimulating proliferation of endothelial cells for detecting the rectal, cervical or inhibiting the binding of C A-peptide to factor VIIA, for inhibiting the differentiation, breast, prostate, rectal, cervical or liver tumour. The oligonucleotide probes are useful for isolating genomic and cDNA nucleotide sequences or are useful for isolating genomic and cDNA nucleotide in chromosome in assays to identify other proteins or molecules involved in binding in assays to identify other proteins or molecules involved in binding conditions of PRO polypeptide, for generating the absorbance of preparation of PRO polypeptide, for generating the absorbance in a screening of therapeutically useful reagents, in gene therapy, for knockout animals which in turn are useful in the development and conconcent of the proposes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g. detecting its expression in specific cells, tissues or serum, and for

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Tumour necrosis factor alpha release; TNP-alpha release;
glucose uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inihibitor; cytokine release stimulator; tumour;
ung tumour; prosest tumour; prosest tumour; rectal tumour;
cervical tumour; liver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
                  sources. (I) and (II) are useful for tissue typing. This sequence encodes a novel human secreted and transmembrane PRO polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypepitides (I). (I) is useful for stimulating the release of TNF-alpha from human blood, for modulating the uptake of glucose or PRA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the release of proteoglycans from cartilage, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the release of a cytokine from PBMC cells, for inhibiting the binding of
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purification of PRO from recombinant cell culture or natural
                                                                                                                                                       Gaps
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Goddard A, Godowski PJ, Gurney AL, Sherwood S;
art TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                     0;
                                                                                                                                                                                           1835 TICTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881
                                                                                                                 DB 1; Length 1129;
                                                                                                                                                                                                                      1129 TTTTTTTTTTTTTTTTTTCAGCTGGCACACAGGCTGGGTTTTATT 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human secreted and transmembrane protein PRO4327 cDNA
                                                                          Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
                                                                                                                                                       16; Indels
                                                                                                               Score 21.4; DB Pred. No. 45; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                             ADB37961 standard; cDNA; 1129 BP.
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99WO-US012252.
99US-00380137.
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01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
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                                                                                                                                   66.0%;
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                             Query Match
Best Local Similarity 66.0
Matches 31; Conservative
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Smith V, Stewa
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02-JUN-1999;
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ADB37961/c
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the presence of tumour in a manmal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour. The oligomuclectide probes are useful for isolating genomic and cDNA nucleotide sequences or antisense probes. (I) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding interaction. A polynucleotide (II) encoding (I) is useful in chromosome of an encoding of the proparation of antisense RNA and DNA, in the preparation of PNO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, in gone therapy, for chromosome identification, as chromosome marker, and for generating probes. An anti-(I)-antibody is useful in diagnostic assays for PNO, e.g. detecting its expression in specific cells, tissues or serum, and for sources. (I) and (II) are useful for tissue typing this sequence encodes
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Tumour necrosis factor alpha release; TNT-alpha release;
glucose uptake modulator; FFA uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inhibitor; cytokine release stimulator; tumour;
und tumous; colon tumour; breast tumour; prostett tumour; rectal tumour;
cervical tumour; liver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte
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                                                                                                                                                                                                                                                                                                                                                         Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                           1.1%; Score 21.4; DB 1; Length 1 66.0%; Pred. No. 45; Artive 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                    a novel human secreted and transmembrane PRO polypeptide.
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98WO-US025108.
99WO-US000106.
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18WO-US014552
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Best Local Similarity
Matches 31; Conserv
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10-SEP-1998;
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99WO-US023089
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28-FEB-2001; 2001WO-US006520
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                                                          99WO-US028301
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28-JUL-2000;
11-AUG-2000;
23-AUG-2000;
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20-DEC-2000;
20-DEC-2000;
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20-DEC-1999)
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08-NOV-2000;
10-NOV-2000;
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24-FEB-2000
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The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (1). (1) is useful for stimulating the transmembrane of TNP-alpha from human blood, for modulating the uptake of glucose or FRA by skeletal muscle cells or adipocyte cells, for glucose or FRA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation of of gene expression in pericyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of proteoglycans from cartilage, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating of cells, for inhibiting the binding of the release of a cytokine from PBMC cells, for inhibiting the binding of the presence of tumour in a mammal. The tumour is lung, colon, breast, cells, for stimulating genomic and cDMA nucleotide sequences or the presence of tumour in a mammal. The tumour is lung, colon, breast, contisense probes. (1) is also useful as therapeutic agent probes are useful for isolating genomic and cDMA nucleotide sequences or confidentify other proteins or molecules involved in binding in assays to identify other proteins or molecules involved in binding interaction. A polynucleotide (1) encoding (1) is useful in chromosome fantisense mapping, in generation of proparation of PRO polypeptide, for generating transgenic animals which in turn are useful in the development and screening of therapeutically useful reagents, and for generating probes. An anti-(1)-antibody is useful in diagnostic assays for PRO, concept probes. An anti-(1) are useful for tissues or serum, and for generating confining its expression in specific cells, itssues or serum, and for affinity purification as at conception of PRO from recombinant cell culture or natural concept human secreted and transmembrane PRO polypeptide.
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New PRO nucleic acid, useful for preparing a e.g. tumor or for tissue typing.
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                                        22-JJN-2011, 2001MG-USC20116.
29-JJN-2001; 2001MG-USC20106.
99-JJU-2001; 2001MG-USC3020735.
18-JJU-2001; 2001MS-00924419.
06-AJG-2001; 2001US-00924419.
16-AJG-2001; 2001US-00931836.
19-DEC-2001; 2001US-00028072.
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ADB89513 standard; cDNA; 1129
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P-PSDB; ADB66434.
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Homo sapiens
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25-AUG-1999;
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                                       Gerritsen Smith V,
                                      Baker KP,
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Best Local Similarity
Matches 31; Conser
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                                                                                            tumour necrosis factor-alpha, TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular modothelial cell; glucose; FRA; skeletal muscle cell; adiporte cell; periotte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
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                                                                         Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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   Human PRO polynucleotide #111
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01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
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99US-00380137
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ME, Goddard
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sequence represents a human PRO polynuclectide of the invention. Note:
The sequence data for this patent is also available in electronic format
from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                               Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; sendothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthitis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
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                                                    Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
                                                                                                       Indels
                                                                                                       16;
                                                                                                       0; Mismatches
                                                                             Score 21.4;
                                                                                            Pred. No.
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99WO-US028551.
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01-WAR-2001; 2001WO-US006666.
09-WAR-2001; 2001US-00802706.
14-WAR-2001; 2001US-0080868.
22-MAR-2001; 2001US-00816744.
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(GETH ) GENENTECH INC

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNP-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. adrenal, lung, certification or differentiation of chondrocyte cells and a method for colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating at attiesnee RNA and DNA and in gene therapy. The polymucleotides may also constain in the development and screening of therapeuticalides may also generating either transgenic animals or knock-out animals which are used in preparing PRO polypeptides by recombinant techniques and in caspens. The PRO polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating differentiation of adipocyte cells, for stimulating of ferentiation of adipocyte cells, for stimulating to the proliferation of adipocyte cells, for stimulating conditions and conditions and conditions and conditions and conditions and conditions and conditions which stimular cartilage are useful for treating various maniform artilage defects, osteoarthritis and rheumacoid arthritis. PRO polypeptides which stimulate scales of protecoglycans articular cartilage defects, osteoarthritis and rheumacoid arthritis. PRO polypeptides which stimulate scales of protecoglycans articular cartilage defects, osteoarthritis and rheumacoid arthritis. Or induces or propagetides which stimulating due to treating various maniform artilage defects, osteoarthritis and rheumacoid arthritis. Or polypeptides are also useful for treating various maniforms and conditions whas benefit from enhanced local immune system cells infilt . 0 Human, secreted and transmembrane protein; PRO; gene; ss;
Tumour necrosis factor alpha release; TNN-alpha release;
glucose uptake modulator; FFA uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation initialior; cytokine release stimulator; tumour;
lung tumoue; colon tumour; breast tumour; prostate tumour; rectal tumour; New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, and in the detection and treatment of tumor in a mammal. is also available in electronic format Gaps Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ge Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; 0 1835 TICTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881 Ouery Match
1.1%; Score 21.4; DB 1; Length 1129;
Best Local Similarity 66.0%; Pred. No. 45;
Matches 31; Conservative 0; Mismatches 16; Indels 0 Novel human secreted and transmembrane protein PRO4327 cDNA. Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; from USPTO at seqdata.uspto.gov/sequence.html. The sequence data for this patent Claim 2; Fig 221; 649pp; English. ADB39346/c ID ADB39346 standard; cDNA; 1129 04-DEC-2003 (first entry) WPI; 2003-743899/70. P-PSDB; ADB90246. 1129 ADB39346; RESULT 128 g KAKAKAKE KAKAKAKA KAKAK ò

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cervical tumour; liver tumour; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker.
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                     Homo sapiens.
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8-FEB-2000;
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                                                                           31-MAR-1997
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28-JUL-2000; 2000WO-US020710.
11-AUG-2000; 2000WO-US022525.
24-AUG-2000; 2000WO-US023128.
08-NOY-2000; 2000WO-US033128.
01-DEC-2000; 2000WO-US033673.
01-DEC-2000; 2000WO-US033673.
01-DEC-2000; 2000WO-US034956.
20-DEC-2000; 2000WO-US034956.
20-DEC-2000; 2000WO-US034956.
20-DEC-2000; 2000WO-US034956.
20-MXR-2001; 2001US-00196498.
21-MXR-2001; 2001US-0019666.
22-MXR-2001; 2001US-0019689.
23-MXR-2001; 2001US-0019689.
25-MXR-2001; 2001US-0019689.
25-MXR-2001; 2001US-0019689.
25-MXR-2001; 2001US-0019689.
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2001US-00874503.
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19-DEC-2001; 2001US-00028072.
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19-JUN-2001;
20-JUN-2001;
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22-JUN-2001;
29-JUN-2001;
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.. 3 Gao Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gr Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-786919/74. P-PSDB; ADB39347.

New secreted and transmembrane PRO polypeptide useful for detecting the presence of tumor in a mammal, or modulating the uptake of glucose or free fatty acid by skeletal muscle cells or adipocyte cells.

## Claim 2; Fig 221; 659pp; English.

The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (1). (1) is useful for stimulating the upcake of release of TNF-alpha from human blood, for modulating the upcake of glucose or FRA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of proteoglycans from cartilage, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating proliferation of individual the between cartilages of a cycokine from PBMC cells, for inhibiting the binding of A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte cells, for stimulating proliferation of endothelial cells, for stimulating proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour. The oligonucleotide probes and misense probes. (1) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding and gene mapping, in generation of antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals or

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knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, in gene therapy, for chromosome identification, as chromosome marker, and for generating probes. An anti-(1)-antibody is useful in diagnostic assays for PRO, e.g. detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. (1) and (11) are useful for tissue typing. This sequence encodes a novel human secreted and transmembrane PRO polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted and transmembrane protein; PRO; gene; ss;
Tumour necrosis factor alpia release; TNF-alpha release;
glucose uptake modulator; PFA uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inhibitor; cytokine release stimulator;
lung tumnoue; colon tumnour; breast tumnour; prostate tumnour; rectal tumnour;
cervical tumnour; liver tumnour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the release of TNF-alpha from human blood, for modulating the uptake of glucose or FRA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation or differentiation of choindrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the release of proteoglycans from cartilage, for
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Goddard A, Godowski PJ, Gurney AL, Sherwood S;
art TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                                                                     Score 21.4; DB 1; Length 1129; Pred. No. 45; 0; Mismatches 16; Indels 0
                                                                                                                                                                                                                                                                                                                                             Novel human secreted and transmembrane protein PRO4327 cDNA.
                                                                                                                                                                                 Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                     1835 ITCITAAITITITCATTICCAGAITICCTICAGITIGGGITITGITT
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01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
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Smith V, Stewart TA,
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ADB46969/C
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continuating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the release of a cytokine from PBMC cells, for inhibiting the binding of A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte cells, for stimulating proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour. The oligonucleotide presence of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour. The oligonucleotide presence of tumour in a mammal. The tumour of endiences or artisense probes. (I) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding in apeneration of antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals or preparation of PRO polypeptide, for generating transgenic animals or chromosome adentification, as chromosome marker, and for generating probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g. effecting the sexpression in specific cells, itssues or serum, and for affinity purification of PRO from recombinant cell culture or natural course. It and (II) are useful for tissue typing. This sequence encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpia; TNF-alpia; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FPA; seeletal muscle cell; adipocyte cell; perfoyte cell; perfoyte cell; perfoyte cell; perfoyte cell; perfoyte cell; perfoyte cell; perfoyte cell; perfoyed; sopports into cell; perfoyed; cartilage disorder; rhownard cell tube formation; bone disorder; cartilage disorder; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                        sources. (I) and (II) are useful for tissue typing. This a novel human secreted and transmembrane PRO polypeptide.
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A, Godowski
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18-0CT-1999; 99US-00403297.
18-FEB-2000; 2000WO-US032472.
01-DEC-2000; 2000WO-US0326782.
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Gerritsen ME, Goddard A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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Page 104

Wood WI, Zhang Z;

Watanabe CK,

Tumas D,

Stewart TA,

10664775-3.rng

New secreted and transmembrane PRO polypeptides, useful in the diagnosis and treatment of cancer. Claim 2; Fig 221; 637pp; English. WPI; 2003-743895/70. P-PSDB; ADB86577. Smith V, 

communication of adoptive cells, for adoptive or grand grand of cells or adoptive cells, for stimulating differentiation of adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating the proliferation of or gene expression in periove cells, for stimulating the proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and carthitis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, collypeptides are also useful for treating various mammalian haemoglobin associated disorders such as various thalassacmias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polynucleotide of the invention. Note: The sequence data for this patent is also available in electronic format. The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimmlating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in useful in the development and screening of therapeutically useful useful in the development and screening of therapeutically useful medicament for treating a condition responsive to the polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of the polypeptides or antibodies or modulation responsive to the polypeptides of the plant of the polypeptides or antibodies, such as tumours, for stimulating and microvascular endothelial cells, for modulating the tells of the public of the polypeptides or antibodies.

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps 0 1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; tive 0; Mismatches 16; Indels 0; 1835 INCIDAATITITICATITICCAGATITICCTICAGTITIGGGTITIGTIT 1881 1129 TITITITITITITITITICGCACACACAGGCIGGGITITIAII 1083 Query Match
Best Local Similarity 66.0
Matches 31, Conservative ઠે

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181/c ADB77181 standard; cDNA; 1129 BP. ADB77181; RESULT 131 

04-DEC-2003 (first entry)

Novel human secreted and transmembrane protein PRO4327 cDNA.

Human; secreted and transmembrane protein; PRO; gene; ss;
Tumour necrosis factor alpha release; TNF-alpha release;
Glucose uptake modulator;
Glucose uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inihibitor; cytokine release stimulator; tumour;
cell differentiation inihibitor; cytokine release stimulator; tumour;
cervical tumour; liver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.

transmembrane) polypeptides (1). (1) is useful for stimulating the uptake of release of TNP-alpha from human blood, for modulating the uptake of glucose or FRA by skeletal muscle cells or adipocyce cells, for glucose or FRA by skeletal muscle cells or adipocyce cells, for stimulating the proliferation of differentiation of chondrocyte cells, for stimulating the proliferation of proteoglycans from cartiage, for cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating of the release of a cytokine from PBMC cells, for inhibiting the binding of A-peptide to factor VIA, for inhibiting the binding of the presence of a cytokine from PBMC cells, for inhibiting the binding of A-peptide to factor VIA, for inhibiting the differentiation of adipocyte cells, for stimulating proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour. The oligonucleotide probes or are useful for isolating genomic and cDMA nucleotide sequences or an essays to identify other proteins or molecules involved in binding interaction A polynucleotide (II) encoding (I) is useful in chromosome condensing the mammal or properation of PMC properating transgent and consone identification, as chromosome marker, and for generating procession in specific cells, itssues or serum, and for generating confined (II) are useful in the development and confined by an anti-(I)-antibody is useful in diagnostic assays for PMC, affinity putification of PMC from ecombinant cell culture or natural confined by an anti-(I) are useful for tissue typing. This sequence encodes confined and the sequence of the sequence of the securing of the properation of PMC from ecombinant cell culture or natural confined by an anti-(I) are useful for tissue typing. This sequence encodes PRO nucleic acid, useful for preparing a composition for treating e.g., The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the Deforge L, Desnoyers L, Filvaroff E, G. A, Godowski PJ, Gurney AL, Sherwood S; Tummas D, Watanabe CK, Wood WI, Zhang Z; Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; a novel human secreted and transmembrane PRO polypeptide. Claim 2; Fig 221; 637pp; English. 01-SEP-1999; 99WO-US020111. 18-OCT-1999; 99US-00403297. 05-JAN-2000; 2000WO-US000219. 18-FEB-2000; 2000WO-US004342. 01-DEC-2000; 2000WO-US032678. 99WO-US020111. 99US-00403297. 22-APR-2002; 2002US-00127848. 98US-0106934P 99US-0145698P tumor or for tissue typing. Gerritsen ME, Goddard A, Smith V, Stewart TA, Tum Beresini M, (GETH ) GENENTECH INC. WPI; 2003-755109/71. P-PSDB; ADB77182 US2003082696-A1. 03-NOV-1998; 26-JUL-1999; 01-MAY-2003 Baker KP, 

Gao W;

ö 1835 TICTTAATITITICATTICCAGATITICCTICAGTITIGGGTITIT 1881 DB 1; Length 1129; 16; Indels Query Match
1.1%; Score 21.4; DB
Best Local Similarity 66.0%; Pred. No. 45;
Matches 31; Conservative 0; Mismatches

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RESULT 132

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TNF-alpha) from human blood, a method for stimulating the proliferation of chondrocyte cells and a method for proliferation or differentiation of chondrocyte cells and a method for colon, breast, prostate, rectal, kidney, cervical and liver tumours). The proliferation probes, in chromosome and gene mapping, in generating antisense RNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in penerating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of thuman microwascular endothelial cells, for modulating the uptake of glucose or FPRA by skeletal muscle cells, for minibating the uptake of stimulating differentiation of adjocyte cells, for stimulating proliferation of and proyte cells, for stimulating
                                                                                                                                                                                                      tumour necrosis factor alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FPA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated, secreted and transmembrane PRO polypeptides and nucleic acids, useful for the diagnosis, prevention and/or treatment of tumors, such as lung, colon, breast, prostate, rectal, cervical and/or liver
                                                                                                                                                                                    gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                              Human PRO polynucleotide SEQ ID NO 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Fig 221; 637pp; English.
                    ADB34338 standard; cDNA; 1129 BP.
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18-OCT-1999; 99US-00403297.
30-NOV-1999; 99WO-US028313.
18-FEB-2000; 2000WO-US0034342.
01-DEC-2000; 2000WO-US034678.
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                                                                                                    (first entry)
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3

Gao

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cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian hamoglobin associated disorders such as various thalasseamias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence acpresents a human PRO polynucleotide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at segdata.uspto.gov/sequence.html.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; perioyte cell; inner ear utricular supporting cell; T-lymphocyte cell; sports injury; proteoglycan; articular cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarchritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
proliferation of inner ear utricular supporting cells or T-lymphocyte
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                                                                                                                                DB 1; Length 1129;
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                                                                                                                                                                                                                                                                                                                                                                                1129 TTTTTTTTTTTTTTTTCAGCTGGCACACAGGCTGGGTTTTTATT 1083
                                                                                                                                                                                                                                           Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                              1.1%; Score 21.4; D
66.0%; Pred. No. 45;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PRO polynucleotide SEQ ID NO 221.
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ADB35442 standard; cDNA; 1129 BP.
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01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
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                                                                                                                                                                                                                                                                                                                         Conservative
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P-PSDB; ADB35443.
                                                                                                                                                                                                                                                                                                      Local Similarity
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ADB35442/c
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Claim 2; Fig 221; 637pp; English

ó 1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; ative 0; Mismatches 16; Indels 0; 1835 TICTIAATTITTCATTICCAGATTICCTICAGTITGGGTTTTGTTT 1881 Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; Conservative Best Local Similarity Matches 31; Conserv Query Match

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ADB33786 standard; cDNA; 1129 BP. 04-DEC-2003 (first entry) ADB33786;

Human PRO polynucleotide SEQ ID NO 221.

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TWF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; PFA; skeletel muscle cell; adipocyte cell; perioyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Homo sapiens.

US2003077716-A1.

24-APR-2003.

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the prosedre of a tumour in a mammal (e.g. adremal, lung, celon, breast, prostate, rectal, kidney, cervical and liver tumours). The prolynucleotides are useful in molecular biology, including uses as hyprication probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also considerable and DNA and in gene therapy. The polynucleotides may also be used in preparing FNO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapoutically useful reagents. The PRO polypeptides or antibodies are used in preparing a rumours, for antibodies, such as tumours, for stimulating and inhibiting proliferation of such an unsole cells, for modulating the uptake of glucose or FRA by skeletal muscle cells, for modulating the uptake of glucose or FRA by skeletal muscle cells, for stimulating the proliferation of or gene expression in periorte cells, for stimulating the proliferation of or gene expression in periorte cells, for stimulating the proliferation of or gene expression in periorte cells, for stimulating the proliferation of condition and for treating such as various bone and/or cartilage disorders such as sports injuries and arthritis: PRO polypeptides are luseful for treating various manials and cartilage are useful for treating various manials and cartilage are useful for treating various manials and cartilage are useful for treating various and remanaled in many benefit from enhanced local immune system cell infilteration. This parent sequence data for this patent is also available in electricity of the may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                      New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in identifying chromosomes.
                                                                                                                                                                                                                                                                                 Beresini M, Daforge L, Desnoyers L, Filvaroff E, Ga
ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Fig 221; 637pp; English.
                                                                                                                 18-FEB-2000; 2000WO-US004342.
10-NOV-2000; 2000WO-US030873.
01-DEC-2000; 2000WO-US32678.
19-DEC-2001; 2001US-00028072.
                                                                        99WO-US020111.
24-APR-2002; 2002US-00131813.
                                                 98US-0103315P
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Gerritsen ME,
                                                 07-OCT-1998;
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                                                                   01-SEP-1999;
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Query Match
1.1%; Score 21.4; DB 1; Length 1129;
Best Local Similarity 66.0%; Pred. No. 45;
Matches 31; Conservative 0; Mismatches 16; Indels 0; 1835 ITCTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881 1129 TITITITITITITITITICAGCIGGCACACGCCIGGCITITITIT 1083 RESULT 135 ADB34890/c

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ADB34890 standard; cDNA; 1129 BP

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Gaps

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10.5EP-1998
14.5EP-1998
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16.5EP-1998
16.5EP-1998
07.0CT-1998
29.0CT-1998
29.0CT-1998
01.DEC-1998
01.DEC-1998
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01.DEC-1998
01.DEC-1998
01.DEC-1998
14.MAX-1999
14.MAX-1999
                                                                                                                                                                                   02-JUN-1999,
01-SEP-1999,
08-SEP-1999;
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01-DEC-1999;
01-DEC-1999;
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22-DEC-1999;
30-DEC-1999;
                                                                      Homo sapiens
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15-SEP-1999;
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           04-DEC-2003
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                                                                                     24-APR-2003
   ADB34890;
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Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; addrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FRD; inser ear unscle cell; adipocyte cell; pericyte cell; endothelial cell; pericyte cell; pericyte cell; pericyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; shorteedlycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration. Human PRO polynucleotide SEQ ID NO 221. 98WO-US012456. 98WO-US014552. 98WO-US017888. 98WO-US022991. 98WO-US022992. 98WO-US025108. 99WO-US005028. 99WO-US005028. 99WO-US006190. 99WO-US006159. 98WO-US018824. 98WO-US019093. 98WO-US019094. 99WO-US028564. 99WO-US028565. 99WO-US030095. 2000WO-US000277. 2000WO-US000376. 2000WO-US003565. 99WO-US028301. 99WO-US028634. 99WO-US028551. 98WO-US019330 98WO-US019437 99WO-US020944 99WO-US021090 99WO-US031243 99WO-US031274 2000WO-US004341 2000WO-US004342 24-APR-2002; 2002US-00131823 99WO-US012252 99WO-US020111 99WO-US023089 99WO-US028313 99WO-US028409 98WO-US019177 98WO-US021141 99WO-US020594 99WO-US021547 99WO-US028214 (first entry) US2003077718-A1

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2000MO-US004914.
2000MO-US005004.
2000MO-US005746.
2000MO-US005841.
2000MO-US006819.
2000MO-US006819.
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2000WO-US008439.
2000WO-US013705.
2000WO-US014941.
2000WO-US015264.
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2001US-00808689.
2001US-00816744.
2001US-00828366.
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2001US-00854280.
2001US-00860216.
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2001WO-US017800.
2001US-00874503.
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2001US-00796498.
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2001US-00887879.
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19-DEC-2001; 2001US-00028072
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02-MAR-2000;
02-MAR-2000;
110-MAR-2000;
120-MAR-2000;
21-MAR-2000;
110-MAR-2000;
110-MAY-2000;
22-MAY-2000;
20-MAY-2000;
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11-AUG-2000;
23-AUG-2000;
08-NOV-2000;
10-NOV-2000;
10-DEC-2000;
20-DEC-2000;
20-DEC-2000;
28-FEB-2001;
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22-MAR-2001;
05-APR-2001;
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10-MAY-2001;
18-MAY-2001;
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25-MAY-2001;
25-MAY-2001;
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06-AUG-2001;
09-AUG-2001;
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### (GETH ) GENENTECH INC

3 Gao Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ga Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

#### WPI; 2003-755073/71. P-PSDB; ADB34891

New isolated, secreted and transmembrane PRO polypeptides and nucleic acids, useful for the diagnosis, prevention and/or treatment of tumors, such as lung, colon, breast, prostate, rectal, cervical and/or liver

## Claim 2; Fig 221; 638pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis

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proliferation or differentiation of chondrocyte cells and a method for proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, widney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating a misses RNA and DNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating of inferation of almoryte cells, for stimulating proliferation of adipocyte cells, for stimulating proliferation of an edipocyte cells, for stimulating proliferation of inner ear utricular supporting cells, or stimulating colliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating cells, for stimulating darbitis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports related joint problems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin-associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This
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The sequence data for this patent is also available in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
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from USPTO at seqdata.uspto.gov/sequence.html.
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ö Gaps ö 1835 TICTIAATITITICATITICCAGAITTICCTTICAGITITIGGITTTIGTIT 1881 1129 rirrirrirrirrirrirrircascrescacacasses rirrirrarr 1083 DB 1; Length 1129; 1.1%; Score 21.4; DB 1; Length 1.66.0%; Pred. No. 45; ive 0; Mismatches 16; Indels Query Match
Best Local Similarity 66.0
Matches 31; Conservative Q ઠે

Human PRO polynucleotide SEQ ID NO 221. ADB35994 standard; cDNA; 1129 BP (first entry) 04-DEC-2003 ADB35994; RESULT 136 ADB35994/ 

Human, gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FRA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; sports injury; proteoglycan; articular cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; heemoglobin-associated disorder thalassaemia; immune system cell infiltration.

99US-0170262P. 2000WO-US032678. 2001US-00028072. 24-APR-2002; 2002US-00131830 09-DEC-1999; 01-DEC-2000; 19-DEC-2001; 24-APR-2003.

US2003077720-A1

Homo sapiens.

(GETH ) GENENTECH INC.

3 Gao Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G. Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

2003-755075/71. P-PSDB; ADB35995 

New isolated, secreted and transmembrane PRO polypeptides and nucleic acids, useful for the diagnosis, prevention and/or treatment of tumors, such as lung, colon, breast, prostate, rectal, cervical and/or liver

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the profileration or differentiation of chondrocyte cells and a method for colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as this matical probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymuclectides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are reagents. The PRO polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies are used in preparing of the proliferation of inner endothelial cells, for modulating the uptake of collumnation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tumbe formation and for treating cells, for arthritis bone and/or cartilage are used in prepared portering are useful for treating exports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans continues and contribute are useful for treating apprex: related of our periodic archivities and rhemmaticid archivities. articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin-asociated disorders such as various thalasseemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polymucleotide of the invention. Note: irom USPTO at segdata.uspto.gov/sequence.html.

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps ö 1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; tive 0; Mismatches 16; Indels 0; 1835 TICTIPATITITICATITICCAGATITICCTICAGITITIGGITITIGITI 1881 31; Conservative Query Match Best Local Similarity Matches

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1129 intrintrintrintrincacciccacacacacacaciccintrain 1083 ADB46389 standard; cDNA; 1129 RESULT 137 ADB46389/ В 

Novel human secreted and transmembrane protein PRO4327 cDNA. Human; secreted and transmembrane protein; PRO; gene; ss;

04-DEC-2003 ADB46389;

Baker KP, Smith V, 

Tumour necrosis factor alpha release; TNF-alpha release; gluose uptake modulator; graduose uptake modulator; graduose uptake modulator; cell proliferation stimulator; cell differentiation stimulator; cell differentiation inhibitor; cytokine release stimulator; tumour; cell differentiation inhibitor; cytokine release stimulator; tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker. Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ge ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; 22-APR-2002; 2002US-00127842. 01-DEC-2000; 2000WO-US032678. (GETH ) GENENTECH INC. Stewart TA, 2003-786906/74. US2003082692-A1. P-PSDB; ADB46390 Gerritsen ME, Homo sapiens. 03-MAR-2000; 01-MAY-2003

New PRO nucleic acid, useful for preparing a composition for treating tumor or for tissue typing.

Claim 2; Fig 221; 637pp; English.

The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the control of the calls or adipocyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, glucose or FFA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells, constimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of cells, for inhibiting the binding of the release of actor VIA, for inhibiting the differentiation of adipocyte cells, for stimulating proliferation of endotherial cells, for stimulating the presence of tumour in a mammal. The tumour is lung, colon, breast, cells, for stolating genomic and cDNA nucleotide sequences or antisense probes. (I) is also useful as therapeutic agent, profit ansays to identify other proteins or molecules involved in binding interaction. A polymucleotide (II) encoding (I) is useful in chromosome and gene mapping, in generation of antisense RNA and DNA, in the correction of therapeutically useful in the development and streams probes. (I) therefore the preparation of therapeutically useful in diagnostic assays for PRO is concover an animals which in turn are useful in the development and streamsome identification, as chromosome marker, and for generating probes. An anti-(I)-antibody is useful in diagnostic assays for PRO concovers. (I) and (II) are inseful in the development and streams probes. (I) and (II) are inseful in the trian main and contained the trian turn and contained the trians and contained the contained and contained the contained and contained the contained and contained the contained and contained and contained the trians and contained the contained and contained the contained and contained the contained and contained the contained and co novel human secreted and transmembrane PRO polypeptide.

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

.; 0 Score 21.4; DB 1; Length 1129; Pred. No. 45; 0; Mismatches 16; Indels 0; 1.1%; Conservative Local Similarity es 31; Conserv Query Match Best Loca Matches

1835 ITCTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881 TITITITITITITITITITITICAGCTGCCACACAGGCTGGGTTTTTATT 1083

ADC50262 standard; cDNA; 1129 BP RESULT 138 ADC50262,

ADC50262;

(first entry) 18-DEC-2003

Novel human secreted and transmembrane protein PRO4327 cDNA.

Human; secreted and transmembrane protein; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; tumour; cancer; adreand; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial call; glucose uptake modulator; PPA uptake modulator; cell proliferation; peril differentiation; PRA uptake modulator; cell proliferation; pericyte call; inner ear utricular supporting cell; Tlymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder; thalassamia; immune system cell infiltration; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker; gene; ss.

Homo sapiens.

Gao W;

US2003092106-A1.

.5-MAY-2003.

24-APR-2002; 2002US-00131822.

98US-0097141P. 99WO-US012252. 99US-00380137. 2000WO-US008439. 2000WO-US032678. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072. 30-MAR-2000; 19-AUG-1998; 02-JUN-1999; 25-AUG-1999;

(GETH ) GENENTECH INC.

3 Deforge L, Desnoyers L, Filvaroff E, Ga A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Matanabe CK, Wood WI, Zhang Z; Gerritsen ME, Goddard Smith V, Stewart TA, Beresini M, Baker KP,

WPI; 2003-801171/75. P-PSDB; ADC50263. New secreted and transmembrane nucleic acid useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome or canner.

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for colon, breast, prostate, rectal, kidney, cervical and liver tumours). The colon, breast, prostate, rectal, kidney, cervical and liver tumours). The colon, breast, prostate, rectal, kidney, cervical and liver tumours). The colon, breast, prostate, rectal, kidney, recvoical and liver tumours). The colon, breast, prostate, rectal, kidney, recvoical and liver tumours). The colon, breast, properties are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, including east and in generating either transgenic animals by recombinant techniques and in generating either transgenic animals of therapeutically useful canearing either transgenic animals of therapeutically useful canearing either transgenic animals of therapeutically useful canearing conficement for treating a condition responsive to the polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for scimulating and inhibiting proliferation of human microvascular endothelial cells, for modulating the uptake of 

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10664775-3.rng

P-PSDB; ADC71810.

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glucose or FFA (free fatty acid) by skeletal muscle cells or adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating proliferation of or gene expression in pericyte cells, for trimulating the proliferation of inner ear utricular supporting cells or treating the proliferation of inner ear utricular supporting cells or treating various bone and/or cartilage disorders such as sports injuries or arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint proteoglycans from cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian hemoglobin-associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence are also useful sales as a proportion. This sequence are those of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at segdata.uspto.gov/sequence.html.
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Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

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1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; tive 0; Mismatches 16; Indels 0
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Human; secreted and transmembrane protein; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; tochondrocyte; tumour; cancer; adrean1; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothalial cell; glucose uptake modulator; mforovascular endothalial cell; perioque cell; inner ear utricular supporting cell; inner ear utricular supporting cell; perioque cell; inner ear utricular supporting cell; representation; bone disorder; cartilage disorder; sports injury; proteodycan; articular cartilage disorder; rheumatoid arthritis; haemoglobin-associated disorder; thalassaemia; immune system cell infiltration; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker; gene; ss.
                                                                                                               Novel human secreted and transmembrane protein PRO4327 cDNA.
                             ADC71809 standard; cDNA; 1129 BP
                                                                                       (first entry)
                                                                                       18-DEC-2003
                                                          ADC71809;
RESULT 139
                ADC71809/
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24-APR-2002; 2002US-00131828 US2003092107-A1. Homo sapiens. 15-MAY-2003

2000WO-US004342. 2000WO-US030873. 2000WO-US032678. 99WO-US020111. 99US-00403297. 98US-0103315P. 19-DEC-2001; 2001US-00028072 07-OCT-1998; 01-SEP-1999; 18-OCT-1999; 18-FEB-2000; 10-NOV-2000; 01-DEC-2000;

Deforge L, Desnoyers L, Filvaroff E, Gao W; A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Beresini M, ME, Goddard P Stewart TA, T (GETH ) GENENTECH INC. Baker KP, Gerritsen Smith V,

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis (collypeptide, a method for stimulating the factor-alpha (TWF-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. adremal, lung, collon, breast, prostate, rectal, kidney, cervical and invertumours). The collon, breast, prostate, rectal, kidney, cervical and liver tumours). The collon, breast, prostate, rectal, kidney, cervical and liver tumours). The collon, breast in proparing PRO polypeptides by recombinant techniques and in thyridisation probes, in chromosome and gene mapping, in generating collon, probes, in chromosome and gene mapping, in generating collons artisense RNA and bin gene therapy. The polywucleotides may also consider the received of propaptides by recombinant techniques and in the development and screening or knock-out animals which are useful in the development and screening or knock-out animals which are useful in the development and screening or knock-out animals which are considered to the propaptides or antibodies are useful in preparing a condition responsive to the polypeptides or antibodies are useful in proliferation of human microvascular endothelial cells, for modulating the proliferation of or gene expression in pericyte cells for stimulating the proliferation of inner ear utricular supporting cells or constituent and architis. PRO polypeptides which simulate the release of treating various bone and/or cartilage disorders such as sports injuries and architists. PRO polypeptides which simulate the release of the problems, articular cartilage are also useful for treating various cartilage are useful for treating various themselved local immune system cells infiltration. Note: The sequence descent the sequence represented infilteration. The sequence represented the t New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or Claim 2; Fig 221; 637pp; English. #XHHHXXXX

Query Match
1.1%; Score 21.4; DB 1; Length 1129;
Best Local Similarity 66.0%; Pred. No. 45;
Matches 31; Conservative 0; Mismatches 16; Indels 0; Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

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Gaps

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ADC59788 standard; cDNA; 1129 BP RESULT 140 ADC59788/c

Novel human secreted and transmembrane protein PRO4327 cDNA.

(first entry)

18-DEC-2003

Human; secreted and transmembrane protein; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothalial cell; glucose uptake modulator; FRA uptake modulator; cell proliferation; cell differentiation; skeletal muscle cell; adipocyte cell; pinner ear utricular supporting cell; T-lymphocyte cell; perioty cell; inner ear utricular supporting cell; T-lymphocyte cell; adipocyte cell; proteoglycan; articular cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; 

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ss; gene.

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human, PRO; membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; cytotoxic factor; differentiation factor; neuropeptide; hormone; cell receptor; receptor-ligand interaction; cytostatic; chondrocyte; tumour;
                                                                                                                                                                                                                                                                                                    Novel human secreted and transmembrane protein cDNA Seq ID221
                                                                                                                                                   ADC52795 standard; cDNA; 1129
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                                                                                                                                                                                                        ADC52795;
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                                                                                                                              ADC52795/
                                                                                                                                                        The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNR-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, proliferation probes, in chromosome and gene mapping, in generaling to polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating thy prolates may also an incleance and an gene therapy. The polynucleotides may also to be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of knock-out animals which are useful in the development and screening of knock-out animals which are useful in the development and screening of knock-out animals which are useful in the development and screening of knock-out animals which are useful in the development as tumours, for stimulating and inhibiting proliferation of man antibodies such as tumours, for stimulating and inhibiting proliferation of such animals and propared of subpocyte cells, for stimulating differentiation of adipocyte cells, for stimulating proliferation of inner as untricular supports related joint stimulating heaptoliferation of inner as untricular supports related joint problems, articular cartilage are also useful for treating various cartilage are also useful for treating various thalasseamias and arthritis. PRO polypeptides which stimulate the release of the problems, articular cartilage defects, osteoathritis and rheumatoid cartilage are also useful for treating various that sequence are research as various cand conditions which may benefit from enhanced local immunesystem cell 
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       disorder; thalassaemia;
rheumatoid arthritis; haemoglobin-associated disorder; thalassaemie
immune system cell infiltration; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker; gene; E
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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01-DEC-2000; 2000WO-US032678.
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98WO-US017888.
98WO-US018824.
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17-SEP-1998;
08-MAY-2003
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Query Match
Best Local Similarity 66.0%; Pred. No. 45;
Matches 31; Conservative 0; Mismatches 16; Indels 0

Gaps

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2000WO-US004414.
2000WO-US004914.
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09-MAR-2001; 2001US-00802706.
14-MAR-2001; 2001US-00808689.
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10-MAY-2001; 2001US-00854208.
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01-JUN-2001; 2001US-00872035.
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## (GETH ) GENENTECH INC

3 Gao Deforge L, Desnoyers L, Filvaroff E, G. A, Godwoski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Beresini M, D ME, Goddard A, Gerritsen ME, Goddard Smith V, Stewart TA, Baker KP,

## WPI; 2003-801150/75. P-PSDB; ADC52796.

PRO nucleic acid, useful for manufacturing a medicament for diagnosing or treating tumor New

# Claim 2; SEQ ID NO 221; 637pp; English.

This invention relates to novel nucleic acids encoding human PRO secreted and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells (for example proliferation,

This invention relates to novel nucleic acids encoding human PRO secreted

migration or differentiation) is typically governed by information received from other cells and the immediate environment. The information is often transmitted by secreted polyapetides (for example mitoganic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaccutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention proteins, along with the cDNA sequences ancoding them. The novel proteins along with the cDNA sequences ancoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present sequence is a cDNA sequence which encodes a human PRO protein of the ö human, PRO, membrane bound protein, membrane bound receptor, cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor, cytotoxic factor; differentiation factor, necropeptide; hormone; cell receptor; receptor-ligand interaction; cytostatic; chondrocyte; tumour; ss; gene. Gao W; Gaps Deforge L, Desnoyers L, Filvaroff E, G. A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; ö Query Match
1.1%; Score 21.4; DB 1; Length 1129;
Best Local Similarity 66.0%; Pred. No. 45;
Matches 31; Conservative 0; Mismatches 16; Indels 0; Novel human secreted and transmembrane protein cDNA Seq ID221. 1835 TICTITAATITITICATITICCAGAITITCCTICAGITITGGGTTTTGTTT 1881 1129 trritritritritritrickáciasákasákásorásásíritritri 1083 New PRO nucleic acid, useful for manufacturing a medicament Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; Claim 2, SEQ ID NO 221; 637pp; English. BP. ADC57149 standard; cDNA; 1129 02-MAR-2000; 2000WO-US005841. 30-MAY-2000; 2000WO-US014941. 01-DEC-2000; 2000WO-US032678. diagnosing or treating tumor. 23-APR-2002; 2002US-00128694 19-DEC-2001; 2001US-00028072 (first entry) Gerritsen ME, Goddard A, Smith V, Stewart TA, Tum (GETH ) GENENTECH INC. Baker KP, Beresini M, WPI; 2003-801151/75. P-PSDB; ADC57150. US2003087366-A1. Homo sapiens 18-DEC-2003 08-MAY-2003. invention. ADC57149; RESULT 142 ADC57149/ 8888888888888888888888888888888888 ઠે g

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and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular or organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information received from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention conditions and proteins, along with the cDNs sequences encoding them. The novel proteins of the invention may have cytostatic activities through the continuation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a undicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or sequence is a cDNA sequence which encodes a human PRO protein of the invention.

XX Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 other;
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Human; secreted and transmembrane protein; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNN-alpha; chondroyte; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose uptake modulator; FFA uptake modulator; cell proliferation; perloye cell; differentiation; Refetal muscle cell; adipocyte cell; perioye cell; inner ear utricular supporting cell; Tlymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; rheumatoid arthritis; haemodobin-associated disorder; thalassaemia; immune system cell infiltration; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker; gene; ss.
                                                                                          Gaps
                                                      Query Match
Best Local Similarity 66.0%; Pred. No. 45;
Matches 31; Conservative 0; Mismatches 16; Indels 0;
                                                                                                                       1835 TICTTAATTTTTCATTTCCAGATTTCCTTCAGTTTTGGGTTTTGTTT 1881
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                                                                                                                                                                                                                                                                                                                                   Novel human secreted and transmembrane protein PRO4327 cDNA.
                       Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
                                                                                                                                                                                                                                        ADC60340 standard; cDNA; 1129 BP
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98WO-US014552.
98WO-US017888.
98WO-US019093.
98WO-US019094.
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98WO-US019330.
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14-SEP-1998;
14-SEP-1998;
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14-JUL-1998;
28-AUG-1998;
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16-SEP-1998;
17-SEP-1998;
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nvention
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99WO-US025108.
99WO-US000106.
99WO-US005028.
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2001WO-US006666.
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                                 99WO-US005190,
2000WO-US006319.
                                                      99WO-US012252
                                                               99WO-US020594
                                            99WO-US008615
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08-NOV-2000;
10-NOV-2000;
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20-DEC-2000;
20-DEC-2000;
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30-MAY-2000;
02-JUN-2000;
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09-MAR-2001;
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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNR-alpha) from human blood, a method for stimulating the release of tumour necrosis factor-alpha (TNR-alpha) from human blood, a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The projumuleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating a this same RNA and an gene therapy. The polymucleotides may also colon, breast, prostated and spene therapy. The polymucleotides may also a this same and in gene therapy. The polymucleotides may also consist the PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful.

Complement for treating a condition responsive to the polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies are used in preparing and inhibiting proliferation of human microvascular andothelial cells, for modulating the proliferation of inner ear unitoulating the uptake of glucose or FRA (free fatty acid) by skeletal muscle cells for stimulating the proliferation of inner ear unitoulate supports injuries stimulating the proliferation of inner ear unitoulate cells or treating various bone and/or cartilage and expression in pericyte cells or treating various bone and/or cartilage disorders such as sports injuries proteoglycans from cartilage disorders such as various thalassaemias and arthritis. PRO polypeptides are also useful for treating various benemial manepulations which may benefit from enhanced local immune system cartilated former inst PRO nucleic acid, useful for preparing a recombinant PRO polypeptide for manufacturing a medicament for diagnosing or treating tumor. infiltration. This sequence represents a human PRO polynucleofide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html. Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gi Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; Claim 2; Fig 221; 638pp; English 14-JJN-2001; 2001US-00886342. 19-JUN-2001; 2001US-00886342. 20-JJN-2001; 2001WS-0S019652. 21-JUN-2001; 2001US-0088799. 22-JUN-2001; 2001WS-0S020116. 2001US-00874503 09-JUL-2001; 2001WO-US021735. 18-JUL-2001; 2001US-00908827. 06-AUG-2001; 2001US-00924419. 2001US-00927796 19-DEC-2001; 2001US-00028072 (GETH ) GENENTECH INC. 2003-801152/75. P-PSDB; ADC60341 09-AUG-2001; New 

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps 0 Query Match
Best Local Similarity 66.0%; Pred. No. 45;
Matches 31; Conservative 0; Mismatches 16; Indels 0

1835 ITCTIAATTITITCATTICCAGATTICCTICAGTITGGGTTTTGTTT 1881

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1129 ITTTTTTTTTTTTTTTCAGCTGGCACACAGGCTGGGTTTTTATT 1083

Human; secreted and transmembrane protein; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose uptake modulator; FPA uptake modulator; cell proliferation; perlation; Reletal muscle cell; adipocyte cell; periation; skeletal muscle cell; adipocyte cell; endothelial cell tube formation; bone disorder; artilage disorder; endothelial cell tube formation; bone disorder; cartilage disorder; rheumatoid arthritis; haemoglobin-associated disorder; halassaemia; immune system cell infiltration; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker; gene; ss. Novel human secreted and transmembrane protein PRO4327 cDNA ADC50815/c ID ADC50815 standard; cDNA; 1129 BP. (first entry) 18-DEC-2003 ADC50815; RESULT 144 

US2003087361-A1.

Homo sapiens.

Gao

08-MAY-2003

22-APR-2002; 2002US-00127841.

18-FEB-2000; 2000MO-US004342. 01-DEC-2000; 2000MO-US032678. 19-DEC-2001; 2001US-00028072. 98US-0099536P 99WO-US020111 99US-00403297 09-SEP-1998; 18-OCT-1999;

(GETH ) GENENTECH INC.

3 Gao L, Desnoyers L, Filvaroff E, G: ski PJ, Gurney AL, Sherwood S; Watanabe CK, Wood WI, Zhang Z; Baker KP, Beresini M, Deforge L, Gerritsen ME, Goddard A, Godowski Smith V, Stewart TA, Tumas D, Wat

WPI; 2003-801146/75. P-PSDB; ADC50816.

nucleic acid, useful for preparing a recombinant PRO polypeptide manufacturing a medicament for diagnosing or treating tumor. New PRO I

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the projection or differentiation of chondrocyte cells and a method for proliferation or factoring the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polyprofess are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and in gene therapy. The polyprolides may also antisense RNA and in gene therapy. The polyprolides and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful testul in the development and screening of therapeutically useful medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for simulating and inhibiting proliferation of human microvascular endothelial cells, for modulating the uptake of

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glucose or FPA (free fatty acid) by skeletal muscle cells or adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating prolliferation of or gene expression in pericyte cells, for stimulating the prolliferation of inner ear utricular supporting cells or 1-lymphocyte cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of prolleng articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin-associated disorders such as various thalassaemias
                                                                                                                                                                                                                                                                                                                                           and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polymicleotide of the invention. Note: The sequence date that this patent is also available in electronic format from USPPTO at seqdata.uspto.gov/sequence.html.
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1129 TTTTTTTTTTTTTTTCAGCTGGCACACAGGCTGGGTTTTATT 1083 1835 TICTIAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT g

Gaps

0

1.1%; Score 21.4; DB-1; Length 1129; ilarity 66.0%; Pred. No. 45; Conservative 0; Mismatches 16; Indels 0;

Query Match Best Local Similarity Matches 31; Conservat

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

BP. ADC65342 standard; cDNA; 1129 Human PRO polynucleotide #111. 18-DEC-2003 (first entry) ADC65342; RESULT 145 ADC65342, 

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; trumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FRA; skeletal muscle cell; adpocyte cell; pericyte cell; pericyte cell; inner ear utricular supporting cell; pericyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; cheumatoid arthritis; haemodybin-associated disorder thalassaemia; immune system cell infiltration;

Homo sapiens

US2003087362-A1

22-APR-2002; 2002US-00127844. 38-MAY-2003.

05-JUN-2000; 2000US-0209832P. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC

ss; gene.

human, PRO, membrane bound protein, membrane bound receptor, cell proliferation, cell migration, cell differentiation, mitogenic factor, survival factor, cytotoxic factor, differentiation factor, neuropeptide, hormone, cell receptor, receptor-ligand interaction, cytostatic, chondrocyte, tumour,

Baker KP, Beresini M, Deforge Li, Desnoyers L., Filvaroff E, G Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-801147/75. P-PSDB; ADC65343.

useful for manufacturing a medicament diagnosing or treating tumor. nucleic acid, PRO New

98WS-0099816P. 99WO-US020111. 99US-00403297.

10-SEP-1998; 01-SEP-1999; 18-OCT-1999;

23-APR-2002; 2002US-00128687

US2003087363-A1.

08-MAY-2003

Homo sapiens

Gao W;

Claim 2; Fig 221; 637pp; English.

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymuclectides encoding them. The invention also relates to an antibody which specifically binds them. The invention also relates to an antibody which specifically binds then the polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymuclectides are useful in molecular biology, including uses a hypridisation probes, in chromosome and gene mapping, in generating any polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapy. The polymuclectides may also generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies such as tumours, for stimulating differentiation of finner for stimulating differentiation of adipocyte cells, for stimulating proliferation of finner artilage defected muscle cells or adipocyte cells, for stimulating adipocyte cells, for stimulating adipocyte cells, for stimulating adipocyte cells, for stimulating adipocyte cells, for stimulating adipocyte cells, for stimulating adipocyte cells or artilage and seventh simulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, articular cartilage are useful for treating sports-related joint problems, articular cartilage are useful for treating sports-related disorders such as various thalassaemas and conditions which requence represents a human PRO polyputors 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from USPTO at seqdata.uspto.gov/sequence.html.
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in the formation, federate to movel muchen and maintenance of multicellular roles in the formation, differentiation and maintenance of multicellular corganisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information, creceived from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytocoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interpreted by diverse and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the cDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the estimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumnor in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumnor associated gene. The present
                                                                                                                                                                                                                                                                                                                                                New PRO nucleic acid, useful for manufacturing a medicament
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; SEQ ID NO 221; 637pp; English.
                                         09-FEB-1999; 99US-0119341P.
01-DEC-1999; 99WO-US028634.
01-DEC-2000; 2000WO-US028678.
19-DEC-2001; 2001US-00028072.
                                                                                                                                                                                                                                                                                                                                                                         diagnosing or treating tumor.
  23-APR-2002; 2002US-00128688.
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                                                                                                                                                                                                                      Gerritsen ME,
                                                                                                                                                                                               Baker KP,
                                                                                                                                                                                                                                        Smith V,
    in transmembrane proteins Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular croganisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytofocal, differentiation factors, cytofocal, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the cDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the proteins of chondroytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or reacting a factoring of the convent of a medicament for measuring or the convent of a membrane base of the convent of a process.
                                                                                                                                                                                                                                                                                                                                                                                         to novel nucleic acids encoding human PRO secreted
                                                                                                                                                                                                                                                                                  nucleic acid, useful for preparing a recombinant PRO polypeptide manufacturing a medicament for diagnosing or treating tumor.
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                                                                                                                                                   Gurney AL, Sherwood S;
                                                                                                                                 Filvaroff E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
                                                                                                                                 Desnoyers L,
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as D, Watanabe CK,
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Pred. No. 45;
0; Mismatches
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                                                                                                                              Deforge L,
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18-FEB-2000; 2000WO-US004342.
01-DEC-2000; 2000WO-US032679.
19-DEC-2001; 2001US-00028072.
                                                                                                                            Baker KP, Beresini M, De
Gerritsen ME, Goddard A,
Smith V, Stewart TA, Tun
                                                                                                                                                                                                                                                                                                                                                                                            This invention relates
                                                                                     (GETH ) GENENTECH INC.
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P-PSDB; ADC54441.
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human PRO secreted

invention relates to novel nucleic acids encoding

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Gao .

Deforge L, Desnoyers L, Filvaroff E, Ga A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z;

Beresini M, De ME, Goddard A,

Stewart TA,

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human, PRO; membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; cytotoxic factor; differentiation factor; neuropeptide; hormone; cell receptor; receptor-ligand interaction; cytostatic; chondrocyte; tumour; ss; gene.
                                             Gaps
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                                                                         1835 ITCTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881
                                                                                                      1129 Trritrrrrrrrrrrrrrrrrrrr 1083
                                                                                                                                                                                                                                                                           Novel human secreted and transmembrane protein cDNA Seg ID221
                                          16; Indels
              DB 1;
             1.1%; Score 21.4; C 66.0%; Pred. No. 45; ive 0; Mismatches
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human, PRO, membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; cytotoxic factor factor; differentiation factor; neuropeptide; hormone; cell receptor; receptor-ligand interaction, cytostatic; chondrocyte; tumour;

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US2003087364-A1. Homo sapiens

08-MAY-2003.

Novel human secreted and transmembrane protein cDNA Seq ID221

(first entry)

18-DEC-2003

ADC53401;

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ADC53401 standard; cDNA; 1129

US2003087359-A1.

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Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

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This invention relates to novel nucleic acids encoding human PRO secreted and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintennance of multicellular corganisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information, crecived from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors may be of use as pharmaceutical and diagnostic agents, such an receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the cDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic activities through the stimulation of chondrocytes. The nucleic activities through the cumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present equence is a cDNA sequence a human PRO protein of the
receptor-ligand interaction; cytostatic; chondrocyte; tumour; ss; gene
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2000WO-US023522.
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23-AUG-2000; 2000WO-US023522
01-DEC-2000; 2000WO-US023578
19-DEC-2001; 2001US-000280778
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1 ME, Goddard /
Stewart TA,
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P-PSDB; ADC55803.
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Best Local Similarity
                                                                                                                 US2003087360-A1
                                                          Homo sapiens.
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Smith V,
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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Pred. No. 45;
0; Mismatches 16; Indels
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01-SEP-1999; 99WG-US020111.
18-OCT-1999; 99US-00403297.
30-NOV-1999; 99WG-US028813.
01-DEC-2000; 2000WG-US033878.
19-DEC-2001; 2001US-00028072.
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Best Local Similarity
Matches 31; Conserv
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 This invention relates to novel nucleic acids encoding human PRO secreted and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The face of many individual calls (for example proliferation, organisms. The face of many individual calls (for example proliferation, migration or differentiation) is typically governed by information. Conserved transmitted by secreted polypeptides (for example mitogration is often transmitted by secreted polypeptides (for example mitogration is often transmitted by secreted polypeptides (for example mitogration is often transmitted by secreted polypeptides (for example mitogration is often transmitted by secreted polypeptides (for example mitogration feachors, cytotoxic factors, differentiation factors, or neuropeptides and hormones) which are received and interpreted by diverse call receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the cDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the simulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating at tumour in a mammal. In addition, they may be useful for measuring or sequence is a cDNA sequence which encodes a human PRO protein of the
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                                        human, PRO; membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; cytotoxic factor; differentiation factor; neuropeptide; hormone; cell receptor; receptor-receptor-ligand interaction; cytostatic; chondrocyte; tumour; ss; gene.
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ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
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1.1%; Score 21.4; DB 1; Length 1129;
Best Local Similarity 66.0%; Pred. No. 45;
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01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
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Smith V, Ste
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Human; secreted and transmembrane protein; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; nehondrocyte; tumour; cancer; adrean1; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial call; glucose uptake modulator; FPA uptake modulator; cell proliferation; peril differentiation; RFA uptake modulator; cell proliferation; perily cell; inner ear utricular supporting cell; lung cell; inner ear utricular supporting cell; ramphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; rheumatoid arthritis; haemoglobin-associated disorder; thalassaemia; immune system cell infiltration; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker; gene; ss.
Novel human secreted and transmembrane protein PRO4327 cDNA.
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2000WO-US000277
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11-FEB-2000;
18-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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2000WO-US003565

ADD03046/c ID ADD03046 standard; cDNA; 1129 BP. XX

2000WO-US004341

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CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for cd etecting the presence of a tumour in a mammal leg, adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as nickediation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymucleotides may also antisense RNA and DNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are used in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a muticodies, such as tumours, for simulating and inhibiting proliferation of antibodies or stimulating differential cells, for modulating proliferation of adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating differentiation of adipocyte cells, for inducing endothalial cells the formation and for treating various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, articular cartilage are also useful for treating sorts injuries arthritis. PRO polypeptides are also useful for treating various cartilage are also useful for treating various cartilage are also useful for treating various cartilage are also useful for treating various cartilage are also useful for treating various cartilage are also useful for treating various cartilage are also useful for treating various infiltration. This sequence represents a human PRO polypucles of the invention. Note: The sequence data for this patent is also available in cells invention. Note: The sequence data for this patent is also available in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
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              %%GGGGGGGGGGGGGGGGGGGGGGGGGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Filvaroff E, Gao W;
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in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 PRO4978, useful in molecular biology, chromosome and gene mapping, generating antisense RNA and DNA, and in gene therapy.
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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2001US-00816744.
2001US-00828366.
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2001US-00854280.
2001US-00860216.
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2001US-00874503
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2001US-00866034
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2001WO-US020116
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                                                                               01-MAR-2000;
02-MAR-2000;
02-MAR-2000;
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08-NOV-2000)
10-NOV-2000)
01-DEC-2000)
20-DEC-2000)
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10-MAY-2001

25-MAY-2001

25-MAY-2001

25-MAY-2001

01-JUN-2001

01-JUN-2001
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28-FEB-2001;
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09-MAR-2001;
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30-MAY-2000;
02-JUN-2000;
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23-AUG-2000
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Tumour necrosis factor alpha release; TMF-alpha release;
Jucose uptake modulator; PFA uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inhibitor; cytokine release stimulator; tumour;
cell und tumour; colon tumour; breast tumour; protester tumour; rectal tumour;
cervical tumour; liver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
                                     Gaps
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DB 1; Length 1129;
                                                                   1835 INCITAATTITITCATTICCAGATTICCTTCAGTTIGGGTTTTGTTT 1881
                                                                                                      1129 riririririririririri 1083
                                                                                                                                                                                                                                                                                                    Novel human secreted and transmembrane protein PRO4327 cDNA
1.1%; Score 21.4; DB 1; Length 1
66.0%; Pred. No. 45;
ive 0; Mismatches 16; Indels
                                                                                                                                                                                             ADC90038 standard; cDNA; 1129 BP
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01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
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                Best Local Similarity 66.0
Matches 31; Conservative
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The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the profess of TWD-alpha from human blood, for modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation of or gene expression in paricyte cells, for stimulating the proliferation of or gene expression in paricyte cells, for stimulating the release of protecogycans from cartilage, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting of the release of a cytokine from PMMC cells, for stimulating the binding of A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte cells, for stimulating proliferation of endothedial cells, for stemulating proliferation of endothedial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour. The oligonucleotide probes are useful for isolating genomic and cDNA nucleotide sequences or antisense probes (I) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding in caraction. A polymucleotide (II) encoding (I) is useful in the genemapping, in generation of antisense RNA and DNA, in the preparation of PNO polypeptide, for generating transgenic animals or knocket animals with the contraction of the profess of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of th
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                         Deforge L, Desnoyers L, Filvaroff E, Ga
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                   nucleic acid, useful for manufacturing a medicament for
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                                                                                                                                                                                                                                                                                                                                                                     Claim 2; SEQ ID NO 221; 637pp; English.
                                                                                                                                                                                                                                                                                                       diagnosing or treating tumor.
                         Baker KP, Beresini M, De
Gerritsen ME, Goddard A,
Smith V, Stewart TA, Tum
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Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps ö 1835 ITCTIAATITITICATITICCAGAITICCTICAGITIGGGITITIGIT 1881 DB 1; Length 1129; 16; Indels 1.1%; Score 21.4; Di 66.0%; Pred. No. 45; cive 0; Mismatches 31; Conservative Query Match Best Local Similarity Matches 31; Conserv ઠે g

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ADC69457 standard; cDNA; 1129 ADC69457; RESULT 153 ADC69457/ 

(first entry) 01-JAN-2004

cDNA encoding human PRO polypeptide #111.

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tummour necrosis factor-alphs; TNT-alpha; chondrocyte cell; tummour; cancer; adrena; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletell muscle cell; adipocyte cell; periotyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Deforge L, Desnoyers L, Filvaroff E, Ga A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; 03-MAX-2000; 2000US-0187202P. 30-MAY-2000; 2000WO-US014941. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072. 21-MAY-2002; 2002US-00152375 Beresini M, Dei ME, Goddard A, (GETH ) GENENTECH INC. ME, Goddard Stewart TA, WPI; 2003-844453/78. US2003194770-A1. Homo sapiens. Gerritsen ME, 16-OCT-2003, Baker KP, Smith V, 

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tumors, New isolated, secreted and transmembrane PRO polypeptides and nucleic acids, useful for the diagnosis, prevention and/or treatment of tumors such as lung, colon, breast, prostate, rectal, cervical and/or liver

P-PSDB; ADC69458.

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the problem or differentiation of chondrocyte cells and a method for colon, breast, prostate, rectal, kidney, cervical and liver tumours). The colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as nisease RNA and DNA and in gene herapy. The polynucleotides may also antisease RNA and DNA and in gene herapy. The polynucleotides may also carisease RNA and DNA and in gene herapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals of therapeutically useful useful in the development and screening of therapeutically useful cagenerating accompants. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies are used in preparing or antibodies, such as tumours, for stimulating and inhibiting proliferation of or gene expression in pericyte cells, for stimulating colliferation of adipocyte cells, for stimulating colliferation of adipocyte cells, for stimulating colliferation of adipocyte cells, for stimulating colliferation of anticollar supporting cells, for rimulating colliferating endothelial cells considered to an end/or cartilage disorders such as sports injuries and arbuits. PRO polypeptides which stimulate the releases of proteoglyvans or enthilist PRO proteoglyvans considered are useful to reach a sports injuries and arbuits are useful to reach a storts related and the release of proteoglyvans of the proliferation of adipocyte cells, for stimulating subject the proliferation of subject to the proliferation of subject to t from cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin-associated disorders such as various thalessaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence encodes a human PRO polypeptide of the invention. Note: The data for this patent is also available in electronic format from the USPTO website at segdata.uspto.gov. sednence

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps ó DB 1; Length 1129; 16; Indels 1.1%; Score 21.4; E 66.0%; Pred. No. 45; ive 0; Mismatches Conservative Local Similarity les 31, Conserv Ouerv Match Best Loca Matches

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1835 ITCITAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT

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Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tummour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tummour, cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; pericyte cell; skeletal muscle cell; adipocyte cell; pericyte cell; endothelial cell tube formation; bone disorder; carliage disorder; sports injury; protecylycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
       ADC48346 standard; cDNA; 1129 BP
                                                           Human PRO polynucleotide #111.
                                          (first entry)
                                                                                                                                                                                             US2003194773-A1.
                                                                                                                                                                             Homo sapiens.
                                          01-JAN-2004
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                        ADC48346;
ADC48346,
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21-MAY-2002; 2002US-00152391

09-DEC-1999; 99US-0170262P. 30-MAY-2000; 2000WO-US014941. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC

Gao Deforge L, Desnoyers L, Filvaroff E, G. A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Beresini M, ME, Goddard Stewart TA, ME, Baker KP, Gerritsen 1 Smith V,

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WPI; 2003-844455/78. P-PSDB; ADC48347. New secreted and transmembrane PRO nucleic acids and polypeptides, useful for detecting a tumor, stimulating the release of tumor necrosis factor alpha and stimulating the proliferation of endothelial cells.

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymclectides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the relaese of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the polypeptide, a method for stimulating the factor at the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The colon, breast, prostate, rectal, kidney, cervical and liver tumours). The colon, breast, prostate, in chromosome and gene mapping, in generating a natisense RNA and DNA and in gene therapy. The polymucleotides may also antisense RNA and DNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are used in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for modulating the uptake of glucose or FFA by skeletal muscle cells for adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating the proliferation of inner ear utricular supporting cells, for T-lymphocyte

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cells, for inducing endothelial cell tube formation and for treating arthritis. PRO polypeptides disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems. Atticular cartilage defects, osteoarthritis and rheumatoria archritis. PRO polypeptides are also useful for treating various mammalian heamoglobin-associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human pRO polymocleotide of the invention. Note: The sequence data for this patent is also available in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNR-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; PFA; skeletal muscle cell; adipocyte cell; glucose; PFA; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; shoutengluly; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; hemoglobin-associated disorder thalassaemia; immune system cell infiltration.
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                                                                                                                              DB 1; Length 1129;
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                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                            1.1%; Score 21.4; D 66.0%; Pred. No. 45; ive 0; Mismatches
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ID ADD09875 standard; cDNA; 1129 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PRO polynucleotide #111.
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01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
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                                                                                                                                                                                                                                                                                                                 31; Conservative
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Smith V, Stewart TA,
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                                                                                                                                                                                                                                                                                             Local Similarity
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P-PSDB; ADD09876.
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                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 155
                                                                                                                                                                                                                                                                                                               Matches
    원
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Gao W;

Deforge L, Desnoyers L, Filvaroff E, G: A, Godowski FJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z;

Beresini M, De ME, Goddard A, Stewart TA, Tum

invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis actor—alpha (TWF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for colon, breast, prostate, rectal, kidney, cervical and liver tumours). The colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as consistence RNA and DNA and in gene therapy. The polynucleotides may also hybridisation probes, in chromosome and gene mapping, in generating either transgenic animals or knock-out animals which are consenting either transgenic animals or knock-out animals which are consenting in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of consential muscle cells for adjocyte cells, for stimulating collevant of inner ear utricular supporting cells, for stimulating proliferation of inner ear utricular supporting cells, for stimulating proliferation of inner ear utricular supporting cells, for stimulating cells, for inducing endechelial cells, for stimulating and ordiniaring discreases and arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, cells, from cartilage are useful for treating sports-related joint problems, articular cartilage are useful for treating sports injuries and conditions which may benefit from enhanced local immune system cell infilteration. This earence represents a human PRO polymolocide of the invention. Note: cells, cells and an also various bene in endored discrete such as various challable in electronic format The sequence data for this patent is also avai from USPTO at seqdata,uspto.gov/sequence.html. 888888888888888888888888888888888888

Gaps ö 1835 TICTIAATITITICATITICCAGAITITCCTICAGITITGGGTTTTGTTT 1881 Score 21.4; DB 1; Length 1129; Pred. No. 45; 0; Mismatches 16; Indels 0; 1129 Trritritritritritrickicrackckckckckckcrcccrcccrtritritr 1083 Query Match 1.1%; Best Local Similarity 66.0%; Matches 31; Conservative ( ò

ADD04450/c ID ADD04450 standard; cDNA; 1129 RESULT 156

BP

ADD04450;

(first entry) 01-JAN-2004 Novel human secreted and transmembrane protein PRO4327 cDNA.

Human; secreted and transmembrane protein; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; condroyte; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose uptake modulator; FFA uptake modulator; cell proliferation; cell differentiation; FFA uptake modulator; cell; proliferation; pericyte cell; inner ear utricular supporting cell; thouse cell; inner ear utricular supporting cell; T-lymphocyte cell; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; theumatoid arthritis; haemoglobin associated disorder; thalassaemia; immune system cell infiltration; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker; gene; ss.

Homo sapiens

US2003087354-A1.

38-MAY-2003

22-APR-2002; 2002US-00127827. 

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New PRO nucleic acid, useful for manufacturing a medicament
                                                                                                                         Claim 2; Fig 221; 637pp; English.
         10-7070-1999; 99W0-US012252.
25-AUG-1999; 99US-00380137.
30-MAR-2000; 2000W0-US014941.
30-MAY-2000; 2000W0-US014941.
01-DEC-2000; 2000W0-US032678.
                                                                                                              diagnosing or treating tumor.
                                                  (GETH ) GENENTECH INC
                                                                                      WPI; 2003-801139/75.
                                                                                             P-PSDB; ADD04451
                                                                     Gerritsen ME,
    17-AUG-1998;
02-JUN-1999;
25-AUG-1999;
                                                                Baker KP,
                                                                           Smith V,
Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the factor-alpha (TNF-alpha) from human blood, a method for stimulating the colon, breast, prostate, rectal, kidney, cervical and a method for clon, breast, prostate, rectal, kidney, cervical and liver tumours). The colon, breast, prostate, rectal, kidney, cervical and liver tumours). The colon, breast, prostate, in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and bNA and in gene therapy. The polynuclectides may also contisense in the development and screening of the polymelectides may also sectul in the development and screening of therapeutically useful reagents. The PRO polypeptides by recombinant techniques and in cagenating either transganic animals or knock-out animals which are cagents. The PRO polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or medicament for treating a condition responsive to the polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or condition responsive to the polypeptides or entibodies are used in periotyce cells, for simulating the proliferation of adipocyte cells, for simulating the proliferation of regene expression in periotyce cells or transition and for transition and for transition and for transition and for transition and periotyce reals, for the proliferation of an expense or the proporting cells or transition and many and the proliferation of an expense or the proporting cells or transition and periotyce reals, for the proliferation of an expense or the proporting cells or transition and the proliferation of an expense or the proporting cells or transition of an expense or th treating various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin-associated disorders such as various thalassemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polynucleotide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at segdata.uspto.gov/sequence.html.

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps ó DB 1; Length 1129; Indels 1.1%; Score 21.4; DB 66.0%; Pred. No. 45; tive 0; Mismatches Conservative Query Match Best Local Similarity Matches 31; Conserv

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1835 ITCTIAATITITCATITCCAGATITCCTICAGITIGGGITITGTIT 1881 1083 1129 trrtrrrrrrrrrrrrrrrrrrrrrr ADC80406 standard; cDNA; 1129 BP. RESULT 157 ADC80406/ ID ADC8 XX AC ADC8 g ò

ADC80406;

arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin-associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polynucleotide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

articular cartilage defects, osteoarthritis and rheumatoid

Gaps

0

Indels

DB 1; Length 1129;

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

1.1%; Score 21.4; D 66.0%; Pred. No. 45; tive 0; Mismatches

Conservative

Local Similarity es 31; Conserv

Human PRO polynucleotide #111.

01-JAN-2004 (first entry)

ADD10913;

1913/c ADD10913 standard; cDNA; 1129

New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 PRO4978, useful in molecular biology, chromosome and gene mapping, generating antisense RNA and DNA, and in gene therapy. Claim 2; Fig 221; 637pp; English. WPI; 2003-801168/75. P-PSDB; ADC80407 

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Query Match
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Matches
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88888888888
                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                      Human; secreted and transmembrane protein; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose uptake modulator; FPA uptake modulator; cell proliferation; pell differentiation; Relecal muscle cell; adipocyte cell; periovte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder; thalassaemia; immune system cell infiltration; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker; gene; ss.
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                                                                         Novel human secreted and transmembrane protein PRO4327 cDNA
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2000WO-US004414.
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19-DEC-2001; 2001US-00028072
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                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beresini M,
ME, Goddard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
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Smith V, Stew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-1999;
22-FEB-2000;
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                         01-JAN-2004
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New secreted and transmembrane PRO nucleic acids and polypeptides, useful for detecting a tumor, stimulating the proliferation or differentiation of chondrocyte cells and stimulating the release of tumor necrosis factor Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; periovte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration. The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymuclectides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the Gao Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ga Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; Claim 2; SEQ ID NO 221; 637pp; English. 03-MAR-2000; 2000US-0187202P. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072. 21-MAY-2002; 2002US-00152399. (GETH ) GENENTECH INC. WPI; 2003-852594/79. P-PSDB; ADDI0914. US2003194774-A1. Homo sapiens. 16-0CT-2003 alpha. The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondroyte cells and a method for colon, breast, prostate, rectal, kidney, cervical and liver tumours). The proliferation probes, in chromosome and gene mapping, including uses as hybridisation probes, in chromosome and gene mapping, including uses as chypridisation probes, in chromosome and gene mapping, in generating antisense RNA and bNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of the cells, for modulating the proliferation of submover cells, for stimulating the proliferation of inner are utricular supporting cells, for stimulating the proliferation of inner are utricular supporting cells, for treating various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint in in

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Gaps ; 0 Score 21.4; DB 1; Length 1129; Pred. No. 45; Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; 16; Indels Mismatches ö 1.1%; 31; Conservative Similarity Query Match Best Local S: Matches 31

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1835 TICTIAATITITICATITICCAGATITICCTTCAGTITIGGGTTTTGTTT 1881 1129 Trritritritritritricagciagcacacadagciaggiritratr 1083 BP. ADC47794/c ID ADC47794 standard; cDNA; 1129 g ò

(first entry) 01-JAN-2004 ADC47794; 

Human PRO polynucleotide #111.

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tummour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tummour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFP; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Homo sapiens.

US2003194771-A1.

16-OCT-2003.

21-MAY-2002; 2002US-00152377.

09-DEC-1999; 99US-0170262P. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC. 

Gao W; Smith V; Beresini M, Deforge L, Desnoyers L, Filvaroff E, 1E, Goddard A, Godowski PJ, Gurney AL, Gurney SL, Tumas D, Watanabe CK, Wood WI, Zhang Z; Baker KP, Beres.... Gerritsen ME, Goddard

WPI; 2003-844454/78. P-PSDB; ADC47795 New secreted and transmembrane PRO polypeptides and nucleic acids useful for detecting a tumor, stimulating the release of proteoglycans from cartilage and stimulating the proliferation of endothelial cells.

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TWP-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. darenal, lung, detecting the presence of a tumour in a mammal (e.g. adrenal, lung, detecting the presence of a tumour in a mammal (e.g. adrenal, lung, antibology, including uses as a series, prostate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as a set in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing of the properties or antibodies, such as tumours, for antibodies are used in preparing of thuman microvascular endothelial cells, for modulating the uptake of altibodies, such as tumours, for stimulating of the polypeptides or attribodies, such as tumours, for stimulating are used in preparing of finer ear unfamily or eclls, for stimulating the uptake of stimulating of finer ear unfamily or supporting cells, for stimulating the polypeptides are useful for treating sports-related joint problems, arthritis. PRO polypeptides which stimulate the release of protecylycans from cartilage are useful for treating sports-related joint problems, arthritis. PRO polypeptides which stimulate the release of protecylycans framical are also useful for treating sports-related joint problems, arthritis and man and/or cartilage disorders such as sports injuries and also useful for treating sports-related joint problems, are useful for treating sports-related joint problems, associated disorders such as various human menalphore and also useful for treating sports-relate from USPTO at segdata.uspto.gov/sequence.html.

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps ô 16; Indels DB 1; 1.1%; Score 21.4; D 66.0%; Pred. No. 45; ive 0; Mismatches Conservative Local Similarity 31; Query Match Matches

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1835 TICTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881 1129 iirrirrirrirrirrirrir 1083 DP ઠે

ADC79854 standard; cDNA; 1129 BP. ADC79854; 

RESULT 160

(first entry) 01-JAN-2004 Novel human secreted and transmembrane protein PRO4327 cDNA.

Human; secreted and transmembrane protein; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; tumour; cancer; adrenal; lung; colon; breast; prostate;

rectum, kidney; cervix; liver; microvascular endothelial cell; glucose uptake modulator; FFA uptake modulator; cell proliferation; cell differentiation; skeletal muscle cell; adlocyte cell; pericyte cell; inner ear uricular supporting cell; T-lymphocyte cell; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder; thalassaemia; immune system cell infiltration; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker; gene; se. 01-SEP-1998; 98US-0098750P. 01-SEP-1999; 99WO-US02011. 18-0CT-1999; 99WS-00403297. 18-FEB-2000; 2000WO-US034342. 08-NOVY-2000; 2000WO-US0319952. 01-DEC-2000; 2000WO-US031678. 19-DEC-2001; 2001US-00028072. 22-APR-2002; 2002US-00127833 (GETH ) GENENTECH INC 2003-801143/75. US2003087358-A1. Homo sapiens. 08-MAY-2003 Smith V, 

Deforge L, Desnoyers L, Filvaroff E, G: A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Baker KP, Beresini M, Gerritsen ME, Goddard Stewart TA,

P-PSDB; ADC79855

New PRO nucleic acid, useful for manufacturing a medicament for diagnosing or treating tumor.

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the release of tumour necrosis of detecting the presence of a tumour in a mammal (e.g. adreral, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The projuctleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymucleotides may also consistence in the development and screening of therapeutically useful color proparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful color setulations the proparing a condition responsive to the polypeptides or medicament for treating a condition responsive to the polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies are used in preparing color of human microvascular endothelial cells, for modulating the profileration of color stimulating differentiation of adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating various bone and/or cartilage disorders such as sports injuries and archaritis. PRO polypeptides which stimulate the release of protecolycans from cartilage are useful for treating sports-related joint of problems, articular cartilage defects, osteoarthritis and rheumatoid carthritis and archaritis are not purpoptides are also useful for treating various that are are useful for treating various that associated disorders such as various cand conditions which may benefit from enhanced local im

ö Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; periove cell; inner ear utricular supporting cell; T-lymphocyte cell; sports injury; proteoglycan; articular cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration. Gaps 0 1835 ITCITAAITITICAITICCAGAITICCTICAGITIGGGITITGTIT 1881 1129 rrrrrrrrrrrrrrrrradcrececacadecrederrrrrrr 1083 DB 1; Length 1129; Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; Indels 16; Score 21.4; Di Pred. No. 45; 0; Mismatches ADD09323 standard; cDNA; 1129 BP Human PRO polynucleotide #111. 1.1%; (first entry) 1.1 Best Local Similarity 66.0 Matches 31; Conservative 01-JAN-2004 ADD09323; RESULT 161 ADD09323, ò g

US2003194775-A1. Homo sapiens.

28-MAY-2002; 2002US-00156848. 16-OCT-2003

03-MAR-2000; 2000US-0187202P. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC

Gao ssini M, Deforge L, Desnoyers L, Filvaroff E, Ga Goddard A, Godowski PJ, Gurney AL, Sherwood S; art TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; Baker KP, Beresini M, Gerritsen ME, Goddard Smith V, Stewart TA,

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2003-852595/79. WPI; 2003-852595 P-PSDB; ADD09324 New secreted and transmembrane PRO nucleic acids and polypeptides, usefu for detecting a tumor, stimulating the release of tumor necrosis factor alpha from blood and stimulating the release of proteoglycans from

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene fherapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in

or in

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generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of thuman microvascular endothelial cells, for modulating the uptake of glucose or PRA by skeletal muscle cells, for adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating the uptake of proliferation of orgene expression in perioyte cells, for stimulating the proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and carthritis. PRO polypeptides which stimulate the release of protecylycans from cartilage are useful for treating sports-related joint problems, arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin-associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polymucleotide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at sequence.html.
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Human; secreted and transmembrane protein; PRO; gene; ss; Tumour necrosis factor alpha release; TNF-alpha release; glucose uptake modulator; PFA uptake modulator; cell proliferation stimulator; or the differentiation stimulator; cell differentiation stimulator; cell differentiation inhibitor; cytokine release stimulator; tumour; clump tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; chromosome mapping; gene mapping; gene mapping; gene therapy; chromosome identification; chromosome marker.
                                                                                                                                                                                                                                                                                                                                           Novel human secreted and transmembrane protein PRO4327 cDNA.
                                                                                     ADD41036 standard; cDNA; 1129
                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                      15-JAN-2004
                                                                                                                                                                          ADD41036;
RESULT 162
                                            ADD41036/c
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16-SEP-1998; 98WO-US019330. 25-AUG-1999; 99US-00380139. 22-FEB-2000; 2000WO-US004414. 2000WO-US032678. 2001US-00028072. 15-MAY-2002; 2002US-00146786 97US-0066511P (GETH ) GENENTECH INC. JS2003203438-A1 01-DEC-2000; 19-DEC-2001; 24-NOV-1997; 16-SEP-1998; 30-OCT-2003. 

US2003194769-A1. Homo sapiens.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gr Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

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The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (1). (1) is useful for stimulating the crelases of INF-alpha from human blood, for modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating proliferation of inner ear utricular supporting cells, for stimulating proliferation of adipocyte cells, for stimulating proliferation of modutelial cells, for stimulating cells, for inhibiting the differentiation of adipocyte cells, for stimulating proliferation of modutelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, cells, for stolating genomic and cDNA nucleotide sequences or antisense probes. (1) is also useful as therapeutic agent, proliferation of in assays to identify other proteins or molecules involved in binding in nersense probes. (1) is also useful as therapeutic agent, in chromosome and gene mapping, in generation of antisense process or chrocosome identification, as chromosome marker, and for generating transgenic animals or chromosome identification, as chromosome marker, and for generating cor probes. An anti-(1)-antibody is useful in diagnostic assays for PRO, erg. chromosome identification of PRO from recombinant cell culture or natural correcting its expression in specific cells, tissue syptomy, and (11) are useful for tissue syptomy, pluming and (11) are useful for tissue syptomy, and (11) are second and transmembrane PRO polymorial and transmembrane PRO polymorial and transmembrane PRO polymorial and transmembrane PRO polymorial and transmembrane PRO polymorial and transmembrane PRO polymorial and transmembrane.
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                                                                  New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 PRO4978, useful in molecular biology, chromosome and gene mapping, generating antisense RNA and DNA, and in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             novel human secreted and transmembrane PRO polypeptide.
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llarity 66.0%; Pred. No. 45;
Conservative 0; Mismatches
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                                                                                                                                                                              Claim 2; SEQ ID NO 221; 637pp; English.
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es 31; Conserv
                      P-PSDB; ADD41037
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ADD52915;

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TWR-alpha) from human blood, a method for stimulating the polypeptide, a method for stimulating the release of tumour necrosis of proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating cartisenses RNA and in gene therapy. The polymucleotides may also a trisense RNA and in gene therapy. The polymucleotides may also color be used in preparing PRO polypeptides by recombinant techniques and in the development and screening of knock-out animals which are useful in the development and screening or knock-out animals which are useful in the development and screening or knock-out animals which are useful structured to treating a condition responsive to the polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of summore ear utricular supporting cells, for stimulating differentiation of adipocyte cells, for stimulating the proliferation of inner ar utricular supporting cells, for stimulating the proliferation of inner ar utricular supporting cells, for stimulating differation of inner ar utricular supporting cells, for medication and for treating various bone and/or cartilage disorders such as sports injuries and cartilage are useful for treating sports-related joint problems, articular cartilage are useful for treating sports-related joint problems are useful for treating sports-related joint problems are useful for treating spo
                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated, secreted and transmembrane PRO polypeptides and nucleic acids, useful for detection of tumors, modulating the uptake of glucose or free fatty acids and stimulating the release of proteoglycans from cartilage.
                                                                                                                                                                                                                                                                Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G.
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                   09-DEC-1999; 99US-0170262P.
01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
                                                                      21-MAY-2002; 2002US-00152374
                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
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P-PSDB; ADD52176.
                    16-OCT-2003.
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ö Gaps , 0 Score 21.4; DB 1; Length 1129; Pred. No. 45; 0; Mismatches 16; Indels 0 1835 TICTTAATTTTTTCATTTCCAGATTTCCTTCAGTTTGGTTT 1881 Query Match
Best Local Similarity 66.0%;
Matches 31; Conservative à

Tirrirrirrirrirrirradciescacacadecrescrirrirrir 1083 RESULT 164 ADD52915/c ID ADD52915 standard; cDNA; 1129 BP. 1129

11-FEB-2000;

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNP-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; Dreast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucoss; PRA; skeletal muscle cell; adpocyte cell; graciote cell; cell; dincer ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; shoutenjulary; proteoglycan; articular cartilage defect, osteoarthritis; rheumatoid arthritis; articular cartilage disorder thalassaemia; immune system cell infiltration. cDNA encoding human PRO polypeptide #111 98WO-US012456 98WO-US014552 2002US-00123156 98WO-US019330 98WO-US018824 2000WO-US006319 98WO-US019093 98WO-US019437 99WO-US005028 99WO-US008615 9WO-US012252 9WO-US020111 9WO-US020594 (first entry) 9WO-US020 99WO-US028 99WO-US02 99WO-US02 99WO-US0 98WO-US 8WO-US SD-OM6 SU-OW6 98WO-US SU-OW86 -0M66 -0M66 US2003194792-A1. Homo sapiens. 15-APR-2002; 15-JAN-2004 16-0CT-2003. 4-JUL-1998 8-AUG-1998 

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001US-00796498,
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10-MAY-2001;
18-MAY-2001;
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25-MAY-2001;
25-MAY-2001;
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09-MAR-2001;
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05-APR-2001;
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Gao W; Deforge L, Desnoyers L, Filvaroff E, Ga A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Tumas D, Gerritsen ME, Goddard A, Smith V, Stewart TA, Tum

#### WPI; 2003-852599/79. P-PSDB; ADD52916.

New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or PRO4978, useful in chromosome and gene mapping, in generating antisense RNA and DNA, and in the treatment of cancer.

# Claim 2; Fig 221; 638pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the

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proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polyunclectides are useful in molecular biology, including uses as antisense RNA and NNA and in gene therapy. The polyunclectides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or knock-out animals which are capents. The PRO polypeptides or knock-out animals which are medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of number of the proliferation of adipocyte cells, for stimulating the uptake of stimulating or firminating cells, for stimulating colliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating cells, for indiving endothelial cell tube formation and for treating articular cartilage defects, osteoarthritis and for treating collipsing collipsing are useful for treating various mammalian haemoglobing associated disorders such as various thelasseamias and conditions which may be entitled for treating various mammalian haemoglobing sequence encodes a human PRO polypeptide of the invention. Note: The sequence catter for this patent is also available in electronic format from conditions and a process of the invention.
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Tumour necrosis factor alpha release; TMR-alpha release;
Jucose uptake modulator; PFA uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inhibitor; cytokine release stimulator; tumour;
lung tumour; cloh rumour; breast tumour; rectal tumour;
cervical tumour; liver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
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66.0%; Pred. No. 45;
:ive 0; Mismatches
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99WO-US012252.
2000US-00380137.
2000WO-US032678.
2001US-00028072.
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Best Local Similarity 66.0
Matches 31; Conservative
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01-DEC-2000;
01-DEC-2000;
19-DEC-2001;
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ADD53467/c
ID ADD534
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(GETH ) GENENTECH INC.

Gao W; Beresini M, Deforge L, Desnoyers L, Filvaroff E, G: ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; Gerritsen ME, Goddard Smith V, Stewart TA, Baker KP,

WPI; 2003-875644/81. P-PSDB; ADD53468.

or in New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 PRO4978, useful in molecular biology, chromosome and gene mapping, generating antisense RNA and DNA, and in gene therapy.

2; SEQ ID NO 221; 659pp; English. Claim

The invertion describes 305 nucleic acids encoding FVC (secreted and release of TNF-alpha from human blood, for modulating the uptake of allocation or differentiation of chondrocyte cells, cor stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of proteoglycans from cartiage, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating proliferation of endothelial cells, for stimulating proliferation of endothelial cells, for detecting the prostate, rectal, cervical or liver tumour. The oligonucleotide probes cells, for inhibiting the probes cells, for inhibiting the probes cells, for inhibiting the probes cells, for inhibiting the defecting in assays to identify other proteins or molecules involved in binding in assays to identify other proteins or molecules involved in binding interaction. A polynucleotide (II) encoding (I) is useful in the development and some propers or propers in turn are useful in the development and some conception in turn are useful in diagnostic assays for PRO, e.g. chromosome identification, as chromosome marker, and for generating probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g. detecting its expression in specific cells, tissues or serum and certain are expression in specific cells, tissues or serum and certain and cells are are expression in specific cells, tissues or serum and cells are are also and serum and cells, tissues or serum and cells are are also and serum and cells. The invention describes 305 nucleic acids encoding PRO (secreted novel human secreted and transmembrane PRO polypeptide. 

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps . 0 1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; cive 0; Mismatches 16; Indels 0 1835 TECTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881 31; Conservative Query Match Best Local Similarity Matches 31; Conserv ò

1129 TTTTTTTTTTTTTTTTCAGCTGGCACACAGGCTGGGTTTTATT 1083

ADD51623 standard; cDNA; 1129 RESULT 166 ADD51623,

ADD51623;

cDNA encoding human PRO polypeptide #111.

(first entry)

15-JAN-2004

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; glucose; FFA; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; catchinge disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; 

rheumatoid arthritis, haemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Homo sapiens

JS2003194779-A1.

16-OCT-2003

30-MAY-2002; 2002US-00160500.

05-JUN-2000; 2000US-0209832P. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC.

Gao W; Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-852597/79. P-PSDB; ADD51624. New secreted and transmembrane PRO nucleic acids and polypeptides, useful for detecting the presence of a tumor, stimulating the release of tumor necrosis factor alpha from human blood and treating, e.g. organ failure.

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for proliferation or differentiation of chondrocyte cells and a method for coll, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, in generating antisense RNA and brook polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful useful in the development and screening of therapeutically useful useful in the development and screening of therapeutically useful antibodies, such as tumours, for attimulating and inhibiting proliferation of funces or FRA by skeletal muscle cells, for modulating the uptake of glucose or FRA by skeletal muscle cells, for stimulating differentiation of adipocyte cells, for stimulating collieration of funce and adipocyte cells, for stimulating effect or gene expression in pericyte cells, for stimulating and condition as sports injuries and cartinage defects, observativities and rhemmatoid arthrities PRO polypeptides which stimulate the release of proteoglycan cartinage defects, observativities and rhemmatoid arthrities and seculated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infilteration. One sequence encodes a human PRO polypeptide of the invention. Note: The reproportion of sequence encodes a human PRO polypeptide of the invention. One is a seculation of sequence encodes a human PRO polypeptide of the invention of the propertion of seq 

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

the USPTO website at segdata.uspto.gov.

Gaps 0 DB 1; Length 1129; 1.1%; Score 21.4; DB 1; Length 166.0%; Pred. No. 45; ive 0; Mismatches 16; Indels 0 Conservative Local Similarity nes 31; Conserv Query Match Matches

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RESULT 167

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polypucletides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TRP-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for according to proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The plynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of the polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, for
                                                                                                                                                                                Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatchd arthritis; hemoglobin-associated disorder thalassaemia; immune system cell infiltration.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 PRO4978, useful in molecular biology, chromosome and gene mapping, generating antisense RNA and DNA, and in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ga
IE, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
tewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
                  ADD02422 standard; cDNA; 1129 BP.
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                                                                                                                                               Human PRO polynucleotide #111.
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18-FEB-2000; 2000WO-US004442.

24-AUG-2000; 2000WO-US0328.

10-DEC-2000; 2000WO-US0328678.
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99WO-US020111.
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                                                                                                      (first entry)
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                                                                                                      15-JAN-2004
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01-SEP-1999;
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                                                            ADD02422;
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ADD02422/
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proliferation of or gene expression in pericyte cells, for stimulating proliferation of or gene expression in pericyte cells, for stimulating cells, for stimulating cells, for inducing endothelial cell tube formation cells, Inner ear utricular supporting cells or I-lymphocyte cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of protegglycans from cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin—associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence date for this patent is also available in electronic format form methods.
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                                                                                                                                                                                                Score 21.4; DB 1; Length 1129; Pred. No. 45;
                                                                                                                                                                                                                                                                                                            Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                        16; Indels
                                                                                                                                                                                                                                                                   from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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02-JUN-1999; 99WO-US012252.
30-MAR-2000; 2000US-00380137.
01-DEC-2000; 2000WO-US028678.
19-DEC-2001; 2001US-00028072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human PRO polynucleotide #111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADD01856 standard; cDNA; 1129
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66.0%;
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                                                                                                                                                                                                                                                                                                                                                                                           31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       Similarity
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Best Local &
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generating antisense RNA and DNA, and in gene therapy

Claim 2; Fig 221; 637pp; English 

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polypucleotides encoding them. The invention also melbods and the polypucleotides encoding them. The invention also melbod for stimulating the polypeptide, a method for stimulating the polypeptide, a method for stimulating the profile from human blood, a method for stimulating the profileration or differentiation of chondrocyte cells and a method for proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colin, breast, prostate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating and in gene therapy. The polymucleotides may also antisense RNA and in gene therapy in polymucleotides may also generating either transgenic animals or knock-out animals which are useful in the development and exceening of therapeutically useful captures. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of aluge or stimulating and inhibiting proliferation of stimer expression in periotyce cells, for stimulating proliferation of adipocyte cells, for stimulating various bene and/or cartilage disorders such as sports injuries and cartilage are useful for treating sports related joint problems, articular cartilage defects, osteoarthriks as sports injuries procession expension the such as sports injuries and cartilage are useful for treating sports related joint problems, articular cartilage defects, osteoarthrikis and rheumatoid architics. PRO polypeptides which stimulate the release of proteoglycans articular cartilage are useful for treating sports related joint problems, as sociated disorders such as various thalassemias and conditions which may benefit from enhanced l from USPTO at segdata.uspto.gov/sequence.html.

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps ; 0 DB 1; Length 1129; 1835 TICTIAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881 1.1%; Score 21.4; D 56.0%; Pred. No. 45; ve 0; Mismatches 66.0%; Conservative Local Similarity tes 31; Conserv Query Match Matches à

1129 Trritrrrrrrrrrrrrrradcrescacacades 엄

ADD54038 standard; cDNA; 1129 BP 15-JAN-2004 ADD54038; RESULT 169 ADD54038/ 

(first entry)

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Novel human secreted and transmembrane protein PRO4327 cDNA.

Human; secreted and transmembrane protein; PRO; gene; ss; Tumour necrosis factor alpha release; TNF-alpha release; glucose uptake modulator; PFA uptake modulator; cell proliferation stimulator; cell differentiation stimulator; cytokine release stimulator; tumour; cloud unity tumour; cloud timulator; cytokine release stimulator; tumour; cloud timulator; tumour; chost tumour; cho

JS2003203432-A1

30-0CT-2003

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;

Human PRO polynucleotide #111.

29-JAN-2004 (first entry)

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The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the criedase of INF-alpha from human blood, for modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation of or gene expression in perioryte cells, for stimulating the proliferation of or gene expression in perioryte cells, for stimulating the proliferation of inner ear utricular supporting cells, cor stimulating the proliferation of inner ear utricular supporting cells, cor stimulating the proliferation of inner ear utricular supporting cells, cor stimulating proliferation of inner ear utricular supporting cells, cor stimulating proliferation of endothelial cells, for stimulating the prostate, rectal, corvical or inhibiting the differentiation of adipocyte cells, for stimulating proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, corstate, rectal, cervical or liver tumour. The oligonucleotide probes are useful for isolating genomic and cond to inching sequences or antisense probes. (I) is also useful as therapeutic agent, in chromosome and gene mapping, in generation of antisense RNA and DNA, in the properation of RNO polypoptide, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, in gene therapy, for chromosome identification, as chromosome marker, and for generating conditions. An anti-condition is useful in diagnostic assays for RNO, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. (I) and (II) are useful for tissue typing. This sequence encodes
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                                                                                                                                                                                 Deforge L, Desnoyers L, Filvaroff E, Ga
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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Pred. No. 45;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; SEQ ID NO 221; 637pp; English.
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                                                        05-JUN-2000; 2000US-0209832P.
01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
               10-MAY-2002; 2002US-00142886
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                                                                                                                                                                                 Beresini M,
1 ME, Goddard A
Stewart TA, T
                                                                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                       WPI; 2003-875639/81.
P-PSDB; ADD54039.
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                                                                                                                                                                                      Baker KP,
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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymuclectides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TMF-alpha) from human blood, a method for stimulating the proliferation of chondrocyte cells and a method for proliferation probes. The mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidatey, cervical and invertumours). The colon, breast, prostate, rectal, kidatey, cervical and liver tumours). The polymuclectides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating colon, breast, propoptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of thuman microvascular endothelial cells, for modulating the uptake of glucose or FRA by skeletal muscle cells, for stimulating differentiation of adipocyte cells, for stimulating the proliferation of adipocyte cells, for stimulating and inhibiting proliferation of adipocyte cells, for stimulating are useful for treating sports related joint problems, articular cartilage are useful for treating sports related joint problems, articular cartilage defects, osceoarthriles and rheumatoid atthering cartilage are useful for treating various mammalian haemoglobin-and/or cartilage are useful for treating various mammalian haemoglobin-and/or artilage are useful for treating various per propertion
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tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; periote cell; inner ear utricular supporting cell; periote cell; endochelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
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                                                                                                                                                                                                       Human, gene; ss, PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNP-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothalial cell; glucose; FRA; skeletal muscle cell; adipocyte cell; perioyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothalial cell tube formation; bone disorder; cartilage disorder; sports injury; protecodyycan; articular cartilage defect; osteoarthritis; rheematoid arthritis; haemoglobin-associated disorder thalassaemia;
                      Gaps
                      0
                                                               1129 ritritritritritritricagciggcacacacagggrigitritrit 1083
 DB 1; Length 1129;
                    16; Indels
                                          1835 TICTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT
Score 21.4; DB Pred. No. 45; 0; Mismatches
                                                                                                          ADD91251/c
ID ADD91251 standard; cDNA; 1129 BP.
                                                                                                                                                                                                                                                                                                         immune system cell infiltration
                                                                                                                                                                                     Human PRO polynucleotide #111.
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2000WO-US006319.
99WO-US008615.
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98WO-US019094.
98WO-US019177.
1.1%;
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98WO-US021141.
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 Query Match
Best Local Similarity 66.0
Matches 31; Conservative
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99WO-US028564

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

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99WO-US030720
99WO-US031243
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        99WO-US030999
                                       000WO-US004414
                 99WO-US031274
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                                    SU-CM000
                                         24-FEB-2000;
24-FEB-2000;
           22-DEC-1999;
30-DEC-1999;
30-DEC-1999;
                                      22-FEB-2000;
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22-JUN-2001
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(GETH ) GENENTECH INC.

Gao W; Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G. Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-900165/82. P-PSDB; ADD91252.

Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis. Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; claim 2; SEQ ID NO 221; 636pp; English. 

DB 1; Length 1129; 1.1%; Score 21.4; DB 1; Length 11: 66.0%; Pred. No. 45; ive 0; Mismatches 16; Indels Query Match Best Local Similarity 66.0' Matches 31, Conservative

1835 ȚICȚIAAȚIȚIȚCAȚITCCAGAȚITCCTTCAGTTTGGGTȚTTGTTT 1881 1129 TTTTTTTTTTTTTTTTCAGCTGGCACACACGCTGGGTTTTTTT 1083 à 셤

Gaps

. 0

ADE03865 standard; cDNA; 1129 BP 29-JAN-2004 (first entry) ADE03865; RESULT 172 ADE03865/ 

Human PRO polynucleotide #111.

Human, gene, ss, PRO, secreted polypeptide, transmembrane polypeptide, tumour necrosis factor-alpha, TNF-alpha, chondrocyte cell; tumour, cancer, adrenal; lung; colon; breast; prostate, rectum; kidney; cervix; liver, microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; perioyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; artilage disorder; sports injury; proteoglycan, articular cartilage defect; osteoarchritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.

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2001WO-US006666
2001US-00802706.
2001US-00808689.
2001US-00816744.
2001US-00828366.
                                                                  2001US-00860216.
2001US-00866028.
2001US-00866034.
2001US-00866034.
2001US-0087035.
2001US-00874503.
                               2001WO-US006520
                                                              2001US-00854280
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2001WO-US019692
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2001WO-US021066.
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                                                                           25-MAY-2001;
25-MAY-2001;
01-JUN-2001;
                                   01-MAR-2001;
09-MAR-2001;
                                            14-MAR-2001;
                                                                       25-MAY-2001;
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# (GETH ) GENENTECH INC

Gao W; Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G. Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

#### WPI; 2003-900167/82. P-PSDB; ADE03866.

Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis.

# Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for cecting the presence of a tumour in a mammal (e.g. adrenal, lung, considering the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and bNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or autibodies, such as tumours, for stimulating and inhibiting proliferation of of human microvacular nucle cells or adipocyte cells, for stimulating cells or timulating cells or proliferation of inner ear utricular supporting or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating

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various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteogyycans from cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin-associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polymucleotide of the invention. Note: The sequence data for this patent is also available in electronic format from USPIO at sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted and transmembrane protein; PRO; gene; ss; Tumour necrosis factor alpha release; TNT-alpha release; glucose uptake modulator; endulator; PFA uptake modulator; cell proliferation stimulator; cell differentiation stimulator; cell differentiation stimulator; cell differentiation inhibitor; cytokine release stimulator; tumour; clup tumour; cloon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the release of INF-alpha from human blood, for modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation or differentiation of chondrocyte cells,
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                                                                                                                     1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; tive 0; Mismatches 16; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                      1129 TITITITITITITITITITICAGCIGGCACACAGGCIGGGTITITATT 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human secreted and transmembrane protein PRO4327 cDNA.
                                                                                                                                                                                                                                    Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE32162 standard; cDNA; 1129
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01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
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Smith V, Stewart TA, Tumas
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les 31, Conservative
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P-PSDB; ADE32163.
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colls, for stimulating the proliferation of or gene expression in pericyce cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of finner ear utricular supporting cells, for stimulating the proliferation of finner ear utricular supporting cells, for stimulating the broliferation of finner ear utricular supporting cells, for stimulating the broliferation of endothelial cells, for stimulating proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour. The oligonucleotide probes center is claring genomic and cDNA nucleotide sequences or antisense probes. (I) is also useful as therapeutic agent. PRO is useful an assays to identify other proteins or molecules involved in binding interaction. A polynucleotide (II) encoding (I) is useful in the preparation of PRO polypeptide, for generating transgents animals or knockout animals which in turn are useful in the development and chromosome identification, as chromosome marker, and for generating probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g. detecting its expression in specific cells, itssues or serum, and for affinity purification of PRO from recombinant cell culture or natural sour anovel human secreted and transmembrane PRO polypeptide.
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stimulating the proliferation of or gene expression in pericyte
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Pred. No. 45
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98WO-US012456.
98WO-US014552.
98WO-US014888.
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98WO-US019330
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Best Local Similarity
Matches 31; Conserv
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12-JUN-1998;
14-JUL-1998;
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14-SEP-1998;
14-SEP-1998;
14-SEP-1998;
16-SEP-1998;
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ADE22094/c
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2001US-00886342.
2001WO-US019692.
2001US-00887879.
    25-MAY-2001; 2001WO-US017092.
01-UUN-2001; 2001US-00872035.
01-JUN-2001; 2001US-00874503.
05-UUN-2001; 2001US-00882636.
                                         22-JUN-2001; 2001WO-US020116.
29-JUN-2001; 2001WO-US021066.
                                                  2001WO-US021735.
2001US-00908827.
2001US-00866034
                                                             1; 2001US-00924419
                                                                 09-AUG-2001; 2001US-00927796
16-AUG-2001; 2001US-00931836
                                                                           19-DEC-2001; 2001US-00028072
                           19-JUN-2001;
                                 20-JUN-2001;
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# (GETH ) GENENTECH INC

3 Gao Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ga Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

### WPI; 2003-900166/82. P-PSDB; ADE22095.

Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis.

# Claim 2; Fig 221; 638pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TWP-alpha) from human blod, a method for stimulating the proliferation of differentiation of chondrocyte cells and amethod for proliferation of aliferentiation of chondrocyte cells and amethod for colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular blology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RAM and DNA and in gene therapy. The polynucleotides may also catistical in the development and screening of therapeutically useful reagents. The PRO polypeptides by knock-out animals which are generating either transgenic animals or knock-out animals which are medicament for treating a condition responsive to the polypeptides or medicament for treating a condition responsive to the polypeptides or medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating of the proliferation of or gene expression in pericyte cells, for stimulating to the proliferation of anexes ear urricular supporting cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating antihities and finer ear urricular supporting cells, for inducing endochelial cell tube formation and for treating crocartilage are useful for treating sports injuries and conditions which associated disorders such as various thalassaemias and conditions which may benefit from enhance date of the invention. Note: The sequence encodes a human PRO polypeptide of the inventions of the invention. Note: The condition conditions are also useful for treating each encodes a human PRO polypeptide of the inventions and provide of the invention. the USPTO website at segdata.uspto.gov.

# Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps ö DB 1; Length 1129; 16; Indels 1.1%; Score 21.4; D. larity 66.0%; Pred. No. 45; Conservative 0; Mismatches Query Match Best Local Similarity Matches 31; Conserv

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an artichody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the prosition or differentiation of chondrocyte cells and a method for detecting the presence of atumour in a meamal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as chybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for modulating the uptake of glucose or FPA by skeletal muscle cells or adipocyte cells, for
                                                                                                                                                                                                                                                                                                                Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostace; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated, secreted and transmembrane PRO polypeptides and nucleic acids, useful for the diagnosis, prevention and/or treatment of tumors, such as lung, colon, breast, prostate, rectal, cervical and/or liver
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
  1881
                         TITITITITITITITITICAGCIGGCACACAGGCIGGGTITITATI 1083
  TICTIAAITITITICAITITCCAGAITITCCTICAGITITGGGITTIGITI
                                                                                                                                                                                                                                                                               cDNA encoding human PRO polypeptide #111.
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                                                                                                                                                     ADD79318 standard; cDNA; 1129
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01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
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Gerritsen ME, Goddard
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1835
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                                                                                                     RESULT 175
ADD79318/c
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stimulating differentiation of adipocyte cells, for stimulating proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, polypeptides are also useful for treating sports-related joint problems, polypeptides are also useful for treating various mammalian haemoglobin-associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence encodes a human PRO polypeptide of the invention. Note: The sequence data for this patent is also available in electronic format from the USPTO website at segdata.uspto.gov.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis.
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
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Best Local Similarity 66.0
Matches 31; Conservative
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Gerritsen ME, Goddard
Smith V, Stewart TA,
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P-PSDB; ADE41855.
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             The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymuclectides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the invention albo an method for stimulating the propriet of conductory cells and a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for proliferation or differentiation of chondrocyte cells and a method for proliferation or differentiation of chondrocyte cells and a method for proliferation probes, in chromosome and gene mapping in generating colls, breast, prostate, rectal, kidney, cervical and liver tumours). The polymuclectides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping in generating colls and the development and screening of therapeutically useful and evelopment and screening of therapeutically useful cuseful in the development and screening of therapeutically useful cuseful in the development and screening of therapeutically useful cuseful in the development and screening of therapeutically useful cuseful in the development and screening of therapeutically useful cuseful in the development and screening of therapeutically useful cuseful in the development and screening of therapeutically useful cuseful in the development of stimulating and inhibiting and inhibiting and medicament for tracting a condition responsive to the polypeptides of stimulating differation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting on and for artilage disorders such as sports righted proteoglycans from cartilage are useful for treating sports-related joint problems, articular cartilage disorders which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, associated disorders such as various thalassaemis and relation. The may benefit from enhanced local immune syst
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1.1%; Score 21.4; DB 1; Length 1129;
Best Local Similarity 66.0%; Pred. No. 45;
Matches 31; Conservative 0; Mismatches 16; Indels 0.
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99WO-US030911.
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2001US-00802706.
2001US-00806689.
2001US-00816744.
2001US-00828366.
2001US-00854208.
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2001US-00872035.
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Smith V, Stewart TA,
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14-MAR-2001; 2
05-APR-2001; 2
10-MAY-2001; 2
10-MAY-2001; 2
18-MAY-2001; 2
25-MAY-2001; 2
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01-JUN-2001;
01-JUN-2001;
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18-JUL-2001;
06-AUG-2001;
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yers L, Filvaroff E, G. Gurney AL, Sherwood S; CK, Wood WI, Zhang Z; Deforge L, Desnoyers L, A, Godowski PJ, Gurney Al Tumas D, Watanabe CK, Woo

Gao W;

Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis.

Claim 2; SEQ ID NO 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the problem to relate the transment of chondrocyte cells and a method for colon, breast, prostate, rectal, kidney, cervical and liver tumours). The colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as thybridisation probes, in chromosome and gene mapping, in generating antisense RNA and bNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are caspents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies are used in preparing coll human microvascular endothelial cells, for modulating the stimulating coll for stimulating differentiation of inner ear utricular supporting cells, for stimulating proliferation of inner ear utricular supporting cells, for inducing endochelial cells for modulating cells, for inducing endochelial cells are supporting cells, for inducing endochelial cells, for modulating carting are useful for treating sports related joint problems, articular cartilage are useful for treating sports related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. Problems associated disorders such as various thalassaemias and conditions which

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may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polymucleotide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html.
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larity 66.0%; Pred. No. 45;
Conservative 0; Mismatches
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                                                                                             Query Match
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Matches
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99WO-US
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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNR-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adremal, lung, coll, breast, prostate, rectal, kidney, cervical and liver tumours). The colynucleotides are useful in molecular biology, in generating to polymucleotides may also constituted by an expensive to the prolifeds may also constituted by the presence of the properties of hybridisation probes, in chromosome and gene mapping, in generating coll preparing prolypeptides by recombinant techniques and in this ensetul in the development and screening of the prolypeptides or antibodies are used in preparing of condition responsive to the polypeptides or antibodies, such as tumours, for stimulating of interacting a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endochelial cells, for medilating the uptake of stimulating differation of another and such an adipocyte cells, for stimulating collication of another are useful for medilating the proliferation of inner ear utricular such as sports injuries and articular cartilage are useful for treating various mammalian hammedlobin. Collicated are useful for treating various mammalian hammedlobined are also useful for treating various mammalian hammedlobined are also useful for treating various mammalian hammedlobined as various thalassaemias and condition. The sequence terpresents as various thalassaemias and condition. The sequence represents a various thalassaemias and condition. The sequence represents a human PRO polymedeced than. Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis. 3 Gao Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G: Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; Claim 2; SEQ ID NO 221; 636pp; English. WPI; 2003-900164/82. P-PSDB; ADD91804. 

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps 0 1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; live 0; Mismatches 16; Indels 0; Query Match
Best Local Similarity 66.0°

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ADE33266 standard; cDNA; 1129 ADE33266; RESULT 179 ADE33266/c 

Novel human secreted and transmembrane protein PRO4327 cDNA

29-JAN-2004 (first entry)

Human; secreted and transmembrane protein; PRO; gene; ss; Tumour necrosis factor alpha release; glucose uptake modulator; FFA uptake modulator; oell proliferation stimulator; cell differentiation stimulator;

818/c ADE33818 standard; cDNA; 1129 BP.

29-JAN-2004 (first entry)

ADE33818;

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The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (1). (1) is useful for stimulating the crelease of TNF-alpha from human blood, for modulating the uptake of glucose or FFA by skeletal muscle calls or adipocyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or spane expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, cor stimulating proliferation of for the binding of the release of a cycokine from PBMC cells, for stimulating cells, for stimulating cells, in the differentiation of adipocyte cells, for stimulating proliferation of endothelial cells, for stimulating cells, in the differentiation of adipocyte cells, for stimulating sproliferation of endothelial cells, for stimulating center tumour. The oligonucleotide probes cells, for stimulating genomic and cDNA nucleotide sequences or antisense probes. (1) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding contensation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and certification, as chromosome marker, and for generating creening of therapeutically useful reagents, in gene therapy, for chromosome identification, as chromosome marker, and for generating correcting in statioday is useful in diagnostic assays for PRO, a probes. (1) and (11) are useful in diagnostic assays for PRO, a probes contend and transmented the forganerating cells, in generating of the cells and transmented the forganerating and the appendix and forganerating and the propertical and the propertion of PRO in the propertion of PRO in the properties or setum, and 
cell differentiation inhibitor; cytokine release stimulator; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker.
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99US-00380137
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01-DEC-2000; 2000WO-US032678
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Best Local Similarity 66.0
Matches 31; Conservative
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Gerritsen ME, Goddard
Smith V, Stewart TA,
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P-PSDB; ADE33267.
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02-JUN-1999;
25-AUG-1999;
                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                           16-OCT-2003
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Human, secreted and transmembrane protein, PRO; gene; ss;
Tumour necrosis factor alpha release; TWP-alpha release;
glucose uptake modulator; FPA uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inhibitor; cytokine release stimulator; tumour;
lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;
cervical tumour; liver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
                                            Novel human secreted and transmembrane protein PRO4327 cDNA
                                                                                                                                                                                                                                98WO-US012456.
98WO-US014552.
98WO-US017888.
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98WO-US019437
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98WO-US019094
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16;

Pred. No. 45; 0; Mismatches

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2001US-00816744.
2001US-00828366.
2001US-00854208.
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2001US-00860216.
2001US-00866028.
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20-DEC-2000;
28-FEB-2001;
11-FEB-2000;
18-FEB-2000;
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# (GETH ) GENENTECH INC

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

#### WPI; 2003-899790/82. P-PSDB; ADE33819.

Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis.

Claim 2; SEQ ID NO 221; 636pp; English

The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the

cc release of TNF-alpha from human blood, for modulating the uptake of glucose or FRA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation or differentiation of condrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells, con stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating of A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte cells, for stimulating proliferation of endothelial cells, for stimulating of the presence of tumour in a mammal. The tumour is lung, colon, breast, professed, cervical or liver tumour is lung, colon, breast, colon, breast, colon, breast, colon, breast, colon, breast, colon, breast, and servical or liver tumour. The oligonucleotide probes are useful for isolating genomic and cDNA mucleotide sequences or antisense probes. (I) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding increaction. A polymicleotide (I) is encoding (I) is useful in chromosome and gene mapping, in generation of antisense RNA and DNA, in the conformation of therapeutically useful reagents, in gene therapy, for chromosome identification, as chromosome marker, and for generating conforms one identification, as chromosome marker, and for generating conformation of the properties of sources. (I) and (II) are useful in diagnostic assays for PRO, encombinant cell culture or natural conformation of PRO from recombinant cell culture or natural conformation than an uncell in diagnostic sequence encodes a novel human secreted and transmembrane PRO polypeptide. ö Gaps ô 1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; ive 0; Mismatches 16; Indels 0 Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; 31; Conservative Similarity Query Match Best Local ( Matches 

### 1835 ITCTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881 1129 rrrrrrrrrrrrrrrrrrrrr 1083 ð . 연

RESULT 181

ADD79870;

ADD79870 standard, cDNA, 1129 BP

cDNA encoding human PRO polypeptide #111. (first entry) 29-JAN-2004

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNP-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvsacular endothelial cell; glucose; FFA; inner ear utricular supporting cell; periotte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; atticular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration. 

### Homo sapiens.

US2003207417-A1.

07-MAY-2002; 2002US-00140805. 06-NOV-2003

97WO-US005230 31-MAR-1997; 2-JUN-1998 .4-JUL-1998

98WO-US012456. 98WO-US014552. 98WO-US017888. 98WO-US018824. 98WO-US019093. 28-AUG-1998; 10-SEP-1998; 14-SEP-1998;

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2001US-00808689.
2001US-00816744.
2001US-00828366.
2001US-00854208.
    98WO-US019177
98WO-US019330
                                     98WO-US024855
98WO-US025108
                     98WO-US021141
98WO-US022991
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                                                 99WO-US000106
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                17-SEP-1998;
07-OCT-1998;
29-OCT-1998;
29-OCT-1998;
                                    20-NOV-1998;
01-DEC-1998;
05-JAN-1999;
08-MAR-1999;
10-MAR-1999;
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Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ge Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; 2001W3-US017800. 2001US-00874503. 2001US-00882636. 2001US-00886342. 2001US-00924419. 2001US-00927796. 2001US-00931836. 2001US-00028072. 2001US-00866034 2001WO-US020116 2001WO-US021066 2001WO-US021735 2001US-00908827 (GETH ) GENENTECH INC 25-MAY-2001; 01-JUN-2001; 19-DEC-2001; 18-MAY-2001; 25-MAY-2001; 01-JUN-2001; 05-JUN-2001; 14-JUN-2001; 19-JUN-2001; 20-JUN-2001; 29-JUN-2001; 09-AUG-2001; 16-AUG-2001; 21-JUN-2001; 22-JUN-2001; 09-JUL-2001; 06-AUG-2001; 25-MAY-2001; 18-JUL-2001 

New PRO nucleic acid, useful for manufacturing a medicament for diagnosing or treating tumor, for chromosome mapping or for tissue 2003-875867/81. P-PSDB; ADD79871.

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Claim 2; Fig 221; 638pp; English.

typing

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for proliferation or differentiation of chondrocyte cells and a method for celecting the presence of a tumour in a mammal (e.g. adrean), lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polyuncleotides are useful in molecular biology, including uses as hybridasation probes, in chromosome and gene mapping, in generating antisense RNA and bin gene therapy. The polyuncleotides may also constrained either transgenic animals or knock-out animals which are useful in the development and screening of knock-out animals which are useful in the development and screening of knock-out animals which are useful in the development and screening of therapeutically useful.

Complement for treating a condition responsive to the polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of mandochelial cells, for medilating the uptake of glucose or FRA by skeletal muscle cells or adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating differentiation of inner ear utricular supporting cells or T-lymphocyte cells, for medicing endochelial cells or adipocyte cells, for stimulating and or gene expression in periors cells, for stimulating are useful for treating sports injuries and articular cartilage are useful for treating sports-related joint problems, articular cartilage are useful for treating sports-related joint problems, articular encodes a human PRO polypeptide of the invention. Note: The sequence encodes a human PRO polypeptide of the invention.

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

DB 1; Length 1129; Score 21.4; 1.1%;

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for proliferation or differentiation of chondrocyte cells and a method for clon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagners. The PRO polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular modothelial cell; glucose; FPA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
                                    Gaps
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                          1835 ITCTIAATITITCATITCCAGAITICCTICAGITIGGGTTTTGTTT 1881
                                                                                                                                                                                                            1129 TITITITITITITITITITITICAGCIGGCACACACACGCIGGCITITIATI 1083
                                    16; Indels
Pred. No. 45;
0; Mismatches
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01-DEC-2000; 2000WO-US03267B.
19-DEC-2001; 2001US-00028072.
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Best Local Similarity 66.0%;
Matches 31; Conservative
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cof human microvascular endothelial cells, for modulating the uptake of glucose or FRA by skeletal muscle cells or adipocyte cells. for stimulating differentiation of adipocyte cells, for stimulating proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating cells, for inducing endothelial cell tube formation and for treating carious bone and/or cartilage disorders such as sports injuries and arthitis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, or polypeptides are also useful for treating sports-related joint problems, propagated disorders such as various thalasseemias and conditions which may benefit from enhanced local immune system cell infiltration. This captured data for this parent is also available in electronic format
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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10-NOV-2000; 2000WO-US030873.
01-DEC-2000; 2000WO-US32678.
19-DEC-2001; 2001US-00028072.
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P-PSDB; ADE19328.
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nes 31; Conserv
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                                                                                                                                                                                                                                                                                                                                                                          Query Match
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the invention relates to isolated number FKO puppetides (secreted and the propertied) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the relates of themour necrois and the polymucleotides are amethod for stimulating the presence of a tumour in a meanmal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The publication probes, in chromosome and gene mapping, in generating the presence of a tumour in a mammal (e.g. adrenal, lung, publication probes, in chromosome and gene mapping, in generating attients probe polypeptides by recombinant techniques and in attients RNA and bNA and in gene therapy. The polymucleotides may also attients RNA and bNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or attibodies, such as tumours, for stimulating and inhibiting proliferation of the proliferation of adipocyte cells, for stimulating of human microvascular endothelial cells or adipocyte cells, for stimulating the proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating endothelial cell tube formation and for treating endothelial cell tube formation and for treating endothelial cell tube formation and for treating endothelial cell tube formation and for treating endothelial cell tube formation and for treating endothelial cell tube formation and for treating endothelial cell tube formation and for treating endothelial cell tube formation and for treating endothelial cell tube formation and for treating endothelial cell tube formation and for treating endothelial cell tube formation and for
                                                                                                                The invention relates to isolated human PRO polypeptides
and/or cartilage disorders, e.g. arthritis.
                                                        Claim 2; SEQ ID NO 221; 648pp; English.
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Gaps ; 0 1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; tive 0; Mismatches 16; Indels 0; Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; Query Match. Best Local Similarity 66.0%

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Human PRO polynucleotide #111. ADE18775 standard; cDNA; 1129 (first entry) 29-JAN-2004 ADE18775; RESULT 184 ADE18775/c 

Human, gene, ss. PRO, secreted polypeptide, transmembrane polypeptide, tummour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tummour, cancer, adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothalial cell; glucoss; FFA; skeletal muscle cell; adipocyte cell; glucoss; FFA; inner ear utricular supporting cell; T-lymphocyte cell; endothalial cell tube formation; bone disorder; cartilage disorder; endothalial cell tube formation; bone disorder; cartilage disorder; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Homo sapiens

US2003199026-A1

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TNR-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for coloribrate, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also antisense RNA and DNA and in gene therapy. The polynucleotides may also consistent transgenic animals or knock-out animals which are usedin in the development and screening of therapeutically useful reagents. The PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are usedicament for treating a condition responsive to the polypeptides or antibodies; such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for stimulating differentiation of adipocyte cells, for stimulating colliferation of animal expension in periovice cells, for stimulating proliferation of animal expension in periovice cells, for stimulating colliferation of animal endothelial cells or adipocyte cells, for stimulating colliferation of animal animal colliferation of animal animal subporting cells or treating proliferation of animal animal subporting cells or treating cartilage defects, osteodicaments and continues and continues and continues and continues and continues and continues and conditions which associated disorders such as sports injuries and associated disorders such as various thalasseamias and conditions when the former expression in perior cells, in a polar or the propertion of any phenefit from enhanced local infimume system cells i Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis. is also available in electronic format Gaps Gao Filvaroff E, Gao AL, Sherwood S; ·. DB 1; Length 1129; Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; Deforge L, Desnoyers L, Filvard A, Godowski PJ, Gurney AL, Sher Tumas D, Watanabe CK, Wood WI, Indels 16; The sequence data for this patent is also availerom USPTO at segdata.uspto.gov/sequence.html. Pred. No. 45; ; Mismatches 1.1%; Score 21.4; 66.0%; Pred. No. 45 Claim 2; SEQ ID NO 221; 636pp; English. · 0 20-MAY-2002; 2002US-00152393, 03-MAR-2000; 2000US-0187202P. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072. Goddard A, Local Similarity 66.0 nes 31; Conservative Beresini M, (GETH ) GENENTECH INC. Gerritsen ME, Goddard Smith V, Stewart TA, WPI; 2003-900157/82. P-PSDB; ADE18776. Baker KP, Query Match Best Loca Matches 

1835 TICTIAATITITICATTICCAGAITICCTICAGITITGGGTTTTGTTT 1881 1129 rrrrrrrrrrrrrrrrrrrradecrecacacadecrederrrrrrrr 2971/c ADE42971 standard; cDNA; 1129 RESULT 185 ADE42971/c ID ADE42 XX ò g

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WPI;
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C cells, for inducing endothelial cell tube formations and artifices and artificals are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rhematoid arthritis. PRO polypeptides which stimulate the release of proteoglycan articular cartilage are useful for treating various mannalian hammologicated disorders such as various prodessing are useful for treati
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                                                                                                                                               Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tummour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tummour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FF; inner ear utricular supporting cell; pericyte cell; endothelial cell; adipocyte cell; pericyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin associated disorder thalassaemia; immune system cell infiltration.
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                           Human PRO polynucleotide #111.
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01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
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                                                            (first entry)
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Gerritsen ME, Goddard A,
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Smith V, Stewart TA,
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                sequence represents a human PRO polynucleotide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at segdata.uspto.gov/sequence.html.
may benefit from enhanced local immune system cell infiltration. This
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Best Local Similarity 66.0
Matches 31; Conservative
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Gao W;

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ga Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

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24-FEB-2000;
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(GETH ) GENENTECH INC

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNP-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for proliferation or differentiation of chondrocyte cells and a method for detecting the presence of tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidhey, cervical and liver tumours). The polymucleotides are useful in molecular bloicgy, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymucleotides may also consecular in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are generating either transgenic animals or knock-out animals which are medicament for treating arcening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for midpodies are used in hisbiting proliferation of inner ear unricular or proliferation of of inner ear unricular supporting cells, for inducing endothelial cells, for modulating the upcase of proliferation of inner ear urricular supporting cells, for inducing endothelial cells, for modulating the proliferation of inner ear urricular supporting cells, for inducing endothelial cells of such as sports injuries and cells, for inducing endothelial cell the release of proteoglycans from cartilage defects, osteoarthitis and rheumatoid arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage defects, osteoarthitis and rheumatoid arthritis in PRO polypeptides which stimulations cells, for may benefit from enhance of sequence repre Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis. Human; gene; ss; PRC; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNR-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; Gaps . 0 1835 ITCTIAATTITICATTICCAGATTICCTICAGTTIGGGTTITGTTT 1881 DB 1; Length 1129; 1129 Trritritritritritricascrescacadascrescritritrit 1083 Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; 1.1%; Score 21.4; DB 1; Length 1.66.0%; Pred. No. 45; cive 0; Mismatches 16; Indels from USPTO at segdata.uspto.gov/seguence.html. cDNA encoding human PRO polypeptide #111. Claim 2; Fig 221; 638pp; English ADE22646 standard; cDNA; 1129 BP (first entry) Best Local Similarity 66.0 Matches 31; Conservative WPI; 2003-900168/82. P-PSDB; ADD95761. 29-JAN-2004 ADE22646; Query Match RESULT 187 ADE22646//
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skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endchelial cell tube formation; bone disorder; axtilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
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2000WO-US030873. 2000WO-US032678. 2000US-00747259. 2000WO-US034956. 2001US-00796498. 2001WO-US019692. 2001US-00887879. 2001WO-US020116. 2001US-00802706. 2001US-00808689. 2001US-00816744. 2001US-00828366. 2001US-00854208. 2001US-00854280. 2001US-00860216. 2001US-00866028. 2001US-00866034. 2001WO-US017092. 2001US-00872035. 2001WO-US017800. 2001WO-US006666. 2001US-00874503 001WO-US021066 2001US-00924419. 2001US-00028072 2001US-00908827 Baker KP, Beresini M, De Gerritsen ME, Goddard A, Stewart TA, (GETH ) GENENTECH INC. WPI; 2003-900169/82. P-PSDB; ADE22647. 24-AUG-2000; 2 08-NOV-2000; 2 10-NOV-2000; 2 01-DEC-2000; 20-DEC-2000; 20-DEC-2000; 28-FEB-2001; 28-FEB-2001; 01-MAR-2001; 09-MAR-2001; 14-MAR-2001; 22-MAR-2001; 05-APR-2001; 10-MAY-2001; 10-MAY-2001; 18-MAY-2001; 25-MAY-2001; 25-MAY-2001; 19-DEC-2001; 19-JUN-2001; 25-MAY-2001; 05-JUN-2001; 20-JUN-2001; 29-JUN-2001; Smith V, 

3 Gao Deforge L, Desnoyers L, Filvaroff E, G. A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z;

Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis.

Claim 2; Fig 221; 638pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TMF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hypridisation probes, in chromosome and gene mapping, in generating hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are generating either transgenic animals or knock-out animals which are reagents. The PRO polypeptides or antibodies are used in preparing a reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or

2000WO-US004341. 2000WO-US004342.

2000WO-US008439

30-MAR-2000;

2000WO-US000376

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antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for modulating the uptake of glucose or FRA by Skabtata musche calls or adipocyte cells, for stimulating circular such calls or adipocyte cells, for stimulating proliferation of anner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and articular cartilage are useful for treating sports relaced joint problems, for markinge are useful for treating sports relaced joint problems, controllar cartilage defects, osteoathritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin may benefit from enhanced local immune system cell infiltration. This sequence date for this parent is also available in electronic format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format from the format format 
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Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps . 0 DB 1; Length 1129; Indels 1.1%; Score 21.4; DB 1; T66.0%; Pred. No. 45; Ative 0; Mismatches 16; Query Match
Best Local Similarity 66.0
Matches 31; Conservative

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cDNA encoding human PRO polypeptide #111. 29-JAN-2004 (first entry) ADD78764; 

Human, gene; ss, PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FRA; skeletal muscle cell; dipocyte cell; pericyte cell; inner ear utricular supporting cell; pericyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteogly/roan; articular cartilage defect; ostecarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration. US2003203429-A1. Homo sapiens.

30-OCT-2003

22-APR-2002; 2002US-00127900.

05-JUN-2000; 2000US-0209832P. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC.

Gao W; Deforge L, Desnoyers L, Filvaroff E, Gr A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Beresini M, De 4E, Goddard A, Stewart TA, Baker KP, Ber Gerritsen ME, Smith V,

WPI; 2003-875636/81. P-PSDB; ADD78765.

ō New isolated, secreted and transmembrane PRO polypeptides and acids, useful for the diagnosis, prevention and/or treatment o

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the invention albe an include which specifically binds to a PRO polypeptide, a method for stimulating the factor-alpha (TWP-alpha) from human blood, a method for stimulating the presence of a tumur in a mammal (e.g. adrenal, lung, colin, breast, prostate, rectal, kidney, cervical and liver tumours). The colymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating colon, breast, prostate, propolypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are generating either transgenic animals or knock-out animals which are useful in the development and screening of therapy. The polypeptides or antibodies are used in preparing a medicament for tracating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for modulating the uptake of glucose or FRA by skeletal muscle cells, for stimulating differentiation of adipocyte cells, for stimulating coliferation of inner ear uricular supporting cells, for inducing endothelial cells or adipocyte cells, for stimulating effects and useful for treating sports-related joint problems, archidas are useful for treating sports-related joint problems, archidas are useful for treating sports-related joint problems, archidas are useful for treating sports-related joint problems, archidas a human PRO polypeptides and manaled local immune system cell infiltration. Note: The sequence encodes a human PRO polypeptide of the invention. Note: The Expense of production of sequence and a human pro polypeptide of the inspect of the propertion of sequence and a human encodes a human pro polypeptide of the inspect of prop
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such as lung, colon, breast, prostate, rectal, cervical and/or liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.1%; Score 21.4; DB
66.0%; Pred. No. 45;
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence data for this patent is also a
the USPTO website at seqdata.uspto.gov.
                                                                             Claim 2; Fig 221; 637pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches
à
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Novel human secreted and transmembrane protein PRO4327 cDNA. BP. ADE32714 standard; cDNA; 1129 29-JAN-2004 (first entry) ADE32714; RESULT 189 ADE32714/c 

Human; secreted and transmembrane protein; PRO; gene; ss; Tumour necrosis factor alpha release; TNR-alpha release; glucose uptake modulator; prA uptake modulator; cell proliferation stimulator; cell differentiation stimulator; cell differentiation inhibitor; cytokine release stimulator; tumour; colon tumour; breast tumour; protestet tumour; rectal tumour; cervical tumour; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker.

Homo sapiens

US2003194766-A1

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The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (1). (1) is useful for stimulating the criesase of TNF-alpha from human blood, for modulating the uptake of glucose or FFRA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating proliferation of T-1ymphocyte cells, for stimulating cells, for inhibiting the binding of A-peptide to factor VIIA, for inhibiting the binding of the presence of tumour in a mammal. The tumour is lung, colon, breast, cells, for stimulating genomic and cDNA nucleotide sequences or are useful for isolating genomic and cDNA nucleotide sequences or antisense probes. (1) is also useful as therapeutic agent. PRO is useful or inseastion of PRO polypeptide, for generating transgenic animals or concour animals which in turn are useful in the development and screening of therapeutically useful in the development and screening of therapeutically useful in the development and screening of therapeutically useful in the development and screening of therapeutically useful in the development and screening of therapeutically useful in the development and screening of therapeutically useful in the development and screening of therapeutically useful in the development and screening of therapeutically useful in diagnostic assays for PRO, ergebecting its expression in specific cells, tissues or serum, and for sentence encodes the faithfication of PRO from recombinant cell culture or natural contracts. (1) and (11) are useful in researce or natural encodes.
                                                                                                                                                                                                                                                                                                                                                                          Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes
                                                                                                                                                                                                                        3
                                                                                                                                                                                                                      Gao 1
                                                                                                                                                                                                                   Beresini M, Deforge L, Desnoyers L, Filvaroff E, G?
.ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           urces, (I) and (II) are useful for tissue typing. This movel human secreted and transmembrane PRO polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; SEQ ID NO 221; 636pp; English.
                                                                                       05-JUN-2000; 2000US-0209832P.
01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
                                               14-MAY-2002; 2002US-00145874
                                                                                                                                                                           (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                               WPI; 2003-899785/82.
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    16-OCT-2003
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Smith V,
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Gaps ô 1835 TICTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTT 1881 1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; ive 0; Mismatches 16; Indels 0 rirrrrritirrritrakkakakakakakakakaka 1083 Query Match
Best Local Similarity 66.0
Matches 31; Conservative 1129 '

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ADE42406 standard; cDNA; 1129 BP. Human PRO polynucleotide #111; (first entry) 29-JAN-2004 ADE42406; ADE42406/ X B X B X B X B X

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; ostecarchritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Homo sapiens.

US2003199032-A1.

23-OCT-2003.

28-MAY-2002; 2002US-00156844.

03-MAR-2000; 2000US-0187202P. 01-DEC-2000; 2000MO-US032678. 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC.

Gao W; Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ga Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-900161/82. P-PSDB; ADE42407 Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis.

Claim 2; Fig 221; 636pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TWP-alpha) from human blood, a method for stimulating the proliferation of chondrocyte cells and a method for proliferation of differentiation of chondrocyte cells and a method for colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymuclectides are useful in molecular biology, including uses as antipolastion probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymuclectides may also colon preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a metibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for modulating the uptake of glucose or FRA by skeltal muscle cells, for stimulating cells, for stimulating cells, for stimulating cells, for inducing endothelial cells, for modulating the uptake of strious bone and/or cartilage disorders such as sports injunies and arthritis. PRO polypeptides which stimulate the release of proteoglycans or arthritis. PRO polypeptides which stimulate the release of proteoglycans cells, for inducing endethelial cell the formation and for treating various bone and/or cartilage disorders such as sports injunies and arthritis. PRO polypeptides which stimulate the release of proteoglycans cells, for inducing endethelial cells the properties of proteoglycans or arthritis. PRO polypeptides which stimulate the release of proteoglycans are also useful for treating sports-related joint problems, ascendants a human PRO polymorione cells, for enarching endethelial cel USPTO at segdata.uspto.gov/sequence.html.

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

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Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-875868/81
0;
                                                                                                                                                                 Human; gene, ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prestate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
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       Length 1129;
                                         1835 TICTIAATITITICATITICAGATITICCTICAGTITIGGGTTTTGTTT 1881
                                                 1129 TTTTTTTTTTTTTTTCAGCTGGCACACAGGCTGGGTTTTTATT 1083
                       Indels
                       16;
      Query Match
Best Local Similarity 66.0%; Pred. No. 45;
Matches 31; Conservative 0; Mismatches 16;
                                                                                                                                                   cDNA encoding human PRO polypeptide #111.
                                                                                                 ADD80422 standard; cDNA; 1129
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98WO-US014552.
98WO-US017888.
98WO-US018824.
98WO-US019093.
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98WO-US022991.
98WO-US022992.
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98WO-US025108.
99WO-US000106.
99WO-US005028.
99WO-US005190.
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98WO-US019330.
98WO-US019437.
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99WO-US012252.
99WO-US020111.
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99WO-US028634.
99WO-US028551.
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99WO-US008615
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                                                                                                                                   29-JAN-2004 (first entry)
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                                                                                                                                                                                                                                                                 Homo sapiens.
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02-JUN-1999;
01-SEP-1999;
08-SEP-1999;
13-SEP-1999;
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01-DEC-1998;
05-JAN-1999;
08-MAR-1999;
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                                                                                                                  ADD80422;
                                                                                  RESULT 191
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2001US-00796498.
2001WO-US006520.
2001WO-US006666.
2000WO-US000219.
2000WO-US000277.
2000WO-US000376.
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2001US-00866028.
2001US-00866034.
                                                 2000WO-US003565
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                                                                   2000WO-US004341
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10664775-3.rng

P-PSDB; ADD80423.

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNP-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The proliferation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymucleotides may also antisense RNA and DNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful canequicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of thuman microvascular endothelial cells, for modulating the uptake of glucose or FRA by skeletal muscle cells, for stimulating differentiation of anipocyte cells, for stimulating che proliferation of inner ear usticular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating che proliferation of inner ear usticular supporting cells, for stimulating che proliferation of since and arrival as sports injuries and arrhitis. PRO Polypeptides which stimulate the release of proteoglycans containing and carthitis and carthitis and cartilage disorders such as sports injuries and arrhitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin-associated disorders such as various thalasseamias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence encodes a human PRO polypeptide of the invantion. Note: The sequence data for this patent is also available in electronic format from
                                                 New PRO nucleic acid, useful for manufacturing a medicament for diagnosing or treating tumor, for chromosome mapping or for tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the USPTO website at segdata.uspto.gov.
                                                                                                                                                                        Claim 2; Fig 221; 638pp; English.
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Gaps .; 0 DB 1; Length 1129; Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; Ouery Match 1.1%; Score 21.4; DB 1; Length 1 Best Local Similarity 66.0%; Pred. No. 45; Matches 31; Conservative 0; Mismatches 16; Indels

ò g

ADD89450 standard; cDNA; 1129 BP ADD89450; RESULT 192 

29-JAN-2004 (first entry)

Human PRO polynucleotide #111.

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; carcilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumarcid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Homo sapiens

US2003199028-A1.

23-OCT-2003

22-MAY-2002; 2002US-00153552.

03-MAR-2000; 2000US-0197202P. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC.

3 Gao Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ge Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-900158/82. P-PSDB; ADD89451 Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis.

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. adrenal, lung, certification probes, in chromosour and newhod for polynucleotides are useful in molecular biology, including uses as colynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also consist in preparing PRO polypeptides by recombinant techniques and in reagents. The PRO polypeptides by recombinant techniques and in reagents. The PRO polypeptides by recombinant techniques and in reagents. The PRO polypeptides or antibodies are used in preparing condition responsive to the polypeptides or antibodies, such as tumours, for attibudiating of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing condition responsive to the polypeptides or antibodies, such as tumours, for stimulating of therapeutically useful colluding antibodies, such as tumours, for stimulating or the polypeptides or cells, for stimulating the uptake of stimulating of finer ear utricular supporting cells, for stimulating cells for stimulating cells, for inducing endothelial cells, for modulating the uptake of stimulating cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycan cells, for inducing endothelial cell tube formation and for treating colludar attributes and secular second second cartilage disorders such as sports injuries and conditions which associated disorders such as various bane and/or cartilage are useful for treating sports related joint problems. The sequence represents a human PRO polypurione The sequence data for this patent is also avai from USPTO at seqdata.uspto.gov/sequence.html.

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps ; 0 DB 1; Length 1129; 16; Indels 1.1%; Score 21.4; Di 66.0%; Pred. No. 45; iive 0; Mismatches Query Match
Best Local Similarity 66.03
Matches 31; Conservative

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8 g

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in amammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymucleotides may also attisense RNA and DNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are used in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides of numbedies, such as tumours, for simulating and inhibiting proliferation of or gene expression in pericyte cells, for stimulating proliferation of or gene expression in pericyte cells, for stimulating cells, for inducing endothelial cell tube formation and for treating cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilades which stimulate the release of proteoglycans arthritis. PRO polypeptides which stimulate the release of proteoglycans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis.
                                                                                                                                                                                                                           Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; inner ear uscle cell; dajpcoyte cell; pericyte cell; endothelial cell; supporting cell; pericyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports alphury; proteoglyron; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deforge L, Desnoyers L, Filvaroff E, Ga
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 221; 637pp; English.
                                           ADE40734 standard; cDNA; 1129 BP
                                                                                                                                                                                    Human PRO polynucleotide #111.
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01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
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                                                                                                                                 29-JAN-2004 (first entry)
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P-PSDB; ADE40735.
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                                                                                          ADE40734;
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RESULT 193
                        ADE40734/
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from cartilage are useful for treating sports-related joint problems, atticular cartilage defects, osteoarthritis and rheumatoid arthritis. PRC polypeptides are also useful for treating various mammalian baemoglobin-associated disorders such as various thalasaeamias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polynucleotide of the invention. Note: The equence data for this patent is also available in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FRA; seeleral muscle cell; adipocyte cell; gricyte cell; inner ear utricular supporting cell; pricyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; shound intitury; proteoglycan; articular cartilage defect; ostecarthritis; sheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                                                                             DB 1; Length 1129;
                                                                                                                                                                                                                                                                                                            1835 ITCTTAATTTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881
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                                                                                                                                                                                    Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
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                                                                                                                                               from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                           / Match
Local Similarity 66.0%; Pred. No. 45;
nes 31; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PRO polynucleotide #111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADE04533 standard; cDNA; 1129
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01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-900163/82.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE04533;
                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 194
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proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as colon, breast, and DNA and in gene therapy. The polynucleotides may also antisense RNA and DNA and in gene therapy. The polynucleotides may also consistence RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgence and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of the proliferation of adipocyte cells, for stimulating collection of stimulating and inhibiting proliferation of inner ear utricular supporting cells, for stimulating consideration of inner ear utricular supporting cells, for stimulating consideration of inner ear utricular supporting cells, for stimulating consideration of inner ear utricular supporting cells, for inauting and childing sports related of joint problems, articular cartilage are useful for treating sports related of joint problems, articular cartilage defects, osteoatthritis and rheumatoid arthritis. Proliferated disorders such as various thatasseamias and conditions which may benefit from enhanced local immune system cell infiltration. Note: consumption at earlier a human PRO polymolectide of the invention. Note: consumption at earlier and an and an analyse and an and an analyse and an and an and an analyse consideration and an analyse and an analyse and an also available in electronic format from the profile.
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                                                  Query Match 1.1%; Score 21.4; DB 1; Length 1129; Best Local Similarity 66.0%; Pred. No. 45; Matches 31; Conservative 0; Mismatches 16; Indels 0.
                                                                                                                                                                  1835 TICTIAATTITICATTICCAGATTICCTICAGITIGGGTTITGTTT 1881
                                                                                                                                                                                                                    1129 rrrrrrrrrrrrrrrrrcagcregeacacacacacacacacacregarrrrarr 1083
Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
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Novel human secreted and transmembrane protein PRO4327 cDNA.
  ADC80958 standard; cDNA; 1129 BP
                  (first entry)
                  15-JAN-2004
          ADC80958;
ADC80958/
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Human; secreted and transmembrane protein; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNT-alpha; chondrocyte; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose uptake modulator; FFA uptake modulator; cell proliferation; cell differentiation; Skeletal muscle cell; adipocyte cell; endothelial cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; networatoid arthritis; haemoglobin-associated disorder; thalassaemia; immune system cell infiltration; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker; gene; SS.

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05-JUN-2000; 2000US-0209832P.
                                  30-MAY-2002; 2002US-00158785
15-MAY-2003
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JS2003092115-A1. Homo sapiens.

Human PRO polynucleotide #111.

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO invention also relates to an antibody which specifically binds to a PRO invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. adrenal, lung, collecting the presence of a tumour in a mammal (e.g. adrenal, lung, collecting the presence of a tumour in a mammal (e.g. adrenal, lung, collecting the presence of a tumour in a mammal (e.g. adrenal, lung, collecting the presence of a tumour in the constant of the polymucleotides may also polymucleotides are useful in Achomosome and gene mapping, in generating chertaing either transgenic animals or knock-out animals which are useful in the development and screening of therapeutical which are useful in the development and screening of therapeutical which are useful in the development and screening of therapeutically which are considered in the development and screening of knock-out animals which are consecuted in the development and screening of knock-out animals which are consecuted in the development and screening of knock-out animals which are the propagatides or antibodies are useful in preparing a tumours, for stimulating of the prolympetides or antibodies are used in preparing a condition responsive to the polympetides or attribuding and inhibiting proliferation of stimulating and inhibiting proliferation of stimulating the proliferation of inference are supported cells or tradition and provide cells for inducing endothelial cell tube formation and for traditing various bone and/or cartilage defects, osteoarthritis and rhemmacoid for problems, articular cartilage are also useful for treating sports related joint and arthritis. PRO polypeptides which may be a unann PRO polympetide are al
                                                                                                                                                                                                                                                  New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or
                                                                                         Gao W;
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                                                                                    Deforge L, Desnoyers L, Filvaroff E, G:
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Fig 221; 637pp; English.
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19-DEC-2001; 2001US-00028072.
                                                                                                                    Gerritsen ME, Goddard A,
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                                                                                                                                          Stewart TA,
                                                 (GETH ) GENENTECH INC.
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Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; trumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; timour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; Tlymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; cheumatoid arthritis; haemoglopin-associated disorder thalassaemia; immune system cell infiltration. 99WO-US031243 99WO-US031274 2000WO-US000277 2000WO-US000376 2000WO-US004341 2000WO-US004342 16-APR-2002; 2002US-00123912 98WO-US019177 98WO-US019330 99WO-US028409 2000WO-US003565 98WO-US017888 98WO-US019093 98WO-US019094 98WO-US019437 98WO-US022992 98WO-US024855 98WO-US025108 99WO-US000106 99WO-US005190 99WO-US008615 99WO-US012252 99WO-US020111 99WO-US020594 99WO-US021090 99WO-US021547 99WO-US023089 99WO-US028214 99WO-US028313 99WO-US028634 99WO-US028565 99WO-US030095 99WO-US030720 98WO-US022991 99WO-US028301 99WO-US028551 99WO-US028564 US2003100087-A1. 01-DEC-1999; 02-DEC-1999; 02-DEC-1999; 18-FEB-2000; Homo sapiens -JAN-2000; 05-OCT-1999; 29-NOV-1999; -DEC-1999; -DEC-1999; -DEC-1999; 30-DEC-1999 02-DEC-1999 16-DEC-1999 NOV-1999 29-MAY-2003 20-APR-1999 30-NOV-1999 

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2001WO-US006666
2001US-00802706
2001US-00808689
2001US-0081844
2001US-00828366
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2001US-00924419.
2001US-00927796.
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2000WO-US034956.
2001US-00796498.
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2001US-00860216.
2001US-00866028.
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2001WO-US021735.
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2001US-00887879
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                 17-MAY-2000;
                                             23-AUG-2000;
24-AUG-2000;
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09-AUG-2001
                                                                                   28-FEB-2001
01-MAR-2001
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                                                                                                                0-MAY-2000
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## (GETH ) GENENTECH INC

Gao Deforge L, Desnoyers L, Filvaroff E, Ga A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Baker KP, Beresini M, Gerritsen ME, Goddard Smith V, Stewart TA,

3

## WPI; 2004-008956/01. P-PSDB; ADD76407.

New PRO nucleic acid, useful for recombinantly producing a PRO polypeptide and for manufacturing a medicament for diagnosing or treating a tumor.

## Claim 2; Fig 221; 638pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polyuclectides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymuclectides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymuclectides may also be used in preparing PRO polypeptides by recombinant techniques and in

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generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are useful in proparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of the man microascular endochelial cells, for modulating the uptake of glucose or FRA by skeletal muscle cells, for modulating the uptake of stimulating differentiation of adipocyte cells, for stimulating the proliferation of orgene expression in periove cells, for stimulating the proliferation of inner ear untricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and carthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, associated disorders such as various thalassaemias and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin-associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polynucleotide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at sequence.html.
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ô Gaps ; 0 DB 1; Length 1129; 1835 TICHTAATHTHTCATHTCCAGATHTCCTTCAGTHTGGGTTTTGTTT 1881 1129 ritritritritritritritricacciccacacacacacacacaciccititrari 1083 1.1%; Score 21.4; DB 1; Length 1 66.0%; Pred. No. 45; ative 0; Mismatches 16; Indels Conservative Local Similarity es 31; Conserv Query Match Matches ð a

770/c ADD87770 standard; cDNA; 1129 BP. Human PRO polynucleotide #111. (first entry) 29-JAN-2004 RESULT 197 ADD87770/ 

Human, gene, ss, PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrend; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FRA; skeletal muscle cell; adipocyte cell; glucose; FRA; inner ear utricular supporting cell; pericyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Homo sapiens.

US2003092113-A1.

15-MAY-2003.

16-MAY-2002; 2002US-00147523.

09-DEC-1999; 99US-0170262P. 01-DEC-2000; 2000WO-US032679. 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC

Gao W; Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ge Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; WPI; 2004-020237/02.

P-PSDB; ADD87771.

New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or cancer

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynuclectides encoding them. The invention also relates to an antibody which specifically binds to a PRO prolypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TWP-alpha) from human blood, a method for stimulating the prolypeptides of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polyprodes are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also the useful in the development and screening of therapeutically useful cuseful in the development and screening of therapeutically useful useful in the development and screening of therapeutically useful andicament for treating a condition responsive to the polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human miscovascular endothelial cells, for modulating the uptake of glucose on FRA by skeletal muscle cells, for adipocyte cells, for stimulating the proliferation of or gene expression in perioyte cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating cells, for inducing endothelial cell tube formation and for treating variation bone and/or cartilade disorders such as sports injuries and continued to the proless of proliferation of a proless of arthuitis. PRO polypetides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems. Atticular cartilage defects, osteoarthitis and rheumatond arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobinassociated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This from esquence represents a human PRO polymucleocide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;

Gaps . 0 DB 1; Length 1129; 16; Indels 1.1%; Score 21.4; D. 66.0%; Pred. No. 45; ive 0; Mismatches Local Similarity 66.0 Query Match Matches

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ADD86174/c

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ADD86174 standard; cDNA; 1129 BP. ADD86174;

Human PRO polynucleotide #111. 29-JAN-2004 (first entry)

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tummour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tummour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; glucose; FFA; inner ear utricular supporting cell; pericyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarchritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; &&&&&&&&&&

Gao W;

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNP-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for colon, breast, prostate, rectal, kidney, cervical and liver tumours). The proliferation probes, in chromosome and gene mapping, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also antisense RNA and DNA and in gene therapy. The polynucleotides may also generating either transgenic animals or knock-out animals which are used in preparing PRO polypeptides or knock-out animals which are used in the development and screening of therapeutically useful captument for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of or gene expression in pericyte cells, for stimulating collecation of or gene expression in pericyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating collieration of or gene expression in pericyte cells, for stimulating collieration of anipocyte cells, for stimulating collieration of anipocyte cells, for stimulating collieration of anipocyte cells, for stimulating endochelial cell tube formation and for treating colliers are useful or artifage disorders such as sports injuries and arthiris. PRO polypeptides which stimulate the release of proteoglyvans of the prolieration of the prolieration and for treating content of the prolieration of the prolieration and for treating content of the prolieration of the prolieration of the prolieration and for treating columns.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 PRO4978, useful in molecular biology, chromosome and gene mapping, generating antisense RNA and DNA, and in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                          Deforge L, Desnoyers L, Filvaroff E, Ga
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Fig 221; 637pp; English.
immune system cell infiltration.
                                                                                                                                                                                                                                                      05-JUN-2000; 2000US-0209832P.
01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
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                                                                                                                                                                                                                                                                                                                                                                                                       Baker KP, Beresini M,
Gerritsen ME, Goddard
Smith V, Stewart TA,
                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-021363/02.
P-PSDB; ADD86175.
                                                                                                    US2003203440-Al.
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may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polynucleotide of the invention. Note: The sequence data for this patent is also available in electronic format Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; from USPTO at segdata.uspto.gov/sequence.html.

PRO

Gaps 0 Indels 16; DB 1; Score 21.4; DB Pred. No. 45; 0; Mismatches 1.1%; Conservative Query Match Best Local Similarity Matches 31, Conserv

1835 ITCTTAATITITICATITICCAGATITICCTTCAGTITIGGGTTTTGTTT 1881 1129 rirrirririririririririris decres de cade cientaririra de 1083

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for certification or differentiation of chondrocyte cells and a method for certification or differentiation of chondrocyte cells and a method for certification broase, in chromosome and gene mapping, including uses as chybridisation probes, in chromosome and gene mapping, in generating antisense RNA and bnNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful.

C useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for modulating the uptake of glucose or FRA by Skeletal muscle cells, for adipocyte cells, for stimulating the proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FPA; skeletal muscle cell; adipocyte cell; periovte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration. New secreted and transmembrane PRO polypeptide and nucleic acid encoding it, for use in gene therapy, as diagnostic markers for the presence of a disease condition, or as therapeutic targets for treating tumors, diabetes, or arthritis. Gao Deforge L, Desnoyers L, Filvaroff E, Ga A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Claim 2; Fig 221; 637pp; English. ADE75622 standard; cDNA; 1129 BP. Human PRO polynucleotide #111. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072. 20-MAY-2002; 2002US-00152405. (first entry) Beresini M, NE, Goddard A Stewart TA, T (GETH ) GENENTECH INC. WPI; 2004-051576/05. P-PSDB; ADE75623. US2003211571-A1 Homo sapiens. 03-MAR-2000; 29-JAN-2004 13-NOV-2003 Baker KP. Gerritsen Smith V, ADE75622; 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or
various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobinassociated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polymucleotide of the invention. Note: The sequence data for this patent is also available in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; periove cell; inner ear utricular supporting cell; T-lymphocyte cell; sports injury; proteoglycan; articular cartilage disorder; sports injury; proteoglycan; articular cartilage dect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
                                                                                                                                                                                                                                                                               Gaps
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                    from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                      Score 21.4; I
Pred. No. 45;
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19-DEC-2001; 2001US-00028072.
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ME, Goddard A,
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Gerritsen ME,
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cc polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the problemation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymucleotides may also antisense RNA and DNA and in gene therapy. The polymucleotides may also consistent in the development and screening of therapeutically useful creagent in the development and screening of therapeutically useful creagents. The RNO polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of furner endothehalial cells, for modulating the uptake of glucose or FFA by skeletal muscle cells, for addipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating colleration of inner ear utricular such as sports injuries and cells, the proliferation of for gene expression in pericyte cells, for stimulating content of inner ear utricular such as sports injuries and arthritis. PRO polypeptides which stimulate the release of protecolly arthritis. PRO polypeptides which stimulate the release of protecollar arthritis. PRO polypeptides which stimulate the release of protecollar arthritis and nematical cell for treating sports-related joint problems, arthritis penetic from cartilage defects, ostecarthritis and rheumatoid arthritis. PRO polypeptides are useful for treating various mammalian haemoglobin-associated disorders such as various thalassemias and conditions which sequence encodes a human PRO polypeptide of the invention. Note: The Sequence date for this patent is also available in electronic format from the colones a human PRO polypeptide of the invention. N
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nes 31; Conservative
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01-DEC-2000;

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a.PRO polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TNF-alpha) from human.Dlood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as thyridisation probes, in chromosome and gene ampping, in generating charter ansigning and the polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in seful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for modulating the uptake of all minds and all properties or antibodies of the polypeptides or all properties or antibodies of the polypeptides or antibodies of the polypeptides or antibodies or antibodies cells, for modulating the uptake of all minds.
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                                                                                                                                                                                                                                                                                                    New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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19-DEC-2001; 2001US-00028072.
                                                                                                            Beresini M, ME, Goddard PStewart TA, T
                                                       (GETH ) GENENTECH INC.
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Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
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SEXEXEXEX
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cDNA encoding human PRO polypeptide #111.

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tummour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tummour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FPA; seeletal miscle cell; adipocyte cell; pericyte cell; endpocyte cell; pericyte cell; endothelial cell; prostagy cell; praphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; endothelial printy; proteoglycan; articular cartilage defect; osteoarthiits; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration. 

US2003092111-A1

15-MAY-2003.

03-MAY-2002; 2002US-00137869.

03-MAR-2000; 2000US-0187202P. 01-DEC-2000; 2000WO-US032678. 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC.

Gao Deforge L, Desnoyers L, Filvaroff E, Ga A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Beresini M, 1 ME, Goddard A Stewart TA, T Baker KP, Gerritsen Smith V,

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WPI; 2004-020236/02. P-PSDB; ADE24394.

New secreted and transmembrane nucleic acid useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome, or cancer.

Claim 2; Fig 221; 637pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. adream) lung, or proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adream) lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymuclectides are useful in molecular biology, including uses as hypridisation probes, in chromosome and gene mapping, in generating antisense RNA and BNA and in Gene therapy. The polymuclectides may also be used in preparing RNO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful.

CC persecting either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful.

CC reagents. The PRO polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or attribodies, such as tumours, for stimulating and inhibiting proliferation of thuman microvascular endothelial cells, for modulating the uptake of slucose or FPA by skeletal muscle cells, for stimulating differentiation of adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating and confirming the proliferation of or gene expression in periopte cells, for stimulating the proliferation of funer ear utricular supporting cells or Tlymphocyte cells, for inducing endothelial cell the formation and for treating various mannal cartilage are useful for treating sports injuries and articular cartilage are useful for treating sports-related joint problems, articular cartilage are useful for treating sports-related joint proble

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                                                                                                                                                                                                                                                                                                                                                                                                                    gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
Smith V, Stewart TA, Tumas D, Matanabe CK, Wood WI, Zhang Z;
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Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
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30-MAR-2000; 2000US-00380137.
30-MAR-2000; 2000WO-US008439.
01-DEC-2000; 2000WO-US032678.
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                                                           Similarity
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be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of thuman microvascular endothelial cells, for modulating the uptake of glucose or FPA by skeletal muscle cells, for stimulating the uptake of proliferation of or gene expression in periotte cells, for stimulating proliferation of inner ear utricular supporting cells, for stimulating to the proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating carbinates and arthritis. PRO polypeptides are useful for treating sports-related joint problems, articular cartilage disorders such as sports injuries and articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence tepresents a human PRO polymucleotide of the invention. Note:

The sequence data for this patent is also available in electronic format
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                                                                                                                                                                                                                                                                                                                                                                                                                                       from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 21.4;
Pred. No. 45;
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98WO-US019330.
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Best Local Similarity 66.0
Matches 31; Conservative
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17-SEP-1998;
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ADE89084/c
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98WO-US024855.
98WO-US025108.
99WO-US000106.
99WO-US005028.
99WO-US005190.
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99WO-US020594.
99WO-US020944.
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99WO-US030095.
99WO-US030911.
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99WO-US021547
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99WO-US030720
    98WO-US022991
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99WO-US028564
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11-FEB-2000;
18-FEB-2000;
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28-FEB-2001;
28-FEB-2001;
01-MAR-2001;
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24-FEB-2000;
24-FEB-2000;
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22-DEC-1999;
30-DEC-1999;
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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymuleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the prosence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and brook polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies such as tumours, for stimulating and inhibiting proliferation of funce or stimulating and inhibiting middle proliferation of or gene expression in pericyte cells, for stimulating the proliferation of adoptore cells, for stimulating effected in of adoptore cells, for stimulating effected in cell tube formation and for treating various bene and/or cartilage disorders such as sports injuries and carthritis and shemmed effects of prolipeptides are useful for treating sports-related joint problems, articular cartilage defects, osteoarthitis and rhemmatoid arthritis. PRO polypeptides which stimulate the release of proteoglycan arthritis and member and success such as various thalassaemias and conditions which may benefit from enhanced local immune system cells in filteration. One of the sequence represents a human PRO polypeptides or a limit problems, articular cartilage are also useful for treating various mammalian hamoglobin. The propose of the propertion of the propertion of the propertio
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                                                                                                                                                                                                                                                                                                                                                                                                                    Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ga
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                2001US-00872035.
2001WO-00817800.
2001US-0088243.
2001US-0088342.
2001US-0088342.
2001US-0088342.
2001US-00883878.
2001WO-US020116.
2001WO-US021166.
2001WO-US021135.
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09-AUG-2001; 2001US-00927796:
16-AUG-2001; 2001US-00928072:
19-DEC-2001; 2001US-00028072:
                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC
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P-PSDB; ADE89085.
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19-JUN-2001; 2
20-JUN-2001; 2
21-JUN-2001; 2
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16-AUG-2001;
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2000WO-US005601.
2000WO-US005746.
2000WO-US005841.
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 30-DEC-1999;
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06-JAN-2000; 2
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10-NOV-2000; 2
01-DEC-2000; 2
20-DEC-2000; 2
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20-MAR-2000;
21-MAR-2000;
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17-MAY-2000;
22-MAY-2000;
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02-JUN-2000;
   Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tummour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tummour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
1129 TTTTTTTTTTTTTTTTCAGCTGGCACACACAGGCTGGGTTTTTATT 1083
                                                                                                         Human PRO polynucleotide #111.
                                                                                                                                                                                                                                                                                                                      98WO-US017888.
98WO-US018824.
98WO-US019093.
96WO-US019094.
96WO-US0193177.
                                                     ADE18223 standard; cDNA; 1129
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98WO-US022991.
98WO-US022992.
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99WO-US010733.
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                                                                                                                                                                                                                          Homo sapiens.
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10-SEP-1998;
14-SEP-1998;
14-SEP-1998;
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16-SEP-1998;
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07-0CT-1998;
29-0CT-1998;
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20-NOV-1998;
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05-JAN-1999;
08-MAR-1999;
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Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; 11 MAR. -2001; 2001WG-US006666.
19 MAR. -2001; 2001WS-US006666.
12 MAR. -2001; 2001WS-US006669.
22 MAR. -2001; 2001WS-USB16744.
10 MAY. -2001; 2001WS-USB1689.
11 MAY. -2001; 2001WS-USB1689.
11 MAY. -2001; 2001WS-USB1686.
12 MAY. -2001; 2001WS-USB66218.
13 MAY. -2001; 2001WS-USB66218.
14 MAY. -2001; 2001WS-USB66218.
15 MAY. -2001; 2001WS-USB17092.
10 -7UN -2001; 2001WS-USB17092.
10 -7UN -2001; 2001WS-USB17092.
11 -7UN -2001; 2001WS-USB17092.
12 -7UN -2001; 2001WS-USB17092.
13 -7UN -2001; 2001WS-USB17092.
14 -7UN -2001; 2001WS-USB17092.
15 -7UN -2001; 2001WS-USB17092.
16 -7UN -2001; 2001WS-USB17092.
17 -7UN -2001; 2001WS-USB17092.
18 -7UN -2001; 2001WS-USB17092. 2000WO-US013705. 2000WO-US014042. 2000WO-US015264. 2000WO-US020710. 2000WO-US022031. 2000WO-US034956. 2001US-00796498. 2001WO-US006520. 2001US-00908827. 2001US-00924419. 2001US-00927796. 2000US-00747259 2001WO-US020116 2001WO-US021066. 2001WO-US021735. 2001US-00028072 (GETH ) GENENTECH INC.

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New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or PRO4978, for use in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymicleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the release of tumour necrosis proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polymuclectides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating cartisenses RNA and bin gene therapy. The polymuclectides may also a hybridisation probes, in chromosome and gene mapping, in generating cartisenses RNA and should name therapy. The polymuclectides may also be used in preparing PRO polypeptides by recombinant techniques and in the development and screening or knock-out animals which are useful in the development and screening or knock-out animals which are useful in the development and screening or knock-out animals which are useful as tumours, for stimulating or inhibiting proliferation of antibodies are used in preparing a condition responsive to the polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or thuman microvascular endothelial cells, for middlating the uptake of glucose or FRA by skeletal muscle cells, for middlating differentiation of alphocyte cells, for stimulating differentiation of alphocyte cells, for stimulating differentiation of alphocyte cells, for stimulating and confidence cells, for inducing endothelial cell tume as sports injuries and arritular cartilage are useful for treating sorts-related joint problems, articular cartilage are useful for treating various manalent may benefit from enhanced local immune system cell infilteration. This sequence represents a human PRO polymuclecti
Claim 2; SEQ ID NO 221; 638pp; English.
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Gaps ; 0 1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; tive 0; Mismatches 16; Indels 0 1129 TTTTTTTTTTTTTTTCAGCTGGCACACAGGCTGGGTTTTTATT 1083 1835 TICTIAATITITICATTICCAGATTICCTICAGTTIGGGTTITGTTI 1881 Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other; Query Match Best Local Similarity 66.0 Matches 31, Conservative g ò

ADE88532 standard; cDNA; 1129 BP Human PRO polynucleotide #111. 29-JAN-2004 (first entry) ADE88532; RESULT 206 ADE88532/c 

Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FRA; inser ear unsole cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; Tlymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; shorteral profesoly/yean; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.

Homo sapiens

US2003199054-A1.

23-OCT-2003

98WO-US019093. 98WO-US019094. 98WO-US019330. 12-APR-2002; 2002US-00121054 98WO-US022991 98WO-US022992 98WO-US018824 98WO-US019437 98WO-US025108 98WO-US019177 98WO-US024855 99WO-US000106 99WO-US005190 99WO-US012252 99WO-US020111 2000WO-US000219 2000WO-US003565 2000WO-US004341 2000WO-US005746 99WO-US010733 99WO-US020594 98WO-US02; 99WO-US02 SD-OM66 80-0M66 3U-0W66 3U-0W66 99WO-US 99WO-US 99WO-US 10-SEP-1998; 14-SEP-1998; 14-SEP-1998; .0-MAR-1999 0-MAR-1999; -SEP-1999 01-MAR-2000 7-MAY-2000 20-MAR-2000 02-JUN-2000 4-MAY-0-NOV- ö

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynuclectides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TWF-alpha) from human blood, a method for stimulating the polypeptide, a method for stimulating the factor-alpha (TWF-alpha) from human blood, a method for stimulating the profileration or differentiation of choadrocyte cells and a method for colon, breast, prostate, rectal, kidney, cervical and liver tumours). The profileration probes, in chromosome and gene mapping, in generating antisense RNA and pNA and in gene therapy. The polyuncleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals of therapeutically useful reagents. The PRO polypeptides by recombinant techniques and in generating either transgenic animals of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of number of adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating condition responsive cells, for stimulating condition expression in pericyte cells, for stimulating conditions are useful for treating sports injuries and various bone and/or cartilage disorders such as sports injuries and cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides of the prolypeptides are useful for treating various memalian haemoglobin-
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bone disorders, arthritis, heart attack, injuries, tumors, and
stimulating release of TNF-alpha from human blood.
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                                                                 09-MAR-2001; 20010S-00802706;
14-MAR-2001; 20010S-00806689;
22-MAR-2001; 20010S-00806689;
05-MAY-2001; 20010S-00854206;
10-MAY-2001; 20010S-00854209;
10-MAY-2001; 20010S-00854280;
25-MAY-2001; 20010S-00860216;
25-MAY-2001; 20010S-00866034;
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01-JUN-2001; 2001WO-US017800.
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2001US-00887879.
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Gerritsen ME, Goddard A,
Smith V, Stewart TA, Tum
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Deforge L, Desnoyers L, Filvaro A, Godowski PJ, Gurney AL, Sher Tumas D, Watanabe CK, Wood WI,

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Human; coagulation; Factor VII; Factor VIIa; blood coagulation; fibrin clot; haemostatic; tissue factor; zymogen; Factor IX; Factor X; prothrombin; Practor V; Factor V; Factor V; Factor V; Factor V; Factor V; Factor V; Factor V; II; fibrinogen; fibrin, plasma factor; bleeding episode; haemophilia A; haemophilia B; thrombus; intimal hyperplasia; restenosis; cardiogenic embolism; stroke; platellet deposition; percutaneous transdermal coronary angioplasty; PTCA; cancer; tumour; anglogenesis; ischaemia; reperfusion; thrombolysis; rheumatoid arthritis; arteriosclerosis; inflammation; septic shock; myocardial infarction; vasotropic; cerebroprotective; ARDS; milbacterial; immunosuppressive; cardiant; gene therapy; ds; pLNI74.
associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO POINTUCIONED of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "No start codon shown. Xaa = gamma carboxylated
                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                      1835 TTCTTAATTTTTCATTTCCAGATTTCCTTCAGTTTGGGTTTTGTTT 1881
                                                                                                                                                                                                                                              1.1%; Score 21.4; DB 1; Length 1129; 66.0%; Pred. No. 45; ive 0; Mismatches 16; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                         1129 ITTITITITITITITITITICAGCIGGCACACAGGCIGGGITITIAII 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l_except= (pos:300. .305, aa:Xaa-Xaa)
11_except= (pos:324. .326, aa:Xaa)
11_except= (pos:330. .334, aa:Xaa.)
11_except= (pos:339. .344, aa:Xaa.Xaa)
11_except= (pos:357. .362, aa:Xaa.Xaa)
11_except= (pos:369. .371, aa:Xaa.Xaa)
11_except= (pos:387. .389, aa:Xaa)
                                                                                                                                                                                    Sequence 1129 BP; 231 A; 369 C; 335 G; 194 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid pLN174 for expressing human coagulation Factor VII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product= "Coagulation Factor VII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
285. .1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_except= (p/transl_exce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABX14193 standard; DNA; 6098 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                        Local Similarity 66.0
nes 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NOVO ) NOVO NORDISK AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-058374/05.
P-PSDB; ABG73119.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABX14193;
                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 207
                                                                                                                                                                                                                                                                                                                            Matches
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                   8X3333X8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Filvaroff E, Gac
L, Sherwood S;
od WI, Zhang Z;
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The invention discloses a human factor VII polypeptide, or a variant or derivative of it, where an amino acid has been modified. This change results in a polypeptide with the same or an increased activity when compared to recombinant wild type human Factor VIIa. Blood coagulation of the haemostation of process is mediated by the formation of a complex between tissue factor or process is mediated by the formation of the Pactor VII zymogen). This complex and Factor VIIa (the active form of the Factor VII zymogen). This complex activates Factors IX and X, converting prothrombin to thrombin, which activates Factors IX and X, converting prothrombin burst. The activates Factors of III leading to a full thrombin burst. The corpusion of activates factor VII zymogen to fibrin resulting in formation of a fibrin clot. The Factor VII zymogen to fibrin tesulting in formation of a fibrin clot. The Factor VII zymogen to fibrin the ability of the Factor VII polypeptide to activate plasma factor X or IX. The factor VII derivative is useful for preparing a medicament for the treatment of beenophilia A or B and for inhibiting thrombus formation. The inactivated factor VII derivatives are useful for treating intimal hyperplasia, restenosis, cardiogenic emboli, platelet deposition the hyperplasia, restenosis, andiogenic emboli, platelet deposition cancer, tumour metastasis, angiogenesis, ischaemia/reperfusion, adult crespiratory distress syndrome (ARDS) and myocardial infarction. The inactivated human coagulation Factor VII polypeptide
Novel factor VII polypeptide, its derivatives useful for preparing medicament for treating bleeding episodes, or for enhancing normal hemostatic system, especially for treating hemophilia.
                                                                                                            Disclosure, Page 82-85; 96pp, English
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Sequence 6098 BP; 1413 A; 1587 C; 1623 G; 1475 T; 0 U; 0 Other;

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                                                                                        TITGTATGCTTCTTGTACCTTGATAGGCATCTCTTTCTCAAGGTTAGGAAATTTTTCTTT 1595
                                                                                                                                      TTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCC 4488
                                                  0; Gaps
                                                                                                                                                                                 1596 TITGGITTICITGAAATATTTTCCCTGCTTTTGACCTGCCTTCTTCCCCT 1646
                                                                                                                                                                                                                            4489 ccrdarircrerddaraaccerarracedecriridagreaecrearaedecr 4539
1.1%; Score 21.4; DB 1; Length 6098;
49.5%; Pred. No. 60;
tive 0; Mismatches 56; Indels 0
                                           55; Conservative
                       Best Local Similarity
                                                                                                                                   4429
                                                                                        1536
Query Match
                                           Matches
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Novel murine polynucleotide isolated using gene trap technology #32
          BP.
         ABS68969 standard; DNA; 305
                              (first entry)
                              21-NOV-2002
                    ABS68969;
RESULT 208
     ABS68969
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Mouse; gene trapped sequence, GTS; functional genomic analysis; phage display system; gene chip; temporal gene expression; tissue specific gene expression; antisense inhibition; gene targeting; development disorder, cell differentiation disorder; aging; cancer; autoimmune disease; lupus; inflammatory disorder; skin disorder; degenerative disorder; ds.

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30-NOV-2000; 2000US-00728445.
US2002102543-A1.
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Mus musculus

US2001051335-A1.

Zea mays.

13-DEC-2001

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The invention describes an isolated murine polymucleotide (1) comprising a contiguous stretch of at least 60 mucleotides of one of 265-677 curdeotide 891 ownInDawk gene trapped sequences (GTSB) (S), given in the specification. The novel genes and development of new therapeutic and diagnostic agains and methods. (I) is useful in functional genomic of diagnostic agains and methods. (I) is useful for identifying the coding regions of the murine genome, to isolate cDNAs, genomic clones, or full-length genes/polymucleotides or homologues, heterologues, paralogues, or crhologues that are capable of hybridising to one or more of the GTSs under stringent conditions. (I) can be incorporated into a phage display system that can be used to screen for protectins, or other ligands, that are capable of binding an amino acid sequence encoded by an coligonucleotide or polymucleotide sequence encoded by an expression, colidonucleotide or polymucleotide sequence in at least one of the TS sequences. (I) is useful in addressable arrays, such as gene chips, to identify and characterise temporal and tissue specific gene expression, to identify and characterise temporal and tissue specific gene expression, colidonucleotides or proteins encoded by (I) is useful for treating development computations such as antisense inhibition and gene targeting. Decreasing the level of expression of (I) and/or down regulating the activity of peptides or proteins encoded by (I) is useful for treating development and cell differentiation disorders, adjug, cancer, autoimmune disease, considered and degenerative disorders. This sequence represents a murine cDNA isolated using gene trap
                                                                                                                                                                                                                                  Novel murine polynucleotides that individually identify novel genes into which a retroviral gene trap vector has integrated, useful in genomic analysis and in discovery, development of therapeutic and diagnostic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 305 BP; 72 A; 96 C; 66 G; 70 T; 0 U; 1 Other;
                                                                                                                                                           Sands AT;
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 36; 296pp; English.
99US-0168358P
                                                                                                                                                           Zambrowicz B,
                                                FRIE/) FRIEDRICH G. (ZAMB/) ZAMBROWICZ B.
                                                                                                                                                                                                            WPI; 2002-690598/74.
                                                                                                      (SAND/) SANDS A T.
01-DEC-1999;
                                                                                                                                                           Friedrich G,
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284 CTGCTCTCAGAACTGCTGCTGCTGCTGCTGGACGAGCTGGAGTCCGAGTCCGAGG 227 CTGCTGGCAATACTTCTGGGGCTGCTGCCTTTCTCCCTGTCTGATTCCTAGGGTGAGG 99 42 ઠે g

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.; 0

0; Mismatches

35; Conservative

Local Similarity

Query Match Matches

38;

Score 21.2; Pred. No. 38

1.1%;

DB 1; Length 305; 23; Indels

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Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPs; inheritance; characteristic; growth; development; disease resistance; environmental adaptability; quality; yield; molecular marker; multigene trait; plant breeding; corn tassel; gene; ss.
                                                                             Corn tassel-derived polynucleotide (cdps) SEQ ID NO:6030.
ABL76656 standard; cDNA; 286 BP.
                                                   (first entry)
                                                   14-MAY-2002
                         ABL76656;
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The present sequence describes a purified corn tassel-derived polymucleotide sequence (cdps) comprising a nucleic acid sequence color polymucleotide sequence (cdps) comprising a nucleic acid sequence selected from those given in ABL70627 to ABL7683. The cdps sequences concode corn tassel-derived polypeptides (CDPs). The cdps sequences (C encode corn tassel-derived polymeptides (EDPs). The cdps sequences (I) can be used for determining altered gene expression, to recover concode corn tassel-through hybrid breeding programs. (I) are also useful in the evaluation, and alteration of desired characteristics associated with growth and development, disease resistance, environmental adaptability, complete traits in a plant breeding program. (I) can be used to produce a tassel-specific profile of gene transcription, a transcript image, to clone regulatory elements for use in transformation vectors, to express a polypeptide, to identify, isolate or extend identical or related corn tassel nucleic acid sequences from DNA libraries, in nucleic acid determine thomology of known sequences, as probe for use in Southern or Northern hybridisation, and to identify the presence of and/or to consume the degree of similarity between two (or more) nucleic acid
                                                                                                                                                                                                                                              Novel purified corn tassel-derived polynucleotide useful for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'n
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Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 286 BP; 96 A; 73 C; 89 G; 27 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 6030; 201pp; English.
                                                                                                                                                                  Sherman BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.18;
99US-00294093.
                                          98US-0082567P.
                                                                                                                                                                    Ito LY,
                                                                                  LALGUDI R V.
                                                                                                        ITO L Y.
SHERMAN B K.
                                                                                                                                                                                                            WPI; 2002-163647/21.
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Best Local Similarity
  16-APR-1999;
                                                                                                                                                                    RV,
                                                                                (LALG/)
(ITOL/)
(SHER/)
                                                                                                                                                                    Lalgudi
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1714 AGACTTAACATTTTCTTTGACCAAGGTATCCATTTCTTCTATCTTGTCTTCACTGCCTGA 1773 TITITGGITITICITGAAATATTITICCCIGCITTITGACCIGCCTTCTTCCCCTTCCTCTA 1653 1654 TICCTITGGTITTIGCATAGTGTCTCTGGCTTCCTGGATGTTTTATGCCTGGATTATTT 1713 141 gresiscricscocori---crrerecricsrecricricaristadresocococosarsrs 85 201 crecacearecerecrierecrececerecricireriererecrececerrerr Gaps GATTCTCTTCTATCTCTTGTATTCTGTCAGTGAGGCTTGTCTCT 1819 9 Matches 104; Conservative 261 1774 84

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AAV88246 standard; cDNA; 267

RESULT 210

(first entry)

12-FEB-1999

AAV88246;

AAV88246/C ID AAV882 XC XX DT 12-FEB XX DX DX EST C1 XX

EST clone EA90.

1543 GCTTCTTGTACCTTGATAGGCATCTCTTTCTCAAGGTTAGGAAATTTTTCTTTTTGGTT 1602 The present sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities heematopoiesis regulating activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, haemostatic and thrombolytic activity, receptor/ligand activity, atti-inflammatory activity, cacherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene therapy ö 243 GAIGCAITGACCICAAACACICICICAGIAICCCAITICIGIIGGAITICITICICAAIC 184 New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries. human; Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding. Gaps Treacy M; Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; hi chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds. Bovine EST associated with lactation/muscle/fat deposition #2260. 1603 TICTIGAAATATHITCCCIGCTTTTGACCTGCCTTCTTCCCCTTCCTC 1651 183 ircircadadaciccacrridecierrecrirrerirececenticee 135 Score 21; DB 1; Length 267; Pred. No. 42; Racie LA, Merberg D, 0, Mismatches 55; Indels Sequence 267 BP; 75 A; 45 C; 90 G; 57 T; 0 U; 0 Other; Lavallie ER, Claim 1; Page 332; 641pp; English. ABX37095 standard; cDNA; 372 BP 98WO-US006956. 97US-00837312. Query Match
Best Local Similarity 49.5%;
Matches 54; Conservative Jacobs K, Mccoy JM, Lava. Spaulding V, Agostino MJ; (first entry) (GEMY ) GENETICS INST INC. Mccoy JM, WPI; 1999-070078/06. 10-APR-1998; Homo sapiens 10-APR-1997; 20-FEB-2003 15-0CT-1998. Bos Taurus ABX37095; RESULT 211 ABX37095, g à à

10664//5-3.rng

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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SENP). The present sequence is one mind probe. The SENPs are defived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                        Probe #10127 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention relates to human single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1614 ATTTTCCCTGCTTTTGACCTGCCTTCTTCCCCTTCCTCTATTCCTTTGGTTTTTGCATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 AATTICTTICCICCICCICCICCICTCICICGCGTICTAGCICCCGCTGCTTTICCAGTIC
                                                                     Probe, human, microarray, gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              liver single exon nucleic acid probe #13528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 263 BP; 91 A; 47 C; 102 G; 23 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.0%; Score 20.8; Di
52.3%; Pred. No. 47;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1674 TGTCTCTGGCTTCCTGGATGTTTATGC 1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; SEQ ID NO 10127; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 cricicca dricca Griciaria con 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABA65223 standard; DNA; 263 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359F.
04-OCT-2000; 2000GB-000424263.
                                                                                                                                                                                                                                                                                                                               2000US-0180312P.
2000US-0207456P.
2000US-00608408.
                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US000670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanzel DK,
                                                                                              cervical cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488901/53.
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                                                                                                                                           Homo sapiens
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ABA65223/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated IMPD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule compising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are if (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3 non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3 end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the 1512 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or the omblement of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid sequences or the complementary nucleic acid sequences or the complementary nucleic acid sequences or the molecule obtained from the bovine cell or tissue. The detection of the complementary nucleic acid is predictive of the level or pattern of the molecule. The LMFD nucleic acid is used for level or pattern of the molecule in the predictive of the later sequence mapping, gene identification and analysis, cattle for genetically improving cattle. The present sequence is one of the present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:

"Sequata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1569 ITICTCAAGGITAGGAAATTTTTTTTTTTGGTTTTTCTTGAAAATATTTTCCCTGCTTTT 1628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
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                                                                                                                                                                                                                                                                                                                               Warren WC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; SEQ ID NO 2260; 245pp; English
                                                                                                                                                                                                                                                                                                                               Tao N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI20194 standard; DNA; 263 BP
                                                                                                                                      12-JAN-1999; 99US-0115707P, 11-JAN-2000; 2000US-00480902.
                                                                                         24-SEP-2001; 2001US-00960352
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                                                                                                                                                                                                          (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN N.
(TAON/) TAO N.
(WARR/) WARREN W C.
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Best Local Similarity
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US2002137139-A1
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                                                                                                                                                                                           genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 AATTICTTICCTCCTCTCCTCTCTCTCTCCCGTTCTAGCTCCCCGCTTTTTCCAGTTG 192
                                                                                                                                                                                                                                                                              The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placente. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New spatially-addressable set of single exon nucleic acid probes, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; microarray; single exon probe; gene expression; breast; disease;
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 263 BP; 91 A; 47 C; 102 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        duman breast cell single exon nucleic acid probe #6033.
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52.3%; Pred. No. 47;
ive 0; Mismatches
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                                                                                                                                                                                                                                                  Claim 25; SEQ ID NO 14080; 654pp; English
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                                                                                                                           Rank DR;
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                                                                                                                                                                                                                  gene expression in human placenta.
                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
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03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
7-SEP-2000; 2000US-023653-99.
04-OCT-2000; 2000GB-00024263.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023559P.
04-OCT-2000; 2000GB-00024263.
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Best Local Similarity 52.3%;
Matches 46; Conservative
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                                                                                                                           Hanzel DK,
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                                                                                                                                                           WPI; 2001-488897/53.
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ABA47338/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 AATTTCTTTCCTCTCTCTCTCTCTCCCCTTCTAGCTCCCGCTGCTTTTCCAGTTG 192
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1.0%; Score 20.8; DB 1; Length 20
Best Local Similarity 52.3%; Pred. No. 47;
Matches 46; Conservative 0; Mismatches 42; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 263 BP; 91 A; 47 C; 102 G; 23 T; 0 U; 0 Other;
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234589P.
04-OCT-2000; 2000GB-00024263.
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
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                                                                         30-JAN-2001; 2001WO-US000669
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                                                                                                                                                                                                                                                                                        Hanzel DK,
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     WO200157277-A2
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                                       09-AUG-2001
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ઠ g ò g WPI; 2001-488899/53.

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nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probes of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for verifying the propassion of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for proposing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this partent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1614 ATTITICCOTGCTTTTGACCTGCCTTCTTCCCCTTTCCTTTGGTTTTTGCATAG 1673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 AATTTGTTCTCTCTCTCTCTCTCTCTCTGCGTTCTAGCTCCGGCTGCTTTTCCAGTTG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                  The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
  for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
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                                                           Claim 4; SEQ ID NO 6033; 327pp + Sequence Listing; English.
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1.0%; Score 20.8; DB 1; Length 2
Best Local Similarity 52.3%; Pred. No. 47;
Matches 46; Conservative 0; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 263 BP; 91 A; 47 C; 102 G; 23 T; 0 U; 0 Other;
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ID ABA32324 standard; DNA; 263 BP
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2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0235559P.
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30-JUN-2000; 2
03-AUG-2000; 2
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27-SEP-2000;
04-OCT-2000;
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1673
                                                                                                              The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular e.g. cardiovascular disease, hypertension, cardiac arrhythmias and e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 AATHTCTTTCCTCTCTCTCTCTCTCTCTCCGTTCTAGCTCCCGCTGCTTTTCCAGTTG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                 Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                         1614 ATTITCCCTGCTTTTGACCTGCCTTCTTTCCCTCTATTCCTTTTGCATAG
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 263;
                                                                                                                                                                                                                                                                                                                                                                   1.0%; Score 20.8; DB 1; Length 2
52.3%; Pred. No. 47;
tive 0; Mismatches 42; Indels
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                                                                                    Claim 4; SEQ ID NO 10790; 530pp; English
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632466.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234589P.
04-OCT-2000; 2000GB-00024263.
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nes 46; Conservative
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATTITCITICCICCICCICCICCICTCICCICCICTICIAGCICCCCCCCCTITITICCAGIIG 192
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                                                                                                                                                                                                             Sequence 263 BP; 91 A; 47 C; 102 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                      Score 20.8; DE Pred. No. 47; 0; Mismatches
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26-MAY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
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nes 46; Conservative
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1614 ATTITICCTGCTTTTGACCTGCCTTCCTTCCTTTCCTTTGCTTTTTGCATAG 1673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                  192
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                                                                                                  251 AATTICITICCICCICTCICCICTCICTCICCGCTTCIAGCICCCGCTGCTTTCCAGTTG
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                           Human; single exon nucleic acid probe; liver; cirrhosis;
hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
coronary heart disease; ss.
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Length 263;
                                Indels
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                                42;
 DB 1;
                                                                                                                                                                                                                                                                                                                                                               Human liver single exon probe, SEQ ID No 13959.
Score 20.8; DB
Pred. No. 47;
0; Mismatches
                                                                                                                                     1674 TGTCTCTGGCTTCCTGGATGTTTTATGC 1701
                                                                                                                                                                      191 CTICICCAGTICCAGTIGICITITICCGC 164
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 1.0%;
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27-SEP-2000; 2000US-0236359P.
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 Query Match
Best Local Similarity 52.3
Matches 46; Conservative
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                                                                                                                                                                                                                           RESULT 219
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1.0%; Score 20.8; DB 1; Length 263;

Query Match

Sequence 263 BP; 91 A; 47 C; 102 G; 23 T; 0 U; 0 Other;

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251 AATTICITICCICCICCICCICCICCICTCICGCGIICIAGCICCCGCIGCITITICCAGIIG 192
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                                                                                     The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory disease and the breast, fibrocystic changes, proliferative breast disease and noncarione tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel single exon nucleic acid probe used to measuring gene expression in a human breast.
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                                                                                                                                            251 AATATCTTCCTCCTCCTCTCTCTCTCCCCTTCTAGCTCCCCCTCCTTTTCCAGTTG
                                 Gaps
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                              Indels
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                                 42;
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1.0%; Score 20.8; DB 1; 1
Best Local Similarity 52.3%; Pred. No. 47;
Matches 46; Conservative 0; Mismatches 42;
   Pred. No. 47;
0; Mismatches
                                                                                                                                                                                                       1674 TGICTCTGGCTTCCTGGATGTTTTATGC 1701
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2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0234587P.
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   Best Local Similarity 52.3%;
Matches 46; Conservative
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from thuman lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes comprising frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes of the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung, measuring gene expression in a sample collection of detectably labeled nucleic acids derived from human lung many, and (b) measuring the label detectably bound to each probe of the algorithmically predicting at least one exon from genomic sequences of the eularyote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several
                                                                                                                                                                                                                                                                                                                            Human, ds, single exon probe; asthma; lung cancer; COPD, ILD, chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histlocytosis; lymphangioleiomyomcosis; Karagener syndrome; pulmonary histlocytosis; lymphangioleiomyomcosis; Karagener syndrome; pulmonary histlocytosis; lymphangioleiomyomcosis; karagener syndrome; pulmonary distinary dyskinesis; plumonary hypertension; hyaline membrane disease; open reading frame; ORF.
                                                                                                                                                                                                                                                                                   Human genome-derived single exon probe ORF from lung SEQ ID No 13459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spatially-addressable set of single exon nucleic acid probes, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               measure gene expression in human lung samples.
1674 TGTCTCTGGCTTCCTGGATGTTTTATGC 1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; SEQ ID NO 13459; 634pp; English.
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                                          191 CTICICCAGTICCAGTIGICITITGCGC
                                                                                                                                                         ВР.
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03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02346359P.
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ABS13468 standard; DNA; 263
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                                                                                                                                                                                                 ABS13468;
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1614 ATTTTCCCTGCTTTTGACCTGCCTTCTCCCCTTCCTTCTATTCCTTTGCATAG 1673

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Gaps

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Indels

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tissues and/or cell types using hybridisation to a single exon
microarrays having a probe with the exon, where a common pattern of
microarrays having a probe with the exon, where a common pattern of
the exons should be assigned to a single gene, a peptide comprising one
of 12011 sequences, mentioned in the specification, or encoded by the
probes/open reading frames (ORP). The probes are used for gene expression
analysis, and for identifying exons in a gene, particularly using human
tung derived mRNA and for the study of lung diseases such as asthma, lung
cancer, chronic obstructive pulmonary diseases such as asthma, lung
disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
tuberous sclerosis, Gaucher is disease, Niemann-Pick disease. Hermansky-
pudlak syndrome, sarcoidosis, pulmonary alveolar proteinosis,
karagener syndrome, ibrocystic pulmonary alveolar proteinosis,
cancer, chronic obstruction and hyaline membrane disease. The
present sequence is a single exon probe open reading frame of the
present squence is a single exon probe open reading frame of the
the printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 263 BP; 91 A; 47 C; 102 G; 23 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 20.8; D
Pred. No. 47;
0; Mismatches
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14-YAR-2000; 2000US-0189467P.
24-YAR-2000; 2000US-0192099P.
29-WAR-2000; 2000US-0193480P.
15-YAY-2000; 2000US-025230P.
09-UNY-2000; 2000US-021115P.
25-JUL-2000; 2000US-02201115P.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                      290 TCTAGATTTAAGCTGTGGTGGTCAGATAGGACATAGAGTATTATTTCAATTGTCTTTTAT 349
                                                                                                                                                                                                                                                                                                                                        91 TCTGGCTCTTGACAAAGATAGACCACTGGAACAATGAGAAGGAGAGAATTCTACTGGTCA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe #1685 for gene expression analysis in human cervical cell sample.
The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
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                                                                                                                                                                                                                                                                                                                                                                                350 CTGTCGAGACTTGCTTTGTTTGAAATATGTATTCA 385
                                                                                                                                                                                                                                                                                                                                                                                                                  151 cagacaagacrererrearergeaaracaacrica 186
                                                                                                                                                                                                                         Score 20.8; DB
Pred. No. 48;
0; Mismatches
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26-MAY-2000; 2000US-0207456P.
30-UNN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
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Bést Local Similarity
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Query Match

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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
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182 ATAATATTCCATTCAGTGTCATTTCATTATAACTTTGATGAGGAAAACAAAAATC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           914 ATCTTTTCTAGAGAAATTAAGATCATTGAGTCATTGATGTTGAGAATTATCAATGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to measure gene expression in human placenta sample.
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                                                                                                  974 GIGITIGIGGALICITGITALCITGCACITGIGAAG 1009
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Local Similarity 51.0%; Pred. No. 54;
les 49; Conservative 0; Mismatches
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; 2000US-0207456P.
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30-JUN-2000; 2
03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
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                                                                                                                                                                                                                                                                                             914 ATCTTTTTCTAGAGAAATTAAGATCATTGAGTCATTGATGTTGAGAATTATCAATGAGGA 973
                                                                                                                                                                                                                                                                                                                                                          ATAATATTCCATTCAGTGTCATTTCATTATAACTTTGATGAGGAAAACAAAAATC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, foetal liver, gene expression, single exon nucleic acid probe, ss.
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                                                                                                                                                               1.0%; Score 20.8; DB 1; Length 474;
51.0%; Pred. No. 54;
tive 0; Mismatches 47; Indels
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                                                                                                     Sequence 474 BP; 121 A; 114 C; 119 G; 120 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human foetal liver single exon nucleic acid probe #1748.
      obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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20-MAY-2000; 2000US-0207456P.

30-JUN-2000; 2000US-00608408.

03-AUG-2000; 2000US-00532366.

21-SEP-2000; 2000US-0234687P.

27-SEP-2000; 2000US-023459P.

04-OCT-2000; 2000GB-00024263.
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914 ATCTTTTTCTAGAGAATTAAGATCATTGAGTCATTGATGTTGAGAATTATCAATGAGGA 973

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ABA23216 standard; DNA; 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from many of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing preast disease. Gene expression analysis is useful for eassessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring case expression, with far less bias then expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                               New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                                 Human; microarray; single exon probe; gene expression; breast; disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID NO 1725; 327pp + Sequence Listing; English.
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                                                     cell single exon nucleic acid probe #1725.
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30-JUN-2000; 2000US-0069408.
03-AUG-2000; 2000US-00632466.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234539P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                        30-JAN-2001; 2001WO-US000662
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Conservative
                          (first entry)
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Matches 49; Conserv
                                                                                                                                                   WO200157271-A2.
                                                      Human breast
                                                                                                                          Homo sapiens
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                            01-FEB-2002
                                                                                                                                                                               09-AUG-2001
                                                                                               cancer; ss.
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ABA43030;
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measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for present sequence is one such probe. The probes may be used for to measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic form at directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single exon nucleic acid probes for analyzing gene expression in human
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                                                                                                         Probe #1682 for gene expression analysis in human heart cell sample.
                                                                                                                                                   Human, gene expression; heart, microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
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27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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2000US-0207456P.
2000US-00608408.
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Best Local Similarity
Matches 49; Conserva
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                                                                                                                                                                                                                                                                                 Homo sapiens.
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ABA23216;
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ID AAK27
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RESULT 227 ABA23216/c

Homo sapiens

09-AUG-2001

Penn SG,

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914 ATCTITITCTAGAGAAATTAAGATCATTGAGTCATTGATGTTGAGAATTATCAATGAGCA 973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                    Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, single exon nucleic acid probe, liver; cirrhosis;
hyperlipoproteinaemia, hyperlipidaemia; hypercholesterolaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; SEQ ID NO 1705; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                     Rank DR
                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                     Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-UTN-2000; 2000US-00608408.
30-3-AUG-2000; 2000US-0053366.
21-SEP-2000; 2000US-0234687P.
                                                                                           26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00633366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0236359P.
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                                     2001WO-US000667
                                                                                                                                                                                                    04-OCT-2000; 2000GB-00024263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coronary heart disease; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 51.0
nes 49; Conservative
                                                                                                                                                                                                                                                                                     DK,
                                                                                                                                                                                                                                                                                                                             WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                     Hanzel
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                                     30-JAN-2001;
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09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 ATAATATTCCÁTTCAGTGTCATTTCATTATAACTTTGATGAGGAAAACAAAATCAATTC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                           Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                   Human bone marrow expressed single exon probe SEQ ID NO: 1723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; SEQ ID NO 1723; 658pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.0%; Score 20.8; DB 1; Length 4
51.0%; Pred. No. 54;
rative 0; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human brain expressed single exon probe SEQ ID NO: 1705.
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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Best Local Similarity 51.0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
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Homo sapiens

05-NOV-2001

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2000US-00608408.
2000US-00632366.
2000US-0234687P.
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2000US-0207456P.
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                                                                               human breast.
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                     Penn SG,
                                                                   Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 232
                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                         The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver. comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS1105 represent human sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at IEEP.wipo.int/pub/published_pct_sequences
                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                   182 ATAATATTCCATTCAGTGTCATTTCATTATAACTTTGATGAGGAAAACAAAATCAATTC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe; human; breast disease; breast cancer; development disorder; ss; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                              914 ATCTTTTTCTAGAGAATTAAGATCATTGAGTCATTGATGATGAGAATTATCAATGAGCA
                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe #1672 used to measure gene expression in human breast sample
                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 474;
                                                                                                                                                                                                                                                                                                                                        Sequence 474 BP; 121 A; 114 C; 119 G; 120 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                      47; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 crárcrágadadacharcragarrariarcasa 87
                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                            1.0%; Score 20.8; Lilarity 51.0%; Pred. No. 54; Conservative 0; Mismatches
                                                                                                                                      Claim 1; SEQ ID NO 1739; 658pp; English.
                                                         Chen W, Rank DR;
                                 (MOLE-) MOLECULAR DYNAMICS INC
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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2000US-0207456P.
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2000US-0234687P.
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2000GB-00024263.
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                                                         Hanzel DK,
                                                                              WPI; 2001-488898/53
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es 49; Conserv
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27-SEP-2000;
04-OCT-2000;
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                                                         Penn SG,
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Best Local S
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The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, particularly those diseases with polygenic aeriology. The diseases include: breast cancer, disorders of development, inflammatory diseases include: breast cancer, the sequence data for this patent disease and noncarcinoma tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in alectronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                   single exon nucleic acid probe used to measuring gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            914 ATCTTTTTCTAGAGAAATTAAGATCATTGAGTCATTGATGTTGAGAATTATCAATGAGCA 973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 474 BP; 121 A; 114 C; 119 G; 120 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                          Claim 25; SEQ ID NO 1672; 322pp; English.
                                                                           Chen W, Rank DR;
(MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                Hanzel DK,
                                                                                                                                                       WPI; 2001-476286/51
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The invention relates to novel serine proteases designated BSSP4

(AABI1700-BI1709), and to nucleic acids encoding them (AAA61695-A61704,
AAA61799). The invention also relates to vectors and transformants

comprising BSSP4 nucleic acids, transgenic animals in which the
expression level of BSSP4 can be varied, and an mBSSP4 knockout mouse.

The invention additionally encompasses anti-BSSP4 antibodies and methods of production of such antibodies, methods of BSSP4 detection using the antibodies, and the use of BSSP4 proteins or fragments as diagnostic markers for certain medical conditions. Nucleotides encoding BSSP4 were initially isolated in a human brain cDNA library using degenerate PCR primers (AAA61715) based on conserved regions of serine proteases and nucleotides encoding them are useful in detecting homologues, mutants and polymorphic variants in biological camples (e.g., blood, urine, brain, prostate gland and testis) as diagnostic markers for diseases associated with altered BSSP4 expression levels. Such diseases include Alzahemer's disease, ocedema (dropsy), cancer or inflammation of brain, prostate, testis or bone. Sequences
AAA61695-A61703 ans AAA61799 represent cDNAs encoding murine contains mutane (BBSSP4), and sequence AAA61704 represents CDNA encoding murine
                                                                                   BSSP4; serine protease; human; hBSSP4; mouse; mBSSP4; brain; diagnostic marker; antibody; transgenic animal; Alzheimer's disease; oedema; dropsy; cancer; inflammation; prostate; testis; bone; ss.
                                            cDNA encoding human serine protease BSSP4 (hBSSP4) SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1036 BP; 205 A; 310 C; 301 G; 220 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serine protease BSSP4 and antibodies recognizing BSSP4 for diagnosis of diseases in which BSSP4 expression is altered.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Uemura H, Okui A, Kominami K, Yamaguchi N, Mitsui
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23-OCT-2000 (first entry)
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                                                                                                                                                                                                                               WO200031277-A1.
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                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                        20-NOV-1998;
                                                                                                                                                                                                                                                                             02-JUN-2000.
    The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12819 open reading frames derived from the 15614 probes. Also included are a microarray comprising the novel set of probes in the human lung, manually expressed in the human lung, measuring gene expression in a sample derived from human lung, measuring gene expression in a sample derived from human lung, measuring gene expression in a sample derived from human lung mRNA, and (D) measuring the label detectably bound to each probe of the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, in dentifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (D) detecting specific hybridisation of detectably having a fragment identical to the predicted exon, the probe is included comprising (a) identifying exons from equomic sequence by the method above and (D) measuring the expression of each of the exons in the tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of the exons should be assigned to a single exon analysis, and for identifying exons in the tissues and/or cell types using plyridisation to a single exon analysis, and for identifying exons in the specification, or encoded by the exons should be assigned to a single gene; a peptide comprising of probes/oper raading frames (ORF). The probes are used for gene expression of each exist and for identifying exons in a gene, particularly using human cancer, chronic obstructive pulmonary diseases such as asthma, language derived mRNA and for the study of lung derived mRNA and for the study of lung derived mRNA and for the study of lung derived manualial idiopathic pulmonary har
                                                                                                                                                                                     Spatially-addressable set of single exon nucleic acid probes, used to
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                                                                                                                                                                                                              measure gene expression in human lung samples.
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                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1708; 634pp; English.
                                                                                             Chen W, Rank DR;
                                                 (MOLE-) MOLECULAR DYNAMICS INC.
    04-OCT-2000; 2000GB-00024263
                                                                                             DK,
                                                                                                                                         WPI; 2002-114183/15
                                                                                             Hanzel
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assay and

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99WO-JP006472.

(FUSO ) FUSO PHARM IND LTD

2000-400084/34.

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Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
                                                                           1131 TTATTTATTATTCATATTTTCTTGAATGTGGGTAACATCTTTAGATTGAAG 1181
                                                                                                        1029 ritririririririririricigaaaraaraarrarigaaaridgag 979
            Length 1036;
                                                                                                                                                                                                                                                                                             Mutant blood coagulant factor VII (FVII-31) coding sequence.
                                           Indels
          Score 20.6; DB 1;
Pred. No. 73;
0; Mismatches 19;
1.0%; Scc.
62.7%; Pred
                                                                                                                                                                                            ВЪ.
                                                                                                                                                                                            AAH19463 standard; DNA; 1206
                                                                                                                                                                                                                                                             (first entry)
                                             Conservative
                           Local Similarity
                                                                                                                                                                                                                                                           31-JUL-2001
                                             32;
                                                                                                                                                                                                                              AAH19463;
            Query Match
                                             Matches
                                                                                                                                                                           AAH194637,
ID AAH1
XX
AC AAH1
XX
DT 31-T
XX
XX
XX
XX
XX
XX
XX
XX
KW HUMA
                                                                                                            셤
                                                              0
                                                                                              914 ATCTTTTTCTAGAGAAATTAAGATCATTGAGTCATTGATGTTGAGAATTATCAATGAGCA 973
                                                                                                                             182 aranarriccarrcagrerererricarraacrireargagaaaacaaaarcaarre 123
                                                                Gapa
                                                             , 0
                             DB 1; Length 474;
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Gaps

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Score 20.8; DB 1; Length 4: Pred. No. 54; 0; Mismatches 47; Indels

0;

Conservative

Query Match Best Local Similarity Matches 49; Conserv

1.0%;

974 GIGITIGIGGALICITGITALCITGCACTIGIGAAG 1009

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122

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AAA61697 standard; cDNA; 1036

AAA61697

AAA61697/C ID AAA616 XX AC AAA616 XX

RESULT 233

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444 Trigoriegearironinintoradanaderarririodacahedaharroakorende 386
                                                                                                                                                                 for substitution therapy in
                                                                                                                                                                                                                                                The present invention relates to mutants of blood coagulant factor VII (FVII) or activated blood coagulant factor VII (FVIIa). The present sequence is the coding sequence for one such mutant FVII: VII-39. The mutants can be used as an agent for the substitution therapy of haemophilia inhibitor patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mutant of blood coagulant factor VII, used for substitution therapy in the treatment of hemophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to mutants of blood coagulant factor VII (FVII) or activated blood coagulant factor VII (FVIIa). The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; haemostatic; blood coagulant factor VII; FVII; haemophilia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 TTCAATTGTCTTTTATCTGTCGAGACTTGCTTTGTTTTGAATATGTATTCAATTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wild-type human blood coagulant factor VII (FVII) coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 1206;
                                                                                                                                                                                                                                                                                                                                                         Sequence 1206 BP; 247 A; 354 C; 387 G; 218 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                           24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         partial
note= "No start codon given"
                                                                                 (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.0%; Score 20.6; D
Best Local Similarity 59.3%; Pred. No. 76;
Matches 35; Conservative 0; Mismatches
                                                                                                                                                                 Mutant of blood coagulant factor VII, used the treatment of hemophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
                                                                                                                                                                                                                     Disclosure; Page 22-23; 29pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 7-8; 29pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .1221
/*tag= a
/product= "FVII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH19459 standard; DNA; 1221 BP
                99JP-00237610.
                                               99JP-00237610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99JP-00237610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-310677/33.
                                                                                                                WPI; 2001-310677/33.
P-PSDB; AAB84871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAB84866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP2001061479-A
                24-AUG-1999;
                                               24-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH19459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 236
AAH19459/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 ITCAATIGICTITIAICTGICGAGACTIGCITITGIITTGAAAIAIGIAITCAAITITGG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         끍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to mutants of blood coagulant factor VII (FVII) or activated blood coagulant factor VII (FVIIa). The present sequence is the coding sequence for one such mutant FVII: VII-31. The mutants can be used as an agent for the substitution therapy of haemophilia inhibitor patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            Mutant of blood coagulant factor VII, used for substitution therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 1206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1206 BP; 244 A; 359 C; 386 G; 217 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coagulant factor VII (FVII-39) coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.0%; Score 20.6; DB 1; Length 12
59.3%; Pred. No. 76;
ive 0; Mismatches 24; Indels
                                                                                                                   *tag= a
product= "FVII-31"
proticial
note= "No start codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  partial
note= "No start codon given"
                                                                                                                                                                                                                                                                                                                                         (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 19-20; 29pp; Japanese.
                                                                               location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag= a
product= "FVII-39"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH19464 standard; DNA; 1206 BP.
                                                                                                                                                                                                                                                                        99JP-00237610.
                                                                                                                                                                                                                                                                                                        99JP-00237610
                                                                                                                                                                                                                                                                                                                                                                                                                                             the treatment of hemophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 59.3
Matches 35; Conservative
                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-310677/33.
P-PSDB; AAB84870.
                                                                                                                                                                                                     JP2001061479-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP2001061479-A.
                            Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mutant blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                      24-AUG-1999;
                                                                                                                                                                                                                                                                                                       24-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-2001.
                                                                                                                                                                                                                                     13-MAR-2001
mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH19464;
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Query Match

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RESULT 235 AAH19464/C

0 392

Gaps

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BP.

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Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
                                                                                                                                       coagulant factor VII (FVII-6) coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
                                              AAH19461 standard; DNA; 1221
                                                                                                                                                                                                                                                                                                                                                                                                                             99JP-00237610,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          99JP-00237610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutant of blood coagulant for the treatment of hemophilia.
                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-310677/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB: AAB84868
                                                                                                                                                                                                                                                                                                                                                                JP2001061479-A.
                                                                                                                                       Mutant blood
                                                                                                                                                                                                                 Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                             24-AUG-1999;
                                                                                                          31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                               13-MAR-2001.
                                                                                                                                                                                      mutant; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334
                                                                            AAH19461,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       444
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                    RESULT 238
AAH19461/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                 Ношо
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0
sequence is the coding sequence for wild-type human FVII. The mutants can be used as an agent for the substitution therapy of haemophilia inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to mutants of blood coagulant factor VII (FVII) or activated blood coagulant factor VII (FVIIa). The present sequence is the coding sequence for one such mutant FVII: VII-5. In the wild-type protein (AAB8466), there is a disulphide bond (159Cys-164Cys). In VII-5, the disulphide bond is disrupted. The mutants can be used as an agent for the substitution therapy of haemophilia inhibitor patients
                                                                                                                                                  334 TICAATIGICTITIAICTGICGAGACTIGCTITGITITGAAATAIGTATICAATTITGG 392
                                                                                                                                                                            444 Tracrescerrirrrrrrrradanahaserarrrrrrescerrescerrarradaerers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mutant of blood coagulant factor VII, used for substitution therapy in the treatment of hemophilia.
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                          haemostatic; blood coagulant factor VII; FVII; haemophilia;
                                                                                                                         .;
0
                                                                                           DB 1; Length 1221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1221;
                                                           Sequence 1221 BP; 248 A; 362 C; 392 G; 219 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1221 BP; 248 A; 365 C; 392 G; 216 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                            Mutant blood coagulant factor VII (FVII-5) coding sequence.
                                                                                                                      Indels
                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /partial
/note= "No start codon given"
                                                                                       Score 20.6; DE
Pred. No. 76;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20.6;
Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 10-11; 29pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=_a
/product= "FVII-5"
                                                                                                                      .;
0
                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.0%;
                                                                                                                                                                                                                                          460/c
AAH19460 standard; DNA; 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99JP-00237610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-00237610
                                                                                       1.0%;
ilarity 59.3%;
Conservative
                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Thes 35; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-310677/33.
P-PSDB; AAB84867.
                                                                            Query Match
Best Local Similarity
Watches 35; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP2001061479-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-AUG-1999;
                                                                                                                                                                                                                                                                                                                31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                           mutant; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                     AAH19460;
                              patients
                                                                                                                                                                                                                                                                                                                                                                             Human;
                                                                                                                                                                                                                          RESULT 23
AAH19460/
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for substitution therapy in

factor VII, used

'partial 'note= "No start codon given"

"FVII-6"

/\*tag= a /product=

location/Qualifiers

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TITGCIGGCATITCTITITICIAGAAIAGGGAITTITCCACAIGGAIAITCAACIGIGG 386
                                                                                                                                                                                                                          ITCAATIGICITITALCIGICGAGACTIGCITIGITITGAAATAIGIATICAATITIGG 392
                                factor VII
                                                                                                                                                                                             Gaps
                           The present invention relates to mutants of blood coagulant factor 'VII' (FVII3), The present sequence is the coding sequence for one such mutant FVII: VII-6. The mutants can be used as an agent for the substitution therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
                                                                                                                                                                                             .
                                                                                                                                                           Length 1221;
                                                                                                                                                                                                                                                                                                                                                                                                                                   coagulant factor VII (FVII-30) coding sequence.
                                                                                                                            Sequence 1221 BP; 248 A; 365 C; 391 G; 217 T; 0 U; 0 Other;
                                                                                                                                                                                           24; Indels
                                                                                                                                                           DB 1;
                                                                                                                                               Score 20.6; DF
                                                                                                                                                                          Pred. No. 76;
Disclosure; Page 13-14; 29pp; Japanese.
                                                                                                                                                                                         .,
                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                             haemophilia inhibitor patients
                                                                                                                                                                                                                                                                                                                    AAH19462/c
ID AAH19462 standard; DNA; 1221
                                                                                                                                                           1.0%;
                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                         35; Conservative
                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutant blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutant; ds
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Gaps

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Indels

24;

0; Mismatches

Conservative

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334 TICAATIGICITITAICIGICGAGACTIGCITIGITITIGAAATAIGIATICAATITIGG 392 irreciedcariricriririciadaraddrariririccacardraricaacherde 386

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Chen X;

Key

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The invention relates to a cell-free, in vitro method of remodeling a peptide. The method involves removing a saccharyl subunit from the peptide. The method involves removing a saccharyl subunit from the conflue forming a truncated glycash, and contacting the truncated glycash, that least one glycosyl transferase and at least one glycosyl color under conditions suitable to transfer at least one glycosyl donor content of the truncated glycash, thus remodeling the peptide. Conjugates can be formed between a granulocyte colony stimulating factor (G-CSF) peptide, interferon alpha peptide, interferon beta peptide, Factor VII a peptide, reactor IX peptide, follicle stimulating formone peptide, erythropoietin (BPO) peptide, interferon-gamma peptide, alpha-1-protease inhibitor (A-L-FI) peptide, interleukin-2 (IL-2) peptide, the saminogen activator (TPA) peptide, interleukin-2 (IL-2) peptide, the saminogen activator (TPA) peptide, interleukin-2 (IL-2) peptide, transminogen activator (TPA) peptide, interleukin-2 (IL-2) peptide, transminogen activator (TPA) peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-respiratory syncytial virus (RSV) F peptide, and modifying group, where the modifying group is covalently attached to the peptide through an inteact glycosyl linking croup. The method is useful for a cell-free, in vitto method of remodeling the above mentioned publice. The present sequence represents
                                                                                                                                                                                                                                                             Remodeling a peptide, by removing a saccharyl subunit from the peptide to form truncated glycan, and adding or deleting glycosyl groups to a peptide and/or adding modifying group of a peptide to remodel the peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             558 iligeledealilerililieladaaladelalilileeakaldealalieaakileide 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334 TICAATIGICTITITATCIGICGAGACTIGCTITGTITIGAAATAIGIATTCAATTITGG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Truncated tissue factor; tTF; factor VIIa; FVIIa; activator;
bleeding disorder; haemophilia; liver cirrhosis; coagulation;
transmembrane domain; extracellular domain; soluble; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 1332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1332 BP; 260 A; 405 C; 426 G; 241 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24; Indels
                                                                                                                                                                                 Hakes D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.0%; Score 20.6; 1
59.3%; Pred. No. 77;
                                                                                                                                                                               Bayer R, Bowe C,
                                                                                                                                                                                                                                                                                                                                                                                      Example; Fig 55A; 900pp; English.
                                                                                                                                        (NEOS-) NEOSE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ62299 standard; cDNA; 1440
                                    2002US-0391777P.
2002US-0396594P.
2002US-0404249P.
                                                                                16-AUG-2002; 2002US-0404249P.
28-AUG-2002; 2002US-0407527P.
2001US-0334301P
                   002US-0387292P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
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hes 35, Conservative
                                                                                                                                                                                 Zopf D,
                                                                                                                                                                                                                      WPI; 2003-449162/42.
P-PSDB; ABR55842.
                   07-JUN-2002;
25-JUN-2002;
17-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
  28-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
27-MAY-1994
                                                                                                                                                                                 De Frees S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ62299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 241
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      음
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 TICAATIGICITITATCIGICGAGACTIGCITTGITTTGAAATATGTATTCAATTTIGG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutant of blood coagulant factor VII, used for substitution therapy in the treatment of hemophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to mutants of blood coagulant factor VII (FVII) or activated blood coagulant factor VII (FVIIa). The present sequence is the coding sequence for one such mutant FVII: VII-30. The mutants can be used as an agent for the substitution therapy of haemophilia inhibitor patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide remodeling, glycoconjugation; glycosyltransferase, glycan;
Factor VIIa; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 1221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1221 BP; 251 A; 357 C; 393 G; 220 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Indels
                                                                                                                               'partial
'note= "No start codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.0%; Score 20.6; D. 59.3%; Pred. No. 76; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .1332
/*tag= a
/product= "Factor VIIa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 16-17; 29pp; Japanese
                                             location/Qualifiers
                                                                                                          "FVII-30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACC78872 standard; DNA; 1332 BP
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19-OCT-2001; 2001US-0344692P.
28-NOV-2001; 2001US-0334233P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-OCT-2002; 2002WO-US032263.
                                                                                                                                                                                                                                                                          99JP-00237610.
                                                                                                                                                                                                                                                                                                                 99JP-00237610
                                                                                      /*tag= a
/product= '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 59.3°
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-310677/33.
                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAB84869
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                                                                                                                                                                                            JP2001061479-A.
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                                                                                                                                                                                                                                                                          24-AUG-1999;
                                                                                                                                                                                                                                                                                                                   24-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-APR-2003
                                                                                                                                                                                                                                   13-MAR-2001
          Synthetic
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RESULT 240 ACC78872/c

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Gaps ·.

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deficient tissue factor (TF) compound that is modified to increase its deficient tissue factor (TF) compound that is modified to increase its biological half-life, but excluding modification that involves attachment to an antibody (or its antigan-binding region) that binds to a component invention are compositions containing any coagulation-deficient TF for promoting coagulation containing any coagulation-deficient TF for promoting coagulation are composition-deficient TF are used to promote coagulation preferentially in prothrombotic vessels, particularly those associated with: (i) bening growths (e.g. bening prostatic hypertrophy); (ii) vascularised, malignant tumours of medium or large size (where they also induce tumour necrosis, or (iii) other disorders that involve angiogenesis, e.g. diabetic retinopathy, restenosis, neovascular glaucoma, psoriasis and rheumatoid arthritis. The composition can be administered sytemically, particularly intravenously, typically at 0.2-coagulation, even though they contain no targeting agent. They cause little if any injury to normal tissue; may produce a symergistic response when used with other antitumour agents and they eliminate the multi-step, and expensive, preparation of antibody-based targeting constructs. The present sequence encodes human Factor VIIa, from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 TTCAATTGTCTTTTATCTGTCGAGACTTGCTTTTGTTTTGAAATATGTATTCAATTTTGG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rrrecrecearircrrrrrcradaaraderarrrrrrccacarerrrrrcaacrered
                                                                                                                                                                                                                                                                    Composition containing coagulation-defective tissue factor for treating, e.g. tumours - useful for, e.g. promoting coagulation in pro:thrombotic and tumour-associated vasculature, used with, e.g. factor 7 or anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 1440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse, scFv; immunoconjugate; IgG1 effector domain; cancer; atherosclerosis; tissue factor; macular degeneration; rheumatoid arthritis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1440 BP; 288 A; 434 C; 464 G; 254 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20.6; DB Pred. No. 78; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HfVIIasm immunoconjugate coding sequence.
                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 195; 225pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.0%;
                                         97US-0035920P.
    98WO-US001012
                                                                                 97US-0042427P
                                                                                                                                                                    Gao B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                          (TEXA ) UNIV TEXAS SYSTEM
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Best Local Similarity 59.3
Matches 35, Conservative
                                                                                                                                                                  King SW,
                                                                                                                                                                                                         WPI; 1998-413821/35.
                                                                                                                                                                                                                               P-PSDB; AAW69606
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    20-JAN-1998;
                                           22-JAN-1997;
                                                                                 27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JAN-2001
                                                                                                                                                                    Thorpe PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
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AAF29715/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A compsn. for treatment of patients with prolonged or excessive bleeding disorders comprises truncated tissue factor (tFT) (AAQ52439) and a substance effective to produce a plasma level of factor VIIa which in combination with tFF will control or stop the excessive bleeding. The substance may be factor VIIa itself or an activator which promotes the conversion of endogenous factor VII to factor VIIa. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 ITCAATTGTCTTTTATCTGTCGAGACTTGCTTTGTTTTGAAATATGTATTCAATTTTGG 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                      of VII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; truncated; tissue factor; tTF; TF; tumour; coagulation; blood vessel; Factor VIIa; FVIIa; benign growth; vascularised; benign prostatic hypertrophy; malignant; necrosis; angiogenesis; diabetic retinopathy; restenosis; neovascular glaucoma; psoriasis; rheumatoid arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                    factor-VIIa or activator o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1440 BP; 288 A; 434 C; 464 G; 254 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20.6; DB Pred. No. 78; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Compsn. of truncated tissue factor and fuseful for treating bleeding disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36. .1436
/*tag= a
/product= "Factor VIIa"
Location/Qualifiers
35. 1436
/*tag= a
/product= "factor_VIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 26-28; 43pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                        (OKLA-) OKLAHOMA MED RES FOUND.
                                                                                                                                                                                                                           92US-00882202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.0%;
idlarity 59.3%;
Conservative (
                                                                                                                                                                                   93WO-US004493
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                                                                                                                                                                                                                                                                                                                                  Comp PC;
                                                                                                                                                                                                                                                                                                                                                                       WPI; 1993-386218/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAR52562
                                                                                                                                                                                                                                                                                                                                  Morrissey JH,
                                                                                                                                                                                                                           13-MAY-1992;
19-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
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                                                                                                    W09323074-A1
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                                                                                                                                              25-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cirrhosis.
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AAV40389/c
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The invention discloses a human factor VII polypeptide, or a variant or derivative of it, where an amino acid has been modified. This change cresults in a polypeptide with the same or an increased activity when cremplated by the the same or an increased activity when compared to recombinant wild type human Factor VIIa. Blood components that compists of a complex interaction of various blood components that compared to a fibrin clot. Initiation of the haemostatic process is mediated by the formation of a complex between tissue factor or and Factor VIIa (the active form of the Factor VII zymogen). This complex activates Factors IX and X, converting prothrombin to thrombin, which activates Factors VII and X, converting prothrombin to thrombin, which activates Factors VII zymogen, or its derivative, can be modified in its clot. The Factor VII zymogen, or its derivative, can be modified to clot. The Factor VII zymogen, or its derivative, can be modified in its clot preparing a medicament for the treatment of the Factor VII polypeptide to activate plasma factor X or IX. The factor VII derivative is useful for preparing a medicament for the treatment of bleeding episodes, for the channed actor X or IX. The factor VII derivative is useful for treatment of haemophilia A or B and for inhibiting thrombus formation. The inactivated factor VII derivatives are useful for treating intimal corpus, percutaneous transdermal coronary angioplasty (PTCA), stroke, cancer, tumour metastasis, analysis, arteriosclerosis, acute and chronic cheurations, such as inflammantion, septic shock, hypotension, adult corpusations, distress syndrome (ARDS) and myocardial infarction. The creations than a such contact and processed the contact than contact the contact than a syndrome (ARDS) and myocardial indication, distress syndrome (ARDS) and myocardial indication. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334 ITCAATIGICTITIATCIGICGAGACTIGCITITITIGAAATAIGIATICAATITIGG 392
/transl_except= (pos:387. .389,aa:Xaa)
/note= "No start codon shown. Xaa = gamma carboxylated
glutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    728 thrgchgccathrcrhrhrhchágaragcharrhhrccacargagarartcaachgig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel factor VII polypeptide, its derivatives useful for preparing medicament for treating bleeding episodes, or for enhancing normal hemostatic system, especially for treating hemophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6098 BP; 1413 A; 1587 C; 1623 G; 1475 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence presented is the plasmid, pLN174, which expresses the inactivated human coagulation Factor VII polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 6098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein 5' EST, SEQ ID NO: 24371.
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1.0%; Score 20.6; D
Best Local Similarity 59.3%; Pred. No. 92;
Matches 35; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 82-85; 96pp; English
                                                                                                                                                                                                                                                                                                                                                                                                        22-MAR-2001; 2001DK-00000477.
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                                                                                                                                                                                                                                                                                                                                11-MAR-2002; 2002WO-DK000189.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-058374/05.
P-PSDB; ABG73119.
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                                                                                                                                                                                                                                                        03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Persson E;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC20296
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AC AAC2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a composition comprising a homodimeric immunoconjugate protein made up of two chains, each containing an 1gG1 FC effector domain and a targeting domain. The targeting domain may be either the human 1gG1 FC region or a mutant form of human factor VII. The immunoconjugate is targeted at the transmembrane receptor tissue factor. This enables the composition to be used in the treatment of diseases associated with neovascularisation, including cancer, atherosclerosis, rheumatoid arthritis and macular degeneration
                                                                                                                                                                                                                                                                                                                                                                                                        Immunoconjugate protein for treatment of neovascularization, comprises protein comprising Fc region of human immunoglobulin (Ig)GI conjugated to the targeting domain which comprises factor VII mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; coagulation; Factor VII; Factor VIIa; blood coagulation; fibrin clot; haemostatic; tissue factor; zymogen; Factor IX; Factor X; prothrombin; thrombin; Factor V; Factor VII; fibrinogen; fibrin, plasma factor; bleeding episode; haemophilia A; haemophilia B; thrombus; intimal hyperplasia; restenosis; cardiogenic embolism; stroke; platelet deposition; percutaneous transdermal coronary angioplasty; PTCA; platelet deposition; percutaneous transdermal coronary angioplasty; PTCA; rheumatoid arthritis; arteriosclerosis; inflammation; septic shock; rheumatoid arthritis; arteriosclerosis; inflammation; septic shock; myoccardial infarction; vasotropic; cerebroprotective; antibacterial; immunosuppressive; cardiant; gene therapy; ds; plN174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 ITCAATIGICITITATCIGICGAGACTIGCTTIGITTIGAAATAIGTATTCAATITTGG 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2138 BP; 459 A; 663 C; 648 G; 368 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid pLN174 for expressing human coagulation Factor VII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .344,aa:Xaa-Xaa)
.362,aa:Xaa-Xaa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .305,aa:Xaa-Xaa)
.326,aa:Xaa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (pos:324. .326, aa: xaa-Xa
(pos:324. .326, aa: xaa)
(pos:330. .332, aa: xaa)
(pos:339. .344, aa: xaa-Xa
(pos:357. .362, aa: xaa-Xa
(pos:369. .371, aa: xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag= a 'rtag= a 'product= "Coagulation Factor VII"
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Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 66-67; 69pp; English
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285. .1505
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                                    14-JUN-2000; 2000WO-US016481.
                                                                                                            99US-0142161P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 59.3
Matches 35; Conservative
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                                                                                                                                                                                (UYYA ) UNIV YALE.
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Unidentified.
Synthetic.
                                                                                                            01-JUL-1999;
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ABX14193;

244 RESULT 24 ABX14193/ ID ABX1

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Gaps

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670

Lander ES;

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The present invention is concerned with a number of human single nucleotide polymorphisms (SNPs) which the inventors identified in human genes. These SNPs can be used in disease diagnosis and prediction of an individual's susceptibility to disease, in forensic and paternity testing and in genetic mapping. In particular, the SNPs of the invention can be used to disgnose susceptibility to diseases of the cardiovascular, endocrine and neurological systems, such as coronary artery disease, schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's diseases. Note: The degenerate codon within the sequence represents the position of an SNP, for example the letter S represents a polymorphism where the nucleotide may be C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid selected from one of 106 genes comprising single nucleotide polymorphisms, allele-specific oligonucleotides to the genes are useful for phenotypic correlations, forensics, paternity testing, medicine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 remucidaarcumcenaguescacemcarecemeaarcherecaremreneae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20.4; DB 1; Length 2 Pred. No. 61; 0; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single nucleotide polymorphism containing sequence #379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 259 BP; 67 A; 61 C; 59 G; 71 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                              Ireland JS,
                                                                                                                                                                                                           (WHED ) WHITEHEAD INST BIOMEDICAL RES. (AFFY-) AFFYMETRIX INC.
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                                                                                                                                                                                                                                                                                                              Cargill M, Daley Patil N, Sklar P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 ACTICTGGGCCAGGGTAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 5; 214pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTGTTTTACACAGTTG 78
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                                                                      30-MAR-2000; 2000WO-US008440.
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Best Local Similarity 53.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-611722/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genetic analysis.
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                                                                                                                                                                                                                                                                                                              Altshuler D,
Lipshutz RJ,
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       05-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
       expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 Triecacracia de la comparación de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra del la contra del la contra del la contra del la contra del la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 24371; 71pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single nucleotide polymorphism containing sequence #379.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Giordano J;
                                        gene therapy; chromosome mapping; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC71307 standard; DNA; 259 BP.
                                                                                                                                                                                                                                                                                                                  21-FEB-2000; 2000EP-00200610.
                                                                                                                                                                                                                                                                                                                                                                                    99US-0122487P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-500381/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1056 TG 1057
5' EST;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200058519-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEST ) GENSET
                                                                                                           Homo sapiens
                                                                                                                                                                         EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-FEB-2001
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AAC71307;

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RESULT 246 AAC71307

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Length 259;

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DNA barley

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1472 CTTTTAGTGATTTGATTATTATGCACTGTGGGGAGTTTCTTTTCCGGTCCAATCTATTTG 1531
                                                                                                                                                                            The present invention relates to oligonucleotide clones originating in barley (Hordeum vulgare) which contain single nucleotide polymorphisms (SNP). The oligonucleotides may be used for analysis of SNPs among barley varieties, identification of particular varieties and genotype-phenotype analysis, isolation of specific genes and creation of new varieties by
                                                                                                                                                                                                                                                                      analysis, isolation of specific genes and creation of new varieties by transformation of barley varieties with them and production of new barley varieties with desired properties. The present sequence represents an oligonucleotide clone DNA sequence featured in the specification. The sequence data for this patent did not form part of the printed at feptimise. The present sequence catalon, the specification of the printed at figure this patent did not form part of the printed at fep.wipo.int/pub/published-pct-sequences. (Updated on 27-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer; cytostatic; carcinogen; pharmacodyanamic marker; marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 crigiadinecaraarratrirgradgradgradgegegearrachradrichtrir 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful
                                   Single nucleotide polymorphism sites in barley varieties and I sequences containing them for analysis and identification of transferies and production of barley transformants with desired characteristics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1532 GIGITITGIAIGCIICTIGIACCIIGAIAGGCAICICIIICICA 1575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 288 BP; 82 A; 75 C; 69 G; 52 T; 0 U; 10 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 ceecrererecercarecernarerarererrirraa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20.4; D
Pred. No. 63;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prostate expression marker cDNA 8812.
                                                                                                                                               Disclosure; SEQ ID XX; 284pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ë
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAR-2000; 2000US-0189862P.
25-MAY-2000; 2000US-0207454P.
09-JUN-2000; 2000US-0211314P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABV08821 standard; cDNA; 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0183319P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUL-2000; 2000US-0219007P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 49.0
hes 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endege WO,
WPI; 2003-587127/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-662795/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; prostate
pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABV08821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                      The present invention is concerned with a number of human single nucleotide polymorphisms (SNPs) which the inventors identified in human genes. These SNPs can be used in disease diagnosis and prediction of an individual's susceptibility to disease, in forensic and paternity testing and in genetic mapping. In particular, the SNPs of the invention can be used to diagnose susceptibility to diseases of the cardiovascular, endocrine and neurological systems, such as coronary artery disease, schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's diseases. Note: The degenerate codon within the sequence represents the position of an SNP, for example the letter S represents a polymorphism where the nucleotide may be C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGTCGAGACTTGCTTTTGAAATATGTATTCAATTTTGGA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis;
                                                                                                                                               Nucleic acid selected from one of 106 genes comprising single nucleotide polymorphisms, allele-specific oligonucleotides to the genes are useful for phenotypic correlations, forensics, paternity testing, medicine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 TTTGCTGGCATTTCTTTTTTTAGAATAGGTATTTTTTCCACATGGATATTCAACTGTGTA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA clone originating in barley containing SNP encoding sequence #11586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 259;
                                          Lander ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 259 BP; 67 A; 61 C; 59 G; 71 T; 0 U; 1 Other;
                                          Daley GQ, Ireland JS, Sklar P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.0%; Score 20.4; E58.1%; Pred. No. 61; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (cul.Akashinriki).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                         Claim 1; Fig 5; 214pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001JP-00387131.
2001JP-00403299.
2001JP-00403300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kohara Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-DEC-2002; 2002WO-IB005403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002JP-00327515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACL21595 standard; DNA; 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYNI-) UNIV JAPAN OKAYAMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334 TICAATIGICITITATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                          Cargill M,
Patil N,
    (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hordeum vulgare; var.
                                                                                                       WPI; 2000-611722/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takeda K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 36; Conserv
                                                                                                                                                                                                                genetic analysis.
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20-DEC-2001;
20-DEC-2001;
27-SEP-2002;
                                        Altshuler D,
Lipshutz RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-DEC-2001;
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17-0CT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sato K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
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ACL21595/c
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibit prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                              83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel serine proteases designated BSSP2 (AAB11695-B11699), and to nucleic acids encoding them (AAA61659-A61663).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 refrerriscaciteacecrearisfrecerererriarirerreaaaaaccarrager
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BSSP2; serine protease; mouse; mBSSP2; human; hBSSP2; brain; diagnostic marker; antibody; transgenic animal; Alzheimer's disease; epilepsy; cancer; inflammation; inflammatory disorder; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine protease BSSP2, useful in detecting homologs, mutants and polymorphic variants as markers for diagnosis of e.g. Altheimer's disease, cancer, inflammation and prostate hypertrophy, using bloodurine or other tissues.
for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA encoding mouse serine protease BSSP2 (mBSSP2), SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                   1.0%; Score 20.4; DB 1; Length 397;
llarity 52.3%; Pred. No. 67;
Conservative 0; Mismatches 41; Indels C
                                                                                                                                                                                                                                                                                                                  Sequence 397 BP; 85 A; 89 C; 82 G; 141 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitsui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamaguchi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1157 TGTGGGTAACATCTTTAGATTGAAGT 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 CTTGGGTAGCGTTTTAATATGGAATT 119
                                   Claim 1; Page 1389; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 55-57; 92pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kominami K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-JP006475
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                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAB11695.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA61659;
                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus sp
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Matches
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The invention also relates to vectors and transformants comprising BSSP2 nucleic acids, transgenic animals in which the expression level of BSSP2 can be varied, and an mBSSP2 knockout meduse. The invention additionally antibodies, methods of BSSP2 and methods of production of such antibodies, methods of BSSP2 detection using the antibodies, and the use of BSSP2 proteins or fragments as diagnostic markers for certain medical conditions. Nucleotides encoding BSSP2 were initially isolated in a mouse brain cDNA library using degenerate PCR primers (AAA61673- AAA61674) based on conserved regions of serine proteases. The BSSP2 serine proteases and nucleotides encoding them are useful in detecting homologues, mutants and polymorphic variants in biological samples (e.g., blood, urine, brain, prostate gland and testis) as diagnostic markers for conditions such as Alzheimer's disease, epilepsy, cancer, inflammation, infertility and prostatic hypertrophy. Sequences AAA61659-A61662 represent cDNA encoding human BSSP2 (hBSSP2), and sequence 107 ragreacrecrecrecrecrateracaerricasecrereceeecrarecaecresces 166 85 26 TATITICITGAAGCCTCTGCTGGCAATACTTCTGGGGCTGCTGCCTTTCTCCCTGTCTGA Gaps .. DB 1; Length 717; Sequence 717 BP; 138 A; 204 C; 221 G; 154 T; 0 U; 0 Other; 41; Indels 1.0%; Score 20.4; DB 52.3%; Pred. No. 77; cive 0; Mismatches TICCTAGGGIGAGGGITACCACIGCT 111 167 rrcargcaggcrggrcagccarggr 192 Local Similarity 52.3 nes 45; Conservative 86 Query Match Best Loc Matches g ò ò 셤

Search completed: August 9, 2004, 17:01:34 Job time : 790 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                  August 9, 2004, 16:49:06; Search time 10 Seconds (without alignments) 3.696 Million cell updates/sec
                                                                                                                                         1 agctttccagagagacttca.....tcaaggaccttttatgaatt 2003
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 250 summaries
                                            OM nucleic - nucleic search, using sw model
                                                                                                                                                                IDENTITY_NUC
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                    20 segs, 9225 residues
                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                  us-10-664-775-3
2003
                                                                                                                                                                                                                                                                                                                                    rnidb:*
                                                                                                                 Title:
Perfect score:
                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                          Sequence:
                                                                                                                                                                                                   Searched:
                                                                     Run on:
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GRUERAL INFORMATION:

APPLICANT: Morrissey, James H.

APPLICANT: Comp, Philip C.

TITLE OF INVENTION: Treatment of Bleeding with Modified

TITLE OF INVENTION: Treatment of Combination with FVIIa

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSED: Richards, Medlock & Andrews

STREET: 1201 Elm Street, Suite 4500

CTTY: Dallas

STATE: Texas COUNTRY: US ZIP: 75270-2197

rnidb:* No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed; derived by analysis of the total score distribution.		nave a ng printed,	ZIP: 75270-2197  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMFUTER: IBW PC compatible  OPERATING SYSTEM: PC-DOS/MS-DOS  SOFTWARE: Patentin Release #1.0, Version #1.25  CURRENT APPLICATION DATA:
SUMMARIES			; APPLICATION NUMBER: US/07/882,202A ; FILING DATE: 13-MAY-1992
	De	Description	
	( )	Sequence 3, Appli	; NAME: Hansen, Eugenia S. ; REGISTRATION NUMBER: 3: 966
3	03	m	REFERENCE/DOCKET NUMBER: OMRF B34290
US-08-321-777-3 US-08-300-317-13	co c	ω, t	; TELECOMMUNICATION INFORMATION:
ı m	3 03	Sequence 13, Appl Sequence 13, Appl	; TELEFRONE: 214-939-4500
т.	CO)	Sequence 3, Appli	: INFORMATION FOR SEC ID NO: 3:
	Se	'n	; SEQUENCE CHARACTERISTICS:
	<b>ம்</b>	m i	; LENGTH: 1440 base pairs
	ž č	ω, t	
	, v	sequence 13, Appl Sequence 13, Appl	; STRANDEDNESS: double
	S	, ,	MOLECULE TYPE: CDNA
	Sec	9	
US-08-849-248-6 Seq	Seg	ý.	; ANTI-SENSE: NO
	ם ממ	- C	CHIGINAL SOURCE:
	מיני מיני	sequence 17, Appl Sequence 16, Appl	) ORGANISM: Homo sapiens
	íš	4 .	PRATIES DICCE
	Š	œ	NAME/KEY: CDS
	Se	13,	; LOCATION: 361433
	S	Sequence 13, Appl	; OTHER INFORMATION: /note= "Coding portion of human
	σ		ORMATION: f
-463-953-7	S.	7,	US-07-882-202A-3
	ּ מֿט	7,	
3892-11357-7	ഗ്ര		1.0%;
3-233-//8-Ib	ימ	9	al Simi
	Š,	17,	Matches 35; Conservative 0; Mismatches 24; Indels
1-838-9/2A-/	י מי	- 1	
7-120-7	<b>0</b> , 0,	Sequence 7, Appli Sequence 7, Appli	Qy 334 TTCAATTGTCTTTTATCTGTCGAGACTTGCTTTGTTTTGAAATATGTAT
7-7	Ö		
-636-9	Se	6	
US-08-955-636-10	o <sub>3</sub>	10,	

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TCTGTCGAGACTTGCTTTTGAATATGTATTCAATTTGG 392 TITITCIAGANIAGGIATITITCCACATGGATATICAACTGTGG 601

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c 34	9.2	0.5	56	_		Sequence 22, Appl
35	9.2	0.5	27		0	Seguence 20, Appl
c 36	8.8	0.4	42	,	US-08-955-636-8	Sequence 8, Appli
c 37	8.6	4.0	27	-	US-08-293-778-20 Se	20
c 38	8.4	4.0	36	ч		٥, ١
<u>გ</u>	8.4	0.4	36	-	US-08-955-636-10 Se	음
40	7.4	4.0	56	7		22,
					-	
					ALIGNMENTS	
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RESULT 1 US-07-882-202A-3/C	02A-3/	υ				
; Sequence 3, Application US/07882202A ; Patent No. 5374617	3, App	olication 617	us/c	1788	12202A	

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Tissue Factor in Combination with FVIIa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 36..1433
OTHER INFORMATION: /note= "Coding portion of human
OTHER INFORMATION: factor VII cDNA"
                                                                                                                                                                                                                                                                                                          OPERALING SYSTEM:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,777
FILING DATE:
CLASSIFICATION 514
PRIOR APPLICATION TOWNER: US/08/321,777
FILING DATE: US/08/321,777
FILING DATE: US/08/321,777
FILING DATE: US/08/321,777
ATONINY/AGENT INFORMATION:
APPLICATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 31,966
REGISTRATION NUMBER: 31,966
REGISTRATION INFORMATION:
TELEPROMUNICATION INFORMATION:
TELEPROMUNICATION SEQUENCE: 214-939-4600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 Dase Pairs
                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: Texas
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 59.3
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sap
TISSUE TYPE: Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA HYPOTHETICAL: NO
     FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-321-777-3
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                                      US-08-021-618-19C

Sequence 3 Application US/08021615A

Parent No. 550064

GENERAL INFORMATION TO SEQUENCE:

PAPPLICANT: Comp. Philip C.

TITLE OF INVENTION: Tissue Factor in Combination with an Activator of TITLE OF INVENTION: Tissue Factor in Combination with an Activator of TITLE OF INVENTION: Tissue Factor in Combination with an Activator of TITLE OF INVENTION: Tissue Factor in Combination with an Activator of TITLE OF INVENTION: Tissue Factor in Combination with an Activator of TITLE OF INVENTION: Tissue Factor in Combination with an Activator of TITLE OF INVENTION: Wall of Tissue Factor in Combination with an Activator of TITLE OF INVENTION: Teach of Title 4500

STRAET: 1201 Elm Street, Suite 4500

STRAET: Texas

COMPUTER: INA FC Compatible

OFFICIATION TYPE: FODS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

COMPUTER: INFO FOR TITLE FORM: FC Compatible

OFFICIATION NUMBER: US/08/021,615A

PILLIA DATE: 19-FEB-1993

CLASSIFICATION DATE: 19-FEB-1993

CLASSIFICATION NUMBER: US/08/021,615A

PILLIA DATE: 11-MY-1993

REGISTRATION NUMBER: OMER B34290CIP

TELEPHONE: 214-939-4600

INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:

LENGTH: 1440 base pairs

TYPE: nucleac acid

TYPE: nucleac acid

TYPE: nucleac acid

TYPE: nucleac acid

TYPE: nucleac acid

TYPE: nucleac acid

TYPE: nucleac acid

TYPE: nucleac acid
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1.0%; Score 20.6; DB 1; Length 1440;
Best Local Similarity 59.3%; Pred. No. 0.85;
Matches 35; Conservative 0; Mismatches 24; Indels 0
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Patent No. 5504067
GENERAL INFORMATION:
APPLICANT: Morrissey, James H.
APPLICANT: Comp, Philip C.
TITLE OF INVENTION: Treatment of Bleeding with Modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | NAME/KEY: CDS | LOCATION: 36..1433 | COCATION: 36..1433 | OTHER INFORMATION: / note= "Coding portion of human oTHER INFORMATION: factor VII cDNA" US-08-021-615A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-08-321-777-3/c
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PCT-US93-04493-3/C

FCT-US93-04493-3/C

Sequence 3, Application PC/TUS9304493
GENERAL INFORMATION:
APPLICANT: Morrissey, James H.
APPLICANT: Comp. Philip C.
ITILE OF INVENTION: Truncated Tissue Factor and FVIIa or TITLE OF INVENTION: FVII Activator for Blood Coagulation NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: AD
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GURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04493
FILING DATE: 1930512
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882202
FILING DATE: 13-MAY-1992
PILING DATE: 13-MAY-1992
PILING APPLICATION NUMBER: US 08/021615
FILING DATE: 19-FEB-1993
ATORINGY/AGENT INFORMATION:
NAME: TITUJ110, Doreen Y.
REGISTRATION NUMBER: 35,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20.6; DB 1;
Pred. No. 0.85;
0; Mismatches 24;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEBAX: 214-939-4600
ORMATION FOR SEC.
APPLICATION NUMBER: US 60/042,427
FILING DATE: 27-MAR-1997
APPLICATION DATA:
APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-JAN-1997
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/035,920
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: UF05: 37
TELEPHONE: 512/418-3000
TELEPHONE: 512/418-3000
TELEPHONE: 512/418-3000
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COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 59.3%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-009-656-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
SOFTWARE: Patentli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
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; Sequence 13, Application Us/09009656
; Patent No. 6132730;
GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: Thorpe, Philip E.
APPLICANT: Thorpe, Philip E.
APPLICANT: Thorpe, Philip E.
APPLICANT: Thorpe, Philip E.
APPLICANT: Thorpe, Philip E.
APPLICANT: Thorpe, Philip E.
APPLICANT: Thorpe, Philip E.
APPLICANT: Thorpe, Philip E.
APPLICANT: Gao, Boning
ITILE OF INVENTION: COMBINED TISSUE FACTOR AND FACTOR VIIA
TITLE OF INVENTION: TREATMENT
ITILE OF INVENTION: TREATMENT
INVERE OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STREET: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 ITCAATIGICITITAATCIGICGAGACTIGCTITGITTIGAAATAIGIATTCAATTTIGG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Indels
                   ZIP: 77210

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,217
FILING DATE: CONCURRENTLY Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,656 FILING DATE: Concurrently Herewith CLASSIFICATION:
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.0%; Score 20.6; DB 1;
59.3%; Pred. No. 0.85;
tive 0; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                FILING DATE:

CLASSIFICATION

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/042,427

FILING DATE: 27-MAR-1997

PRIOR APPLICATION NUMBER: US 60/036,205

FILING DATE: 27-JAN 1997

APPLICATION NUMBER: US 60/035,920

FILING DATE: 22-JAN 1997

APPLICATION NUMBER: US 60/035,920

FILING DATE: 22-JAN 1997

APPLICATION NUMBER: US 60/035,920

FILING DATE: 22-JAN 1997

APPLICATION NUMBER: US 60/035,920

FILING DATE: 22-JAN 1997

APPLICATION NUMBER: US 60/035,920

TELEPHONE: 512/418-3000

TELEPHONE: 512/418-3000

TELEPHONE: 512/418-3000

TELEPHONE: 512/418-3000

TELEPHONE: 512/418-3000

TELEPHONE: 512/418-3000

TELEPHONE: 512/418-3000

TELEPHONE: 512/418-3000

SEQUENCE CHARACTERISTICS: TENTITY: 1440 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 59.3
Matches 35; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Gaps

0

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LOCATION: 36..1433
OTHER INFORMATION: /note= "Coding portion of human
OTHER INFORMATION: factor VII cDNA"
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ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08021615A Patent No. 5504064 GENERAL INFORMATION:
                                                                                                                                                                             Query Match 0.8%;
Best Local Similarity 64.1%;
Matches 25; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sap
TISSUE TYPE: Blood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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ANTI-SENSE: N
                                                                                            ;
US-07-882-202A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Tissue Factor"
/note= "Coding portion of human factor VIII cDNA"
/citation= ([1])
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US-07-882-202A-3
US-07-882-202A-3
; Sequence 3, Application US/07882202A
; Sequence 3, Application US/07882202A
; Patent No. 2374617
; APPLICANT: Morrissey, James H.
; APPLICANT: Comp. Philip C.
; APPLICANT: Comp. Philip C.
; TITLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Tissue Factor in Combination with FVIIa
NUMBER OF SECUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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1.0%; Score 20.6; DB 1; Length 1440;
Best Local Similarity 59.3%; Pred. No. 0.85;
Matches 35; Conservative 0; Mismatches 24; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USE

COUNTRY: USE

ZIP: 75270-2197

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/882,202A
FILING DATE: 13-MAY-1992
CLASSIFICATION NUMBER: 31,966
REGISTRATION NUMBER: 31,966
REFRENCE/DOCKET NUMBER: 31,966
REFRENCE/DOCKET NUMBER: 31,966
REFRENCE/DOCKET NUMBER: 31,966
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Blood
                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
TISSUE TYPE: Blood
                      NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 36..1433
OTHER INFORMATION: /
OTHER INFORMATION: /
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                                                          STRANDEDNESS: douk
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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N
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ORIGINAL SOURCE:
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NAME/KEY: CDS

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APPLICANT: Comp. Philip C.
TITLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Tissue Factor in Combination with an Activator of
TITLE OF INVENTION: FVII
NUMBER OF SEQUENCES:
ADDRESSES: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
                                                                                                                          Gaps
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Pred. No. 12;
0; Mismatches 14; Indels 0;
Score 16.6; DB 1; Length 1440; Pred. No. 12; 0; Mismatches 14; Indels 0
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LOCATION: 36..1433

OTHER INFORMATION: /note= "Coding portion of human oTHER INFORMATION: factor VII cDNA"

US-08-021-615A-3
                                                                                                                                                                                                                              1655 ICCTTTGGTTTTGCATAGTGTCTTGGCTTCCTGGATG 1693
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 1993
CLASSIFICATION NUMBER: 08/021,615A
FILING DATE: 19-FEB-1993
ATPONENTY ADDATE: 13-MAY-1992
ATTONNEY ADDER: 13-MAY-1992
ATTONNEY ADDATE: 13-MAY-1992
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ATTONNEY ADDATE: 31,966
REFERENCE/DOCKET NUMBER: 31,966
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REFERENCE/DOC
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Best Local Similarity 64.1%;
Matches 25; Conservative
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APPLICANT: Thorpe, Philip E.
APPLICANT: King, Steven W.
APPLICANT: King, Steven W.
APPLICANT: Gao, Boning
TITLE OF INVENTION: COMMINED TISSUE FACTOR AND
TITLE OF INVENTION: CHEMOTHERAPEUTIC METHODS AND COMPOSITIONS FOR COAGULATION
TITLE OF INVENTION: AND TUMOR TREATMENT
THIRE OF INVENTION: AND TUMOR TREATMENT
NUMBER OF SEQUENCES: 2
CORRESPONDENCES: 27
CORRESPONDENCES: Annold, white & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/09009656
Patent No. 6132730
GENERAL INFORMATION:
APPLICANT: Thorbe, Philip E.
APPLICANT: Gao, Boing
ITLE OF INVENTION: COMBINED TISSUE FACTOR AND FACTOR VIIA
TITLE OF INVENTION: TREATMENT
TITLE OF INVENTION: TREATMENT
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,217
FILING DATE: CONCURTENTLY Herewith
CLASSIPICATION NUMBER: US 60/042,427
FILING DATE: 27-MAR-1997
PRIOR APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-JAN-1997
PRIOR APPLICATION NUMBER: US 60/035,920
FILING DATE: 22-JAN-1997
ATORNEY/AGENT INFORMATION:
NAME: Hibler: David W ...
REGISTRATION NUMBER: 41,071
REGISTRATION NUMBER: 41,071
REGISTRATION NUMBER: 41,071
FELEFMA: 512/418-300
TELEFMA: 512/418-300
TELEFMA: 512/418-301
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
L'ENGTH: 1440 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 16.6; DB
Pred. No. 12;
0; Mismatches
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Best Local Similarity 64.1<sup>1</sup>
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                  CITY: nc.
STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-09-009-656-13
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                                                                                                                             US-08-321-777-3

US-08-321-777-3

Sequence 3, Application US/08321777

Patent No. 5504067

GENERAL INFORMATION:

APPLICANT: Morrissey, James H.

APPLICANT: Morrissey, James H.

APPLICANT: Treatnent of Bleeding with Modified

TITLE OF INVENTION: Treatnent of Bleeding with Modified

TITLE OF INVENTION: Treatnent of Bleeding with FVIIa

CORRESPONDENCE ADDRESS.

ADDRESSEE: Richards, Medlock & Andrews

STATE: 1201 Elm Street, Suite 4500

CITY: Dallas

STATE: Texas

CONTRY: US

ZIP: 75270-2197

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/321,777

FILING DATE: USMONTA:
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Outlier 140;
Best Local Similarity 64.1%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 14; Indels 0
1655 TCCTTTGGTTTTTGCATAGTGTCTCTGGCTTCCTGGATG 1693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS

LOCATION: 36.1433
COTHER INFORMATION: /note= "Coding portion of human of There Information: factor VII cDNA"
US-08-321-777-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1655 TCCTTTGGTTTTTGCATAGTGTCTCTGGCTTCCTGGATG 1693
                                            58 rcircricricricridentrasederecirederie 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION ......
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882202
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: OMRF B34290C
TELEPHONE: 214-939-4600
TELEPAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo say
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NC
ANTI-SENSE: NO
ORIGINAL SOURCE:
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3: Arnold, White & Durkee P.O. Box 4433

RESULT 10 US-09-009-217-13 ; Sequence 13, Application US/09009217

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ADDRESSEE: Bacon and Thomas
STREET: 625 Slaters Lane, 4th Floor
CITY: Alexandria
FILING DATE: 13-WAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021615
FILING DATE: 19-FEB-1993
ATTORNEY/AGBNT INFORMATION:
NAME: Trujillo, Doren Y.
REGISTRATION NUMBER: 35,719
REFERENCS/DOCKET NUMBER: OMRP B3429
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4600
TELEPAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-849-248-6/c
; Sequence 6. Application US/08849248
; Patent No. 5948759
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1440 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE TYPE: Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US93-04493-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
0.8%; Score 16.6; DB 1; Length 1440;
Best Local Similarity 64.1%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application PC/TUS9304493
GENERAL INFORMATION:
APPLICANT: MORTISSEY, James H.
APPLICANT: Comp. Philip C.
TITLE OF INVENTION: Truncated Tissue Factor and FVIIa or
TITLE OF INVENTION: FVII Activator for Blood Coagulation
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1655 TCCTTTGGTTTTTGCATAGTGTCTCTGGCTTCCTGGATG 1693
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                                                                                                                                                       COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NAMBER: US/09/009,656
FILING DATE: CONCURTENTLY Herewith
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04493
FILING DATE: 19930512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Richards, Medlock & Andrews STREET: 1201 Blm Street, Suite 4500 CITY: Dallas STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRICE APPLICATION DATA:
APPLICATION NUMBER: US 60/042,427
FILING DATE: 27-MAR-1997
PRIOR APPLICATION UNDER: US 60/036,205
FILING DATE: 27-JAN-1997
PRIOR APPLICATION UNDER: US 60/036,205
FILING DATE: 27-JAN-1997
APPLICATION UNDER: US 60/035,920
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W.
41,071
Tr. UTSD:537
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIF: 75270-2197
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                               Texas
                                                                                                                               77210
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                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
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LOCATION: 36..1433
OTHER INFORMATION: /product= "Tissue Factor"
OTHER INFORMATION: /note= "Coding portion of human factor VIII cDNA"
OTHER INFORMATION: /citation= ([1])
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0.8%; Score 16.6; DB 1; Length 1440;
Best Local Similarity 64.1%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 14; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Husbyn, Mette
APPLICANT: Fischer, Peter
APPLICANT: Fischer, Peter
APPLICANT: Orining, Lars
TITLE OF INVENTION: Factor VII Fragment 82-128 and its use
TITLE OF INVENTION: in blood clotting disorders
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: BW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/849,248
FLING DATE: 37 Aug 1997
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
ITYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1655 TCCTTTGGTTTTTGCATAGTGTCTCTGGCTTCCTGGATG 1693
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OMRF B34290CIPC/PCT
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ADDRESSEE: No. 55806600 No. 5580560disk of No. 5580560th America, Inc. STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10.74-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,7.78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 27;
                                                                                                                                             Length 38;
                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                           Score 12; DB 1;
Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Nicolaisen, Else M.
APPLICANT: Nicolaisen, Else M.
APPLICANT: Wiberg, Finn C.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIA
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 11.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
FILING DATE: 25-UN-1987
FILING DATE: 25-UN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/434,149
FILING DATE: 33.00.1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 24-UN-1988
FILING DATE: 12-UN-1988
FILING DATE: 12-UN-1992
ATTORNEY/AGBNT INFORMATION:
NAME: AGITS, CHETYI H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3129.224-US
                   ; SEQ ID NO 4
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-558-027-4
                                                                                                                                                                                                                                                                                                                            RESULT 16
10S-08-293-778-17/c
1 Sequence 17, Application US/08293778
Patent No. 5580560
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REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
                                                                                                                                                                                                                           787 AGGCCATTTGCTTAGAATA
                                                                                                                                           0.6%;
ilarity 75.0%;
Conservative 0
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                     Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE:
US-08-293-778-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
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0
                                                                                 DB 1; Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 12.6; DB 1; Length 141; 55.8%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                        Factor VII Fragment 82-128 and its use in blood clotting disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1288 TTCTAAGTGCAGTAGTCTGGCCTGACATCTGTAGTCTCTTGGA 1330
                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/849,248
FILING DATE: 27 Aug 1997
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base ---
TYPET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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APPLICANT: Wiberg, Finn
APPLICANT: Wiberg, Finn
APPLICANT: Wiberg, Finn
APPLICANT: Wiberg, Finn
ATITUE OF INVENTION: Method for the Production of FVII
FILE REPRENCE: 5565_204-US
CURRENT APPLICATION NUMBER: US/09/558,027
CURRENT FILING DATE: 2000-04-25
PRIOR FILING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                           0.6%; Score 12.8; D
70.8%; Pred. No. 61;
tive 0; Mismatches
;
US-08-849-248-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: ALOURESS:
STREET: 625 Slaters Lane, 4th Floor CITY: Alexandria STATE: Virginia COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "recombinant DNA'
                                                                                                                                                             41 TCTGCTGGCAATACTTCTGGGGCT 64
                                                                                                                                                                                                 25 rcaecreercarccrrerecercr 2
                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08849248
Patent No. 5948759
GENERAL INFORMATION:
APPLICANT: HUBDYN, Mette
APPLICANT: Fischer, Peter
APPLICANT: Corning, Lars
TITLE OF INVENTION: in blood clott
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bacon and Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOSTWARE: Patentin Palace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "recombinar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-558-027-4/c
, Saquence 4, Application US/09558027
; Patent No. 6329176
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 141 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                         Query Match
Best Local Similarity 70.8'
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 55.8
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                   US-08-849-248-6
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RESULT 18
US-09-558-027-4
; Sequence 4, Application US/09558027
; Patent No. 6329176
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Matches 20; Conserv
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US-08-756-506-13/c
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 4
LENGTH: 38
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Sequence 16, Application US/08293778
Sequence 16, Application US/08293778

Bapticant Nicolaisen, Else M.
APPLICANT Nicolaisen, Else M.
APPLICANT Wiberg, Finn C.
APPLICANT Woodbury, Richard
TITLE OF INVENTION: WOOTFIED FACTOR VII/VIIa
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: 405 Lexington Avenue, 62nd Floor
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
COUNTRY: United States of America
21P: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM FC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAMES: US/08/293,778
                        ë.
81.2%; Pred. No. 47; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
APPLICATION NUMBER: DK 3235/87
FILING DATE: 25-UUN-1987
PRIDR APPLICATION DATE: 25-UUN-1987
FILING DATE: 13-NOV-1989
FILING DATE: 13-NOV-1989
PRIDR APPLICATION NUMBER: US 07/434,149
FILING DATE: 47-UUN-1988
PRIDR APPLICATION DATE: 47-UUN-1988
PRIDR APPLICATION NUMBER: US 07/899,248
FILING DATE: 12-UUN-1992
ATTORNEY/AGBNT INFORMATION:
NAME: AGIS, Cheryl H.
REGISTRATION NUMBER: 3129.224-US
REFERENCE/DOCKET NUMBER: 3129.224-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHRACATERISTICS:
LENGTH: 27-2867-0123
TELESTAX: 212-867-0123
TELESTAX: 212-867-0123
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
                                                                        1682 GCTTCCTGGATGTTT 1697
                                                                                                                        23 GCGTCCTGGAAGATT
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Best Local Similarity 81.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 rcrrcaaggac 21
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US-08-293-778-16
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                                                                                                                                                                                                  RESULT 17
US-08-293-778-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 0.5%; Score 11; DB 1; Length 38; 1 Similarity 57.1%; Pred. No. 83; 20; Conservative 0; Mismatches 15; Indels
GENERAL INFORMATION:
APPLICANT: Woldike, Helle
APPLICANT: Wiberg, Finn
APPLICANT: Wiberg, Finn
APPLICANT: Wiberg, Finn
APPLICANT: Wiberg, Finn
APPLICANT: Wiberg, Finn
APPLICANT: Wiberg, Finn
APPLICANT: Method for the Production of FVII
FILE REPERENCE: 5565.204-US
CURRENT APPLICATION NUMBER: US/09/558,027
CURRENT FILING DATE: 2000-04-25
FRIOR APPLICATION NUMBER: 60/108,065
FRIOR APPLICATION NUMBER: 60/108,065
FRIOR APPLICATION NUMBER: 4
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-955-636-8
; Sequence 8, Application US/08955636A
; Patent No. 6617882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: POLYPEPTIDES
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REPERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT APPLICATION NUMBER: 197-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           527 GACCTAACTGTTGGAGAGAATGGGGTATTGAAGTA 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GAATICACIAGICIAGGGAAAIGGGGCICGCAGGA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 CACTICIGGGCCAGGGTAGGGGCAC 156
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APPLICANT: Garner, lan APPLICANT: Temperley, Simon M. APPLICANT: Foster, Donald C.; APPLICANT: Sprecher, Cindy A.; APPLICANT: Prunkard, Donna E.
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
CRGANISM: Saccharomyces cerevisiae
US-09-558-027-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
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0.5%; Score 10.4; DB 1; Length 45; 60.7%; Pred. No. 1.6e+02; Live 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HOLLY, Richard D.
APPLICANT: HOLLY, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESSE:
ADDRESSES: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower,
CITY: STREET: Twentieth Floor
CITY: CAN Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DUS
SOUTHWARE: Patentin Release #1.0, Version #1.25
CUGRENT APPLICATION DATA:
FILING DATE: 19921230
CLASSIFICATION: 435
FILING DATE: 19921230
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/860,701
FILING DATE: 19922
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAMM: PATHOLISE: 13.990
REFERENCE/POCKET NUMBER: 13.990
REFERENCE/POCKET NUMBER: 13.990
REFERENCE/POCKET NUMBER: 13.990
TELEPHONE: 206-46-9600
TELEPHONE: 206-46-9600
TELEPHONE: 206-46-9600
TELERATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        536 GIIGGAGAAIGGGGIAIIGAAGIAGC 563
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ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-998-972A-7/c
; Sequence 7, Application US/07998972A
; Patent No. 5476777
                                                CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 95-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

CLONE: ZC6337

US-08-756-506-13
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Best Local Similarity
Matches 17; Conserv
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STRANDEDNESS:
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0.5%; Score 10.6; DB 1; Length 45;
Best Local Similarity 57.6%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cottingham, Ian R.
APPLICANT: Cottingham, Ian R.
APPLICANT: Temperlay, Simon M.
APPLICANT: Temperlay, Simon M.
APPLICANT: Sprecher, Condy A.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Prunkard, Donna B.
ITTLE OF INVENTION: AND A.
ITTLE OF INVENTION: ANIMALS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSED: ZymoGenetics, Inc.
    PROTEIN C PRODUCTION IN TRANSGENIC ANIMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                     CAMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,506
FILING DATE:
CLASSIFICATION: BOOTA:
NAME: SAWIBLAK, DEBOTA A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 95-28
TELEFAX: 206-442-6672
TELEFAX: 206-442-6673
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: MULDIC CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: MULDIC CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: MULDIC CHARACTERISTICS:
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                                                                                                                                                                                ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-756-506-13

Sequence 13, Application US/08756506

Patent No. 2805185

GENERAL INFORMATION:

APPLICANT: Garner, lan
TITLE OF INVENTION: PRO
TITLE OF INVENTION: ANN
NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE
CLONE: ZC6337
                                                                                                                                                                                                                                                                                                                    STATE: WA
COUNTRY: US
ZIP: 98102
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                                                                                     Length 35;
                                                                                                                                                                                                                                                                                            RESULT 23
US-08-463-7/C
Sequence 7, Application US/08463953
Sequence 7, Application US/08463953
Fatent No. 5502034
GENERAL INFORMATION:
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend
STREET: Twentieth Floor
STREET: Twentieth Floor
CITY: San Francisco
STATE: CASH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,953
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
0.5%; Score 10; DB 1; Le
Best Local Similarity 72.2%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 5;
                                                                                     Score 10; DB 1; 1 Pred. No. 1.7e+02;
                                                                         0.5%; bcc...
72.2%; Pred. No. ...
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
PRILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: PARMELSE, Steven W
REGISTRATION NUMBER: 31,990
REPERRENCE/DOCKET NUMBER: 31,990
REPERRENCE/DOCKET NUMBER: 13952-12-2
TELECHONE: 206-457-9600
TELEPHONE: 206-457-9600
TELEPHONE: 206-457-9600
TELEPHONE: 206-457-9600
TELEPHONE: 206-457-9600
TELEPHONE: 206-457-9600
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TELEPHONE: 206-457-9600
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                                                                                        Query Match 0.5
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
CLONE: ZC1324
8-463-957
IMMEDIATE SOURCE:
                      ;
US-07-998-972A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-463-953-7
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> RESULT 24 US-08-462-261-7/c

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Sequence 17, Application US/08293778
Patent No. 5580560
GENERAL INFORMATION
APPLICANT: Bjorn, Soren E.
APPLICANT: Wicolaisen, Else M.
APPLICANT: Wicolaisen, Else M.
APPLICANT: Wicolaisen, Else M.
APPLICANT: Wicolaisen, Else M.
APPLICANT: Wicolaisen, Else M.
APPLICANT: Wicolaisen, Else M.
APPLICANT: Wicolaisen, Else M.
APPLICANT: Wicolaisen, Else M.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa
NUMBER OF SEQUENCES: 26
NUMBER OF SEQUENCES: 26
NUMBER OF SEQUENCES: ADRESS:
ADDRESSEE: No. 5580560ch America, Inc.
CITY: New York
STATET: New York
STATET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
FILING DATE: 25-UUN-1987

PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989

PRICR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 24-UUN-1988

PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-UUN-1992
ATTORNEY,AGENT INPORMATION:
NAME: AGLIS, Cheryl H
REGISTRATION NUMBER: 34,086

REGISTRATION NUMBER: 34,086

REFERENCE/DOCCOMINICATION INPORMATION:
TELECEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION 1935
PRIOR APPLICATION NUMBER: US/08/104,509
FILING DATE:
APPLICATION NUMBER: US/08/104,509
FILING DATE:
APPLICATION NUMBER: US 035/87
FILING DATE: 13-NOV-1989
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 24-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STAIE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          447 GTCTGTAAATATCTCTAGGTC 467
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                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7<sup>3</sup>
Matches 14; Conservative
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; MOLECULE TYPE: CDNA
US-08-293-778-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 27
US-08-293-778-17
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APPLICANT: Bjorn, Soren E.
APPLICANT: Bjorn, Soren E.
APPLICANT: Bjorn, Soren E.
APPLICANT: Wiberg, Finn C.
APPLICANT: Woodbury, Finn C.
APPLICANT: Woodbury, Finn C.
APPLICANT: Woodbury, Finn C.
APPLICANT: Woodbury, Finn C.
APPLICANT: Woodbury, Finn C.
APPLICANT: Woodbury, Finn C.
APPLICANT: Woodbury, Finn C.
APPLICANT: Woodbury, Finn C.
APPLICANT: New York
COUNTRY: United States of America
APPLICATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BARCHIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 10; DB 1; Length 35;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7e+02; -
ss 5; Indels
                COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURBATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURBATING DATE: 19921230
CLASSIFICATION NUMBER: PCT/US92/11357
FILING DATE: 31.MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/866,701
FILING DATE: 31.MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 31.992
PRIOR APPLICATION NUMBER: 31.992
FILING DATE: 31.DEC-1991
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 13952-12-2
TELECOMMUNICATION INFORMATION:
TELEFHONE: 206-467-9600
TELEFHOME: 415-543-5043
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LEDGTH: 35 base pairs
TYPE: NUCLEIC ACID
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.5%; Score 10; DB Best Local Similarity 72.2%; Pred. No. 1.7e Matches 13; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PILING DATE:
CLASSIPICATION: 435
RICR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/08293778
Patent No. 5580560
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1296 GCAGTAGTCTGGCCTGAC 1313
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

IMMEDIATE SOURCE:

CLONE: ZC1324

PCT-US92-11357-7
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US-08-293-778-16/c
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Score 9.8; DB 1; Length 27; Pred. No. 1.6e+02; 0; Mismatches 7; Indels
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                                                                                                              Length 35;
                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08463953;
Sequence 7, Application US/08463953;
Patent No. 5502034
GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend STREET: One Market Plaza, Stewart Street Tower, STREET: Thentieth Floor
CITY: San Francisco
STREET: CANTE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,953
FILING DATE: US/08/463,953
FILING DATE: US/08/463,953
FILING DATE: WS 07/860,701
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: PATMELS: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 7:
SEQUENCE CRARACTERISTICS:
LENGTH: 35-Dase pairs
LENGTH: 35-Dase pairs
                                                                                                            Score 9.4; DB 1;
Pred. No. 2.7e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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                                                                                                                                                                                                            1683 CTTCCTGGATG 1693
                                                                                                                   Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTCCTGGAGG 31
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IMMEDIATE SOURCE:
CLONE: ZC1324
                            IMMEDIATE SOURCE:
CLONE: ZC1324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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US-08-462-261-7
                                                                     US-07-998-972A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                           RESULT 29
US-08-463-953-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/07998972A;
Sequence 7, Application US/07998972A;
GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend STREET: One Market Plaza, Stewart Street Tower, STREET: Twentieth Floor
CITY: San Francisco
STARET: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: BENCOMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/998,972A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19921230
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-WAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
ATTONIEY/AGENT INFORMATION:
NAME: PARMELS, 31-DEC-1991
ATTONIEY/AGENT INFORMATION:
NAME: PARMELS, 31,990
REGISTRATION NUMBER: 31,990
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-12-2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
PRIOR APPLICATION DATA:

PRIOR APPLICATION UNBER: US 07/898,248

FILING DATE: 12-UTN-1992

ATTORNEY/AGENT INFORMATION:

NAME: AGTIS, Cheryl H.

REGISTRATION NUMBER: 34,086

REFERENCE/DOCKET NUMBER: 3129.224-U;

TELECHOWINICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEPHONE: 212-867-0123

TELEPHONE: 212-867-0123

TELEPHONE: 212-867-0123

TELEPHONE: 212-867-0123

TELEPHONE: 212-867-0123

TELEPHONE: 212-867-0123

TELEPHONE: 212-867-0123

TYPE: UNCORPATION OF SEQ IN NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs

TYPE: nucleic acid

STARNDEDNESS: single

TOPOLOGY: linear

105-08-293-778-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-543-5043
FORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1981 TCTTCAAGGAC 1991
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 9.4; DB 1; Length 35;
Pred. No. 2.7e+02;
); Mismatches 1; Indels',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 36;
                                   COMPUTER READBELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Data PC-DOS/MS-DOS
SOFTWARE: PATHING NG-DOS
SOFTWARE: PATHING NAMES: PCT/US92/11357
FILING DATE: 19921230
FILING DATE: 19921230
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
PRIOR APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: PATMING NUMBER: 31,990
REGISTRATION NUMBER: 31,990
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-12-2
TELEPHONE: 206-467-9600
TELEPHONE: 206-467-9600
TELEPHONE: 206-467-9600
TELEPHONE: 206-467-9600
TELEPHONE: 206-467-9600
TELEPHONE: 206-467-9600
TTELEPHONE: 206-467-9600
TTELEPHONE: 206-467-9600
TTELEPHONE: 206-467-9600
TTELEPHONE: 206-4019
TYPE: NUCLEIC ACID
COMPUTER ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE: OTHER INFORMATION: Protein C mutagenic oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGS-08-95-636-9

Sequence 9, Application US/08955636A

Sequence 9, Application US/08955636A

PAPELICANT: Nelsestuen, Gary

TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT;

TITLE OF INVENTION: POLYPEPIED VITAMIN K-DEPENDENT;

TITLE OF INVENTION: POLYPEPIED VITAMIN K-DEPENDENT;

TITLE OF INVENTION: POLYPEPIED VITAMIN K-DEPENDENT;

CURRENT APPLICATION NUMBER: US/08/955,636A

CURRENT FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 35

SEQ ID NO 9

SEQ ID NO 9

LENGTH: 36
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0.5%; Score 9.4; DB 1; L
Best Local Similarity 68.4%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 6;
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ORGANISM: Artificial Sequence
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Best Local Similarity 90.9
Matches 10; Conservative
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IMMEDIATE SOURCE:
CLONE: ZC1324
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Sequence 7, Application US/08462261

Patent No. 5527632

GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
ITILE OF INVENTION: METHODS FOR PRODUCING THROMBIN NUMBER OF SEQUENCES:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower, STREET: Twentieth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,261
FILING DATE: 30-DEC-1992
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-MAR-1992
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-MAR-1992
APPLICATION NUMBER: 31,990
REGISTRATION NUMBER: 31,990
REGISTRATION NUMBER: 31,990
REGISTRATION NUMBER: 31,990
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REGISTRATION NUMBER: 31,990
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GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
ITILE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower,
STREET: Twentieth Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 9.4; DB 1;
Pred. No. 2.7e+02;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 206-467-9600
TELEPAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.5
Best Local Similarity 90.9
Matches 10; Conservative
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Sequence 20, Application US/08293778
Sequence 20, Application US/08293778
Seturn No. 5580560
GENERAL INFORMATION:
APPLICANT: Nicolaisen, Else M.
APPLICANT: Wiberg, Finn C.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: WODIFIED FACTOR VII/VIIa
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 55805600 NO. 5580560disk of No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3129.224-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
FILING DATE:
APPLICATION NUMBER: DX 3235/87
FILING DATE: 25-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 24-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 31.
TELECOMMUNICATION INFORMATION.
TELEPHONE: 212-867-0123
REFERENCE/DOCKET NUMBER: 3:
TELECOMMUNICATION INFORMATION
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                      1814 GTCTCTGAGGTTCC 1827
                                                              INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 26 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GICTCCGACCTICC 12
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Agris, Cheryl H. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 78.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 35
US-08-293-778-20
                                                                                                                                                                                                                                                               US-08-293-778-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred, No. 2.76+02;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Protein C mutagenic oligonucleotide US-08-955-636-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/293,778 FILING DATE:
                         Sequence 10. Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Nicolaisen, Else M.
APPLICANT: Bjorn, Soren E.
APPLICANT: Wiberg, Finn C.
APPLICANT: Woodbury, Richard
APPLICANT: Woodbury, Richard
NUMBER OF INVENTION: MODIFIED FACTOR VII/VIIA
CORRESPONDENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRICATION NUMBER: US 07/434,149
PRICATION NUMBER: US 07/434,149
PRICATION DATA:
APPLICATION DATA:
PLING DATE: 24-JUN-1988
PRICATION NUMBER: PCT/DK88/00103
PRICATION NUMBER: US 07/898,248
PILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: AGIST Cheryl H.
REGISTRATION NUMBER: 34,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
FILING DATE:
APPLICATION NUMBER: DK 3235/87
FILING DATE: 25-UN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/434,149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
COUNTY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 34
US-08-293-778-22/c
; Sequence 22, Application US/08293778
Patent No. 5580560
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 GCACTACCGCATTCCCTCT 171
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 68.4%;
Matches 13; Conservative
               US-08-955-636-10/c
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SSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
T: 405 Lexington Avenue, 62nd Floor
New York
0.5%; Score 9.2; DB 1; Length 26; 78.6%; Pred. No. 2.5e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
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0.4%; Score 8.4; DB 1; Length 36; 66.7%; Pred. No. 4.4e+02; tive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Protein C mutagenic oligonucleotide US-08-955-636-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 38
US-08-955-636-9/c
; Sequence 9, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT;
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION VUMBER: US/08/955,636A
; CURRENT FILING DAITE: 1997-11-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PastSEQ for Windows Version 3.0
; LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
0.4%; Score 8.5; DB 1; I
Best Local Similarity 60.9%; Pred. No. 3.9e+02;
Matches 14; Conservative 0; Mismatches 9;
                  FILING DATE:
APPLICATION NUMBER: DK 3235/87
FILING DATE: 25-JUN-1987
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-MOV-1989
PRICH APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 12-JUN-1988
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-JUN-192
ATTOCHARM INDOMATION:
NAME: AGIIS, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129.224-US
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
TELECOMATONICATION INFORMATION:
TELECOMATONICATION INFORMATION:
TELECOMATONICATION INFORMATION:
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APPLICATION NUMBER: US/08/104,509
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: CDNA
US-08-293-778-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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US-08-955-636-10
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APPLICANT: Bjorn, Soren E.
APPLICANT: Wiberg, Finn C.
APPLICANT: Wiberg, Finn C.
APPLICANT: Wiberg, Finn C.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS: 26
CORRESPONDENCE ADDRESS: 36
CORRESPONDENCE ADDRESS: 36
CORRESPONDENCE ADDRESS: 36
CONTRY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER: RabDable FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: BAPPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
FILING DATE:
CLASSIFICATION DATA:
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                                                                                                                                         Query Match 0.5%; Score 9.2; DB 1; Length 27; Best Local Similarity 78.6%; Pred. No. 2.6e+02; Matches 11; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.4%; Score 8.8; DB 1; Length 42; Best Local Similarity 52.8%; Pred. No. 3.7e+02; Matches 19; Conservative 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
; OTHER INFORMATION: Protein C mutagenic oligonucleotide US-08-955-636-8
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08955636A
Sequence No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED UTAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REPERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT APPLICATION NUMBER: 197-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 TICTIGAAGCCICIGCIGGCAAIACTICIGGGGCIG 65
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Patent No. 5580560
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                           134 CTTCTGGGCCAGGG 147
                                                                                                                                                                                                                                                                                          2 cracredaccrede 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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US-08-293-778-20/c
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APPLICANT: Nicolaisen, Else M.
APPLICANT: Nicolaisen, Else M.
APPLICANT: Nicolaisen, Else M.
APPLICANT: Wiberg, Finn C.
APPLICANT: Wiberg, Finn C.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: MODIFTED FACTOR VII/VIIa
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 55805600 No. 5580560th America, Inc.
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CONTYRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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0.4%; Score 8.4; DB 1; Length 36;
Best Local Similarity 66.7%; Pred. No. 4.4e+02;
Matches 12; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Protein C mutagenic oligonucleotide
US-08-955-636-10
APPLICANT: Nelsestuen, Gary III-E OF INVENTION: MODIFIED VITAMIN K-DEPENDENT III-E OF INVENTION: MODIFIED VITAMIN K-DEPENDENT III-E OF INVENTION: POLYPEPTIDES FILE REFERENCE: 09531/002001 WINMER: US/08/955,636A; CURRENT PILING DATE: 1997-10-23 NUMBER OF SEQ ID NOS: 35 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 10 SEQ ID NOS: 36 LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE:
CLASSIFICATION: 435
PILING DATE:
PLING APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
FILING DATE:
APPLICATION NUMBER: US/335/87
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,149
FILING DATE: 25-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/434,149
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/898,248
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: AGISTRATION NUMBER: 34,086
RESISTRATION NUMBER: 34,086
RESISTRATION NUMBER: 34,086
RESISTRATION NUMBER: 3129.224-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
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US-08-293-778-22
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| JENGTH: 26 base pairs |
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Sequence 7, Ag
Sequence 7, Ag
Sequence 7, Ag
Sequence 7, Ag
Sequence 13, A
Sequence 12, Ag
                                                                      (without alignments)
3.874 Million cell updates/sec
                                                                                                 us-10-664-775-3
2003
1 agctttccagagagacttca......tcaaggaccttttatgaatt 2003
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                                                              9, 2004, 16:49:40 ; Search time 26 Seconds
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       5.1.6
Compugen Ltd.
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US-10-411-026-7
US-10-411-046-7
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US-10-617-619-9
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                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                              SUMMARIES
       GenCore version
Copyright (c) 1993 - 2004
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Maximum Match 100%
Listing first 250 summaries
                                            nucleic search, using sw model
                                                                                                                                      IDENTITY NUC Gapop 10.0 , Gapext 0.5
                                                                                                                                                                  61 segs, 25143 residues
                                                                                                                                                                                                       length: 0
length: 2000000000
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Match 1
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US-10-029-386-9623 US-10-029-386-23323 US-10-029-386-9623

-09-918-995-8429

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2040 1338 1357

-248-35 -995-8429

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APPLICANT: DeFees Shawn
APPLICANT: DeFees Shawn
APPLICANT: Zopf, David
APPLICANT: APPLICANT: ADSERT SOCIETY
APPLICANT: Hakes, David
APPLICANT: Hakes, David
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APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: CHORN
TITLE OF INVENTION: PROTEIN REMOBELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
TITLE OF INVENTION: PROTEIN UNDER: US 6/324, 23
FILE REPRENCE: 040853-01-5053
CURRENT FILING DATE: 2003-04-09
PRIOR PLING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/387, 292
PRIOR APPLICATION NUMBER: US 60/387, 292
PRIOR APPLICATION NUMBER: US 60/391, 777
PRIOR APPLICATION NUMBER: US 60/391, 777
PRIOR APPLICATION NUMBER: US 60/391, 777
PRIOR PLING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: US 60/404, 249
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: US 60/404, 249
PRIOR PLING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407, 227
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Publication No. US20040077836A1
GENERAL INRORMATION:
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
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APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
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APPLICANT: Bowe, Caryn
TITLE OF INVENTION: GENOURCETE COLONY STIMULATING FACTOR: REMODELING AND
TITLE OF INVENTION: GENOURCETE COLONY
TITLE OF INVENTION: GENOURCETE COLONY
TITLE OF INVENTION: GENOURCETE COLONY
TITLE OF INVENTION: GENOURCET: US 60/328,523
FRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
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PRIOR APPLICATION NUMBER: US 60/394,249
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PRIOR FILING DATE: 2002-08-16
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PRIOR FILING DATE: 2002-08-16
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                     APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-410-962-7/c
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APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
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APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Caryn
TITLE OF INNENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
ITITLE OF INNENTION: GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
ITITLE OF INNENTION: GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
ITITLE OF INNENTION: GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
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ITITLE OF INNENTION: GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
ITITLE OF INNENTION: 2003-04-09
PRIOR PELLING DATE: 2001-04-09
PRIOR PELLING DATE: 2002-06-25
PRIOR PELLING DATE: 2002-06-16
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1.0%; Score 20.6; DB 1; Length 1332;
Best Local Similarity 59.3%; Pred. No. 2.2;
Matches 35; Conservative 0; Mismatches 24; Indels 0
                                                                                                     US-09-951-121A-14
US-09-951-121A-15
US-10-295-682-14
US-10-295-682-14
US-09-933-16-8
US-10-281-727-6
US-10-281-727-6
US-10-281-727-6
US-10-281-727-6
US-10-281-727-6
US-09-951-121A-2
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Publication No. US20040043446A1
GENERAL INFORMATION:
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US-10-411-026-7/c
Sequence 7, Application US/10411026
Publication No. US20040063911A1
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; ORGANISM: Homo sapiens
US-10-411-037-7
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APPLICANT: Harse, Javid
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: INTERPRON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
TITLE OF INVENTION: BETA
FILE REFRENCE: 040853-01-5066
CURRENT APPLICATION NUMBER: US/10/410,930
CURRENT FILING DATE: 2003-04-09
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR PELING DATE: 2002-06-07
PRIOR PELING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
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PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-18
NUMBER OF SEQ ID NOS: 75
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APPLICANT: Defrees, Shawn
APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF TITLE OF INVENTION WIMBER: US 60/328, S23
FILE REFERENCE: 0408323.01-5059
CURRENT FILING DATE: 2001-10-10
FRIOR FILING DATE: 2001-10-10
FRIOR APPLICATION NUMBER: US 60/387, 292
FRIOR FILING DATE: 2002-06-07
FRIOR FILING DATE: 2002-06-07
FRIOR FILING DATE: 2002-06-15
FRIOR APPLICATION NUMBER: US 60/391, 777
FRIOR APPLICATION NUMBER: US 60/391, 777
FRIOR APPLICATION NUMBER: US 60/404, 249
FRIOR APPLICATION NUMBER: US 60/407, 527
FRIOR APPLICATION NUMBER: US 60/407, 527
FRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
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Pred. No. 2.2;
0; Mismatches 24; Indels 0;
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Publication No. US20040126838A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
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Best Local Similarity 59.39
Matches 35, Conservative
                                     Bayer, Robert
Hakes, David
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CORGANISM: Homo sapiens
US-10-410-930-7
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APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Zopf, David
APPLICANT: Applicant: Ai
APPLICANT: Applicant: Ai
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONUGATION OF INTERFERON
TITLE OF INVENTION: INTERFERON ALPHA
FILE REFRERENCE: 040853-01-5055
CURRENT FILING DATE: 2003-04-09
FRIOR APPLICANTON NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2002-06-07
PRIOR PLING DATE: 2002-06-07
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PRIOR PLING DATE: 2002-06-16
PRIOR PLING DATE: 2002-07-17
PRIOR PRING APPLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR PRING DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-16
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1.0%; Score 20.6; DB 1; Length 1332;
Best Local Similarity 59.3%; Pred. No. 2.2;
Matches 35; Conservative 0; Mismatches 24; Indels 0
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59.3%; Pred. No. 2.2;
tive 0; Mismatches 24; Indels 0
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Publication No. US20040115168A1
GENERAL INFORMATION:
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Publication No. US20040082026A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.2
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 59.3
Matches 35; Conservative
                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                  SEQ ID NO 7
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APPLICANT: Hakes, David
APPLICANT: Chen, XI
APPLICANT: Chen, XI
APPLICANT: Chen, XI
APPLICANT: Chen, XI
APPLICANT: Chen, XI
APPLICANT: Chen, XI
TILE OF INVENTION: GLYCOCONJUGATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
TILLE OF INVENTION: METHODS
FILE REPERENCE: 040853-01-5081
CURRENT APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2002-06-25
PRIOR PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR PLING DATE: 2002-06-25
PRIOR PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR PLING DATE: 2002-07-17
PRIOR PLING DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-28
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                         APPLICANT: Hakes, David
APPLICANT: Chen, Xi
TITLE OF INVENTION REMODELING AND GLYCOCONJUGATION OF PEPTIDES
FILE OF THE REPERENCE: 040855-01-5052-00
CURRENT APPLICATION NUMBER: US/10/28/523
FRICK APPLICATION NUMBER: US 60/344,692
PRIOR PILING DATE: 2001-10-19
PRIOR PLING DATE: 2001-10-19
PRIOR PLING DATE: 2002-06-07
PRIOR PELING DATE: 2002-06-07
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PRIOR PELICATION NUMBER: US 60/391,777
PRIOR PELING DATE: 2002-06-15
PRIOR PELING DATE: 2002-06-16
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Publication No. US20040142856A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
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Best Local Similarity 59.3
Matches 35, Conservative
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Zopf, David
Bayer, Robert
Hakes, David
     Bowe, Caryn
Hakes, David
Chen, Xi
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APPLICANT:
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Chen, Xi
APPLICANT: Bayer, Caryne
TITLE OF INVENTION: GLYCOPEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
TITLE OF INVENTION: METHOSS
TITLE OF INVENTION: METHOSS
TITLE OF INVENTION: METHOSS
TITLE OF INVENTION: WINDER: US/10/411,012
CURRENT APPLICATION NUMBER: US 60/38,533
PRIOR PLING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR PLING DATE: 2002-06-07
PRIOR PLING DATE: 2002-06-16
PRIOR PLING DATE: 2002-06-16
PRIOR PLING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
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Best Local Similarity 59.3%; Pred. No. 2.2;
Matches 35; Conservative 0; Mismatches 24; Indels 0
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; Publication No. US20040137557A1
; GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Copf, David
APPLICANT: Rayer, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/10411012
Publication No. US20040132640A1
SOFTWARE: Patentin version 3.2
SEQ ID NO 7
LENGTH: 1332
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Best Local Similarity 59.3%;
Matches 35; Conservative C
                                                                                                                                               TYPE: DNA
CORGANISM: Homo sapiens
US-10-410-997-7
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US-10-411-012-7
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| Publication No. US20040058347A1
| Publication No. US20040058347A1
| GENERAL INFORMATION:
| APPLICANT: Alsobrook, et al.
| TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
| FILE REFERENCE: 21402-568C
| CURRENT APPLICATION NUMBER: US/10/382,248
| PRIOR PLING DATE: 2003-03-05
| PRIOR PAPLICATION NUMBER: 60/366,928
| PRIOR FILING DATE: 2002-03-22
| PRIOR FILING DATE: 2002-03-22
| PRIOR FILING DATE: 2002-03-06
| PRIOR FILING DATE: 2002-03-19
| PRIOR PILING DATE: 2002-03-19
| PRIOR FILING DATE: 2002-03-19
| PRIOR FILING DATE: 2002-03-19
| PRIOR FILING DATE: 2002-03-19
| PRIOR FILING DATE: 2002-03-19
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Publication No. US2040110929A1

GENERAL INFORMATION:
APPLICANT: Bjorn, Soren E

APPLICANT: Jorgensen, Anker S

TITLE OF INVENTION: TF Binding Compound
FILE REFERENCE: 645: 2003-07-11

PRIOR APPLICATION NUMBER: US/10/617,619

CURRENT FILING DATE: 2003-07-11

PRIOR FILING DATE: 2002-07-12

PRIOR FILING DATE: 2002-07-12

PRIOR FILING DATE: 2002-07-12

PRIOR FILING DATE: 2002-07-12

PRIOR FILING DATE: 2002-07-13

SPIOR APPLICATION NUMBER: US 60/404,568

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin version 3.2

SOFTWARE: Patentin version 3.2

SOFTWARE: Patentin version 3.2
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                                                                                                                                                                   Score 20.6; DE Pred. No. 3.1; 0; Mismatches
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                                                                                                                                                                   Query Match
Best Local Similarity 59.3%;
Matches 35; Conservative
                                                           FEATURE:
COTHER INFORMATION: Synthetic
US-10-617-619-12
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TYPE: DNA ORGANISM: Artificial
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APPLICANT: Thorpe, Philip E
APPLICANT: Thorpe, Philip E
APPLICANT: Thorpe, Philip E
APPLICANT: King, Steven W
TITLE OF INVENTION: TREATMENT
TITLE OF INVENTION: TREATMENT
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TITLE OF INVENTION: TREATMENT
TITLE OF INVENTION: TREATMENT
FILING DATE: 2001-02-27
FRICE REPERENCE: 4001-01999
CURRENT APPLICATION NUMBER: 09/573,835
PRIOR FILING DATE: 1996-01-20
PRIOR PELING DATE: 1996-01-20
PRIOR FILING DATE: 1997-01-27
PRIOR FILING DATE: 1997-01-27
PRIOR FILING DATE: 1997-01-27
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; Publication No. US20040110929A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bjorin, Soren E
APPLICANT: Dioclaisen, Else M
APPLICANT: JOYGENSEN, Anker S
TITLE OF INVENTION: TF Binding Compound
FILE REFERENCE: 6455.200-US
CURRENT APPLICATION NUMBER: US/10/617,619
FRIOR PRILING DATE: 2003-07-11
PRIOR FILING DATE: 2002-07-12
PRIOR FILING DATE: 2002-07-12
PRIOR FILING DATE: 2002-08-19
PRIOR FILING DATE: 2002-08-19
PRIOR FILING DATE: 2002-07-12
PRIOR FILING DATE: 2002-07-13
SOFTWARE: Patentin version 3.2
SEQ ID NO 12
LENGTH: 2040
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1.0%; Score 20.6; DE
Best Local Similarity 59.3%; Pred. No. 2.3;
Matches 35; Conservative 0; Mismatches
                                                                                                                Score 20.6; DI
Pred. No. 2.2;
0; Mismatches
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                                                                                                             Query Match
Best Local Similarity 59.3%;
Matches 35; Conservative
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; CRGANISM: Homo sapiens
US-10-375-741-13
  TYPE: DNA
ORGANISM: Homo sapiens
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TITLE OF INVENTION: PROTEIN REMODBLING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE TITLE OF INVENTION: METHODS PROTEINS/PEPTIDES PRODUCED BY THE PRICE OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVINGES OF SERVI
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                                                    PRIOR APPLICATION NUMBER: 05 00,000.
PRIOR FILING DATE: 2002-00.
PRIOR FILING DATE: 2002-08.16
PRIOR PLING DATE: 2002-08.16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR PILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SEQ TO NO 7
LENGTH: 132
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PRIOR PLILING DATE: 2001-10-10

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PRIOR PLLING DATE: 2001-10-19

PRIOR PLLING DATE: 2002-06-07

PRIOR PLLING DATE: 2002-06-07

PRIOR PLLING DATE: 2002-06-25

PRIOR PLLING DATE: 2002-06-25

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PRIOR PLLING DATE: 2002-06-16

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Pred. No. 7
FILING DATE: 2002-06-25
APPLICATION NUMBER: US 60/396,594
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Best Local Similarity 59.2%;
Matches 29; Conservative
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APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
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US-10-411-026-7
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US-10-410-962-7
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APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: David
APPLICANT: Bayer: Robert
APPLICANT: Bayer: Robert
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
TITLE OF INVENTION: GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
TITLE OF INVENTION: GALACTOSIDASE A: CURRENT APPLICATION NUMBER: US/10/411,037
CURRENT APPLICATION NUMBER: US/10/411,037
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERSONCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Mindows Version 3.0
SEQ ID NO 8429
LENGTH: 483
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                                                                                                                                                                                                                                                                                                                                                                                      22; Indels
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0.9%; Score 17.8; D
Best Local Similarity 58.5%; Pred. No. 18;
Matches 31; Conservative 0; Mismatches
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PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION UNMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR PELLING DATE: 2002-06-07
PRIOR PLLING DATE: 2002-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8429, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-8429
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LOCATION: (1)...(483)
                                                                       FEATURE:

// NAME/KEY: CDS

// LOCATION: (45)..(1301)

US-10-382-248-35
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                                 ORGANISM: Homo sapiens
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Matches 29; Conserv
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US-09-918-995-8429
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## APPLICANT: Hakes, David
### APPLICANT: Hakes, David
### APPLICANT: Chen, Xi
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llarity 59.2%; Pred. No. 27;
Conservative 0; Mismatches 20; Indels
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Pred. No. 27;
0; Mismatches
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR PLILAGATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin version 3.2
LENGTH: 1332
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Publication No. US20040115168A1
GENERAL INFORMATION:
APPLICANT: Necse Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
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US-10-410-997-7
; Sequence 7, Application US/10410997
; Publication No. US20040126838A1
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Best Local Similarity 59.2
Matches 29; Conservative
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CORGANISM: Homo sapiens
US-10-410-930-7
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 29; Conser
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Sequence 7, Application US/10411049

Publication No. US20040082026A1

GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Caryn
APPLICANT: Bowe, Caryn
APPLICANT: Bowe, Caryn
APPLICANT: Bowe, Caryn
APPLICANT: Bowe, Caryn
APPLICANT: Bowe, Caryn
APPLICANT: Bowe, Caryn
APPLICANT: Bowe, Caryn
APPLICANT: Bowe, Caryn
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APPLICANT: WHORER: US/10/411,049
CURRENT FILING DATE: 2003-04-09
PRIOR PILING DATE: 2001-10-10
PRIOR PILING DATE: 2001-10-10
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-25
PRIOR PILING DATE: 2002-06-25
PRIOR PILING DATE: 2002-06-17
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PRIOR FILING DATE: 2002-06-17
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APPLICANY: Bayer, Robert
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APPLICANY: Bayer, Robert
APPLICANY: Bayer, Robert
APPLICANY: Bayer, Robert
APPLICANY: Bayer, Robert
APPLICANY: Bayer, David
APPLICANY: Bayer, Saryn
TITLE OF INVENTION: GENOUS TIMULATING FACTOR: REMODELING AND
TITLE OF INVENTION: GENOUS CONSUMENTION OF G-CSF
FILE REFERENCE: 040853-01-554
CURRENT APPLICATION NUMBER: US 60/328,523
FRIOR APPLICATION NUMBER: US 60/328,523
FRIOR FILING DATE: 2001-10-19
FRIOR FILING DATE: 2001-10-10
FRIOR FILING DATE: 2001-10-10
FRIOR FILING DATE: 2002-06-07
FRIOR APPLICATION NUMBER: US 60/387,292
FRIOR APPLICATION NUMBER: US 60/396,594
FRIOR APPLICATION NUMBER: US 60/396,594
FRIOR FILING DATE: 2002-08-16
FRIOR APPLICATION NUMBER: US 60/404,249
FRIOR FILING DATE: 2002-08-16
FRIOR FILING DATE: 2002-08-16
FRIOR FILING DATE: 2002-08-18
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
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Best Local Similarity 59.2
Matches 29; Conservative
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; ORGANISM: Homo sapiens
US-10-410-962-7
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FILE REPERENCE: 040853-01-5052-00
CURRENT APPLICATION NUMBER: US/10/287,994
CURRENT FILING DATE: 2002-11-05
PRIOR PELICATION NUMBER: US 60/328,523
PRIOR PELICATION NUMBER: US 60/328,523
PRIOR PELICATION NUMBER: US 60/344,692
PRIOR PELING DATE: 2001-10-19
PRIOR PELING DATE: 2001-10-19
PRIOR PELING DATE: 2002-06-05
PRIOR PELING DATE: 2002-06-05
PRIOR PELING DATE: 2002-06-05
PRIOR PELING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR PELING DATE: 2002-06-15
PRIOR PELING DATE: 2002-06-16
PRIOR PELING DATE: 2002-06-16
PRIOR PELING DATE: 2002-06-16
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59.2%; Pred. No. 27;
tive 0; Mismatches 20; Indels
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PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SEQ ID NO 7
LENGTH: 1332
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Publication No. US20040137557A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
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APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Bowe, Caryn
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.8
Best Local Similarity 59.2
Matches 29; Conservative
                                                                                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: Homo sapiens
US-10-411-012-7
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US-10-287-994-7
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APPLICANT: Befrees, Shawn
APPLICANT: Defrees, Shawn
APPLICANT: Defrees, Shawn
APPLICANT: Defrees, Shawn
APPLICANT: Defrees, Shawn
APPLICANT: Befree, David
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Bayer, Robert
APPLICANT: Bowe, Carry
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION WIMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION WIMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-15
PRIOR APPLICATION WIMBER: US 60/391,777
PRIOR APPLICATION WIMBER: US 60/391,777
PRIOR APPLICATION WIMBER: US 60/391,777
PRIOR APPLICATION WIMBER: US 60/391,777
PRIOR APPLICATION WIMBER: US 60/391,777
PRIOR APPLICATION WIMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-08-16
                                                                                                      APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
APPLICANT: Bowe, Caryn
APPLICANT: Bowe, Caryn
APPLICANT: Bowe, Caryn
APPLICANT: Bowe, Caryn
APPLICANT: Powention: FSH
TITLE OF INVENTION: FSH
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27;
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Pred. No. 27;
0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: FSH
CURRENT APPLICATION NUMBER: US/10/410,997
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US/00/410,997
PRIOR PILING DATE: 2001-10-10
PRIOR PELING DATE: 2001-10-10
PRIOR PELING DATE: 2001-10-19
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-17
PRIOR PILING DATE: 2002-06-17
PRIOR PILING DATE: 2002-06-16
PRIOR PILING DATE: 2002-06-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-18
NUMBER: OF SEQ ID NOS: 75
SEQ ID NO 7
LENGTH: 1332
LENGTH: 1332
                                                                    Neose Technologies, Inc.
DeFrees, Shawn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/10411012 Publication No. US20040132640A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 59.2%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
COGANISM: Homo sapiens
US-10-410-997-7
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US-10-411-012-7
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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23 TCCTCTGCCTTCTGCTTTGGGCTTCAGGGCTGCCTGGCTGCAGTCTTCGT 71
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Pred. No. 31;
0; Mismatches 14; Indels
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                                                                                                                                           Sequence 2, Application US/09782587B
Sequence 2, Application US/09782587B
Publication No. US20030096338Ai
Seduence 2, Application No. US20030096338Ai
Sebricant NFORMATION: ANDERS H.
APPLICANT: PEDERSEN, KIM V.
APPLICANT: BORNARS, CLAUS
TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
FILE REFERENCE: 31-001100US
CURRENT FILING DATE: 2002-03-26
FRIOR APPLICATION NUMBER: US/09/782,587B
CURRENT FILING DATE: 2000-02-11
FRIOR PILING DATE: 2000-02-21
FRIOR FILING DATE: 2000-02-22
FRIOR FILING DATE: 2000-03-22
FRIOR FILING DATE: 2000-03-22
FRIOR FILING DATE: 2000-03-22
FRIOR FILING DATE: 2000-03-22
FRIOR FILING DATE: 2000-03-22
FRIOR FILING DATE: 2000-03-22
FRIOR FILING DATE: 2000-03-22
FRIOR APPLICATION NUMBER: 60/241,916
FRIOR PRICH DATE: 2000-10-18
SOFTWARE: PALENTIN VET: 2.1
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Publication No. US20030096338A1
GENERAL INFORMATION:
APPLICAMT: PEDERSEN, ANDERS H.
APPLICAMT: ANDERSON, KIM V.
APPLICAMT: BORNAES, CLAUS
TITLE REFERENCE: 31-00100US
CURRENT APPLICATION NUMBER: US/09/782,587B
CURRENT FILING DATE: 2002-03-26
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/184,036
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/241,916
PRIOR FILING DATE: 2000-02-12
PRIOR FILING DATE: 2000-02-13
PRIOR FILING DATE: 2000-10-18
PRIOR FILING DATE: 2000-10-18
PRIOR FILING DATE: 2000-10-18
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ORGANISM: Artificial Sequence
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Best Local Similarity 64.11
Matches 25; Conservative
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Best Local Similarity 64.1
Matches 25; Conservative
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; LOCATION: (115)..(1332)
US-09-782-587B-2
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ORGANISM: Homo sapiens
                                                                                        RESULT 25
US-09-782-587B-2/c
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US-09-782-587B-4/c
g
                                                                                                         APPLICANT: Bowe, Caryn
TITLE OF INVENTION: GIYCOCONJUGATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
TITLE OF INVENTION: METHODS.
TITLE OF INVENTION: METHODS.
TITLE OF INVENTION: METHODS.
THE REPERRINCE: 040855-01-5081
CURRENT APPLICATION NUMBER: US/10/410,913
CURRENT FILING DATE: 2003-04-09
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; Sequence 12, Application US/10617619
; Publication No. US20040110929A1
; GENERAL INFORMATION:
    APPLICANT: Bjorn, Soren E
; APPLICANT: Nicolaisen, Else M
    APPLICANT: Nicolaisen, Else M
    APPLICANT: OF INVENTION: TF Binding Compound
; TILE REPERENCE: 645.200-US
; CURRENT APPLICATION NUMBER: US/10/617,619
CURRENT FILING DATE: 2003-07-11
; PRIOR PILING DATE: 2003-07-11
; PRIOR PILING DATE: 2002-07-12
; PRIOR FILING DATE: 2002-07-12
; PRIOR FILING DATE: 2002-07-12
; PRIOR FILING DATE: 2002-07-12
; PRIOR FILING DATE: 2002-07-13
; SOFTWARE: PatentIn version 3.2
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0.8%; Score 17; DB 1
Best Local Similarity 59.2%; Pred. No. 23;
Matches 29; Conservative 0; Mismatches
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PRIOR PILING DATE: 2001-10-0

PRIOR FILING DATE: 2001-10-0

PRIOR FILING DATE: 2001-10-19

PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR FILING DATE: 2001-10-19

PRIOR FILING DATE: 2002-06-07

PRIOR FILING DATE: 2002-06-07

PRIOR FILING DATE: 2002-06-18

PRIOR FILING DATE: 2002-06-19

PRIOR PLING DATE: 2002-06-19

PRIOR PILING DATE: 2002-06-16

PRIOR PILING DATE: 2002-06-16

PRIOR PILING DATE: 2002-06-16

PRIOR FILING DATE: 2002-06-16

PRIOR FILING DATE: 2002-06-16

PRIOR FILING DATE: 2002-06-16

PRIOR FILING DATE: 2002-08-16

PRIOR FILING DATE: 2002-08-16

PRIOR FILING DATE: 2002-08-16

PRIOR FILING DATE: 2002-08-16

PRIOR FILING DATE: 2002-08-16

PRIOR FILING DATE: 2002-08-18

SOFTWARE: PATENTIN VERSION 3.2
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US-10-410-913-7
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Best Local Similarity
Matches 29; Conserv
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LENGTH: 2040
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; Publication No. US20040110929A1
; Publication No. US20040110929A1
; GENERAL INVORMATION:
    APPLICANT: Bjorn, Sen. Blse M
    APPLICANT: Discolaisen, Blse M
    APPLICANT: USCSENSEN, Anker S
; TITLE OF INVENTION: TP Binding Compound
    FILE REFERENCE: 4455.700-US
; CURRENT FILING DATE: 2003-07-11
    PRIOR APPLICATION NUMBER: US/10/617,619
    PRIOR PRILING DATE: 2002-07-12
    PRIOR PILING DATE: 2002-07-12
    PRIOR FILING DATE: 2002-07-12
    PRIOR FILING DATE: 2002-08-19
    NUMBER OF SEQ ID NOS: 13
    SOFTWARE: PatentIn version 3.2
    SEQ ID NO 9
    LENGTH: 2106
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                                                            Length 1440;
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; Sequence 8429/C
; Sequence 8429, Application US/09918995
; Publication No. USC030073623A1
; GENERAL INFORMATION:
APPLICANT: Hyesq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
; FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT APPLICATION NUMBER: US/09/235,076
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 38054
; SEQ ID NOS: 38054
; SEQ ID NOS: 38054
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; SEQ ID NOS: 38054
; SEQ ID NOS: 38054
; PRANTH: 483
; TYPE: DNA
ORGANISM: HOMO SapienS
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                                                            Score 16.6; DB 1; Length 1
Pred. No. 30;
0; Mismatches 14; Indels
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| LOCATION: (1)...(483)
| OTHER INFORMATION: n = A,T,C or G
                                                            Query Match 0.8%;
Best Local Similarity 64.1%;
Matches 25; Conservative (
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Best Local Similarity 64.1%;
Matches 25; Conservative
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Best Local Similarity
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US-10-375-741-13
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Sequence 13, Application US/2003023753A1

Publication No. US2003023753A1

SEDERAL INFORMATION: Philip E

APPLICANT: Thorgo, Philip E

APPLICANT: Thorgo, Philip E

APPLICANT: Thorgo, Philip E

APPLICANT: Thorgo, Philip E

APPLICANT: Thorgo, Steven W

APPLICANT: Thorgo, Steven W

APPLICANT: Thorgo, Steven W

APPLICANT: Thorgo, Steven W

APPLICANT: Thorgo, Steven W

APPLICANT: Gao, Boning

TITLE OF INVENTION: TISSUE FACTOR METHODS AND COMPOSITIONS FOR COAGULATION AND TUMOR

TITLE OF INVENTION: TISSUE FACTOR METHODS AND COMPOSITIONS FOR COAGULATION AND TUMOR

FILE REFERENCE: 2003-02-27

PRIOR APPLICATION NUMBER: 6,126,321

PRIOR PILING DATE: 1997-03-27

PRIOR PILING DATE: 1997-03-27

PRIOR PILING DATE: 1997-03-27

PRIOR APPLICATION NUMBER: 60/035,920

PRIOR APPLICATION NUMBER: 60/035,920

PRIOR PILING DATE: 1997-01-27

PRIOR PILING DATE: 1997-01-27

PRIOR PILING DATE: 1997-01-27

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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-5686
CURRENT APPLICATION NUMBER: US/10/382,248
CURRENT FILING DATE: 2003-03-05
PRIOR PELLING DATE: 2003-03-05
PRIOR PELLING DATE: 2002-03-05
PRIOR PELLING DATE: 2002-03-05
PRIOR PELLING DATE: 2002-03-19
PRIOR PELLING DATE: 2002-03-19
PRIOR PELLING DATE: 2002-03-19
PRIOR PELLING DATE: 2002-03-19
PRIOR PELLING DATE: 2002-03-19
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PRIOR PELLING DATE: 2002-03-10
PRIOR PELLING DATE: 2002-03-10
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0.8%; Score 16.6; DB 1; Length 1361;
Best Local Similarity 64.1%; Pred. No. 31;
Matches 25; Conservative 0; Mismatches 14; Indels 0;
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                                          1122 GGCCTGGAATTATTTATTCATATTTCTTGAATGTG 1160
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                                                                                                      580 GCCCTGGGGTTTGCTAGCGTTCCGCTTTTCTAGAATGGG 542
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SEQ ID NO 13
LENGTH: 1440
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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; LOCATION: (45)..(1301)
US-10-382-248-35
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US-10-375-741-13
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US-10-382-248-35
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Sequence 9623, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR (TITLE OF INVENTION: HUMAN GENOME-STAND)
FILE REFERENCE: AEOMICA-x-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION UNDER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SEQ ID NOS: 34288
SEQ ID NO 9623
LENGTH: 555
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N: EXPRESSED IN BRAIN, SIGNAL = 1
N: EXPRESSED IN LUNG, SIGNAL = 0.46
N: EXPRESSED IN LONG, SIGNAL = 1.2
N: EXPRESSED IN PLACENTA, SIGNAL = 0.95
N: EXPRESSED IN HEART, SIGNAL = 1.3
N: EXPRESSED IN HEART, SIGNAL = 1.3
N: SIRSEPROT HIT: P00709, EVALUE 7.00e-63
N: NT HIT: J02933.1, EVALUE 0.00e+70
N: EST_HUMAN HIT: AL531727.1, EVALUE 5.00e-76
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         EXPRESSED IN PLACENTA, SIGNAL = 0.95
EXPRESSED IN HEART, SIGNAL = 1.3
NT HIT: gil4783796, EVALUE 1.00e-122
EST HUMAN HIT: AL531727.1, EVALUE 3.00e-26
SWISSPROT HIT: P08709, EVALUE 3.00e-37
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Pred. No. 75;
0; Mismatches
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Pred. No. 60;
0; Mismatches
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Publication No. US20030180748A1
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR GENERATING D
TITLE OF INVENTION: GENERIC MARKERS
TITLE REPRENCE: 24736-2033E
CURRENT FILING DATE: 2002-10-15
CURRENT FILING DATE: 2002-10-15
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PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR FLING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/159,176
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Best Local Similarity 54.7
Matches 29; Conservative
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ORGANISM: Homo sapiens
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Matches 29; Conser
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US-10-029-386-23323
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US-10-029-386-9623/c
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OTHER INFORMAT
US-10-029-386-9623
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Penn, Sharron G.
APPLICANT: Penn, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: BYPESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: BXPRESSION ANALYSIS TWO
TITLE OF INVENTION: BXPRESSION ANALYSIS TWO
CURRENT APPLICATION NUMBER: US/10/029,386
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 23323
LENGTH: 222
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                                           580 AGGICAAIAIGIGAITITAGCIGIAGCIGIGCTIGITITAIGAACITGGGIGACALIG 637
         Gaps
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N: EXPRESSED IN BRAIN, SIGNAL = 1
N: EXPRESSED IN BRAIN, SIGNAL = 0.46
N: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
N: EXPRESSED IN PLACENTA, SIGNAL = 0.95
N: EXPRESSED IN HEART, SIGNAL = 0.95
N: EXPRESSED IN HEART, SIGNAL = 1.3
N: MISSEROT HIT: POGTO9, EVALUE 7.00e-63
N: NI HIT: JO2933.1, EVALUE 0.00e+00
N: EST_HUMAN HIT: AL531727.1, EVALUE 5.00e-76
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      Indels
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EXPRESSED IN BAAIN, SIGNAL = 1
SYPRESSED IN LUNG, SIGNAL = 0.46
EXPRESSED IN BONE MARROW, SIGNAL = 1.2
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LENGTH: 555
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    Mismatches
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56.0%; Pred. No. 70;
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CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
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Publication No: US20030194704A1
GENERAL INFORMATION:
                                                                                                                                                                                            Sequence 9623, Application US/10029386
Publication No. US20030194704A1
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
Matches 28; Conserv
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ilarity 62.9%; Pred. No. 29;
Conservative 0; Mismatches
  PRIOR APPLICATION NUMBER: 05/10/27,756

PRIOR FILING DATE: 2002-10-15

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 118

SEQ ID NO 22

LENGRARE: FastSEQ for Windows Version 4.0

SEQ ID NO 22
CURRENT APPLICATION NUMBER: US/10/272,756
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Best Local Similarity 62.9%;
Matches 22; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
FEATURE:
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Best Local Similarity
Matches 22; Conserv
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US-10-272-665-107/c
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; Sequence 22, Application US/10273321
; Sequence 22, Application US/10273321
; Sequence 22, Application US/20030180749A1
; GERRAL INFORMATION:
    APPLICATION WOUNDERS OR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PG
; TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PG
; TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PG
; TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PG
; TITLE OF INVENTION UNMERS: US/10/273,321
; CURRENT FILING DATE: 2000-07-10
; PRIOR FILING DATE: 2000-07-10
; PRIOR FILING DATE: 1999-10-13
; PRIOR FILING DATE: 2000-07-10
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 118
; SEQ ID NO 22
LENGTH: 60
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Publication No. US20030190644A1
GENERAL INFORMATION:
APPLICANT: Braun et al.
APPLICANT: Braun et al.
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
TITLE OF INVENTION: GENETIC MARKERS
FILE REFERENCE: 24736-2033C
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Pred. No. 29;
0; Mismatches
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62.9%; Pred. No. 29;
        PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: FASTEEQ for Windows Version 4.0
SEQ ID NO 22
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Best Local Similarity 62.9%;
Matches 22; Conservative
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Best Local Similarity 62.9
Matches 22; Conservative
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                                                                                                                                                                                                                                      , OTHER INFORMATION: Probe US-10-272-665-22
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ORGANISM: Homo Sapien
FEATURE:
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US-10-272-756-22/c
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US-10-273-321-22/c
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                                                                                                                                                              LENGTH:
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Sequence 107, Application US/10272756
| Publication No. US20030190644A1
| GENERAL INFORMATION:
| APPLICANT: Braun et al. |
| TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC |
| TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC |
| TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC |
| TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC |
| FILLE OF INVENTION: METHOD FOR IS 2002-10-15 |
| PRIOR PAPLICATION NUMBER: 09/687,483 |
| PRIOR PILING DATE: 2000-07-10 |
| PRIOR FILING DATE: 2000-07-10 |
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Sequence 107, Application US/10273228
Publication No. US2003020729741
GENERAL INFORMATION:
FULL CALLON NO. US2003020729741
GENERAL INFORMATION:
FILLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC
TITLE OF INVENTION: GENERAL WARKERS
FILLE REPRENCE: 24736-2033D
CURRENT APPLICATION NUMBER: 09/687,483
FRICH APPLICATION NUMBER: 09/687,483
FRICH FILING DATE: 2000-07-10
FRICH APPLICATION NUMBER: 60/217,658
FRICH APPLICATION NUMBER: 60/217,658
FRICH APPLICATION NUMBER: 60/217,251
FRICH APPLICATION NUMBER: 60/217,251
FRICH APPLICATION NUMBER: 60/217,251
FRICH APPLICATION NUMBER: 60/217,251
FRICH APPLICATION NUMBER: 60/217,251
FRICH APPLICATION NUMBER: 09/63,968
FRICH FILING DATE: 2000-09-19
FRICH FILING DATE: 2000-09-19
FRICH FILING DATE: 2000-09-19
FRICH FILING DATE: 2000-09-19
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Pred. No. 45;
0; Mismatches
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Pred. No. 45;
0; Mismatches
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Best Local Similarity 62.9%;
Matches 22; Conservative
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Best Local Similarity 62.9%;
Matches 22; Conservative
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US-10-273-228-107/c
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; ORGANISM: HOMO
US-10-272-756-107
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; ORGANISM: Hom
US-10-273-228-107
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                                               ## APPLICANT: Braun et al.

### APPLICANT: Braun et al.

### TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC

### TITLE OF INVENTION: GENERATING MARKERS

### TITLE OF INVENTION: GENERATING DATABASES FOR IDENTIFYING PC

### TITLE OF INVENTION: GENERALING DATABASES FOR IDENTIFYING PC

### CURRENT APPLICATION NUMBER: US/10/272,665

### CURRENT APPLICATION NUMBER: 09/687,483

### PRIOR FILING DATE: 2000-07-10

### PRIOR FILING DATE: 2000-07-10

### PRIOR FILING DATE: 2000-07-10

### PRIOR FILING DATE: 2000-07-10

### PRIOR FILING DATE: 2000-07-10

### PRIOR FILING DATE: 2000-07-10

### PRIOR FILING DATE: 2000-07-10

### PRIOR FILING DATE: 2000-09-19

### NUMBER OF SEQ ID NOS: 118

### SOFTWARE: FastSEQ for Windows Version 4.0

### SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: GENERAL MARKERS
FILE SPERSONS: 24756-20338

CURRENT APPLICATION NUMBER: US/10/273,321

CURRENT APPLICATION NUMBER: US/10/273,321

CURRENT APPLICATION NUMBER: 0S/687,483

PRIOR APPLICATION NUMBER: 0S/687,483

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 1999-10-13

PRIOR APPLICATION NUMBER: 60/159,176

PRIOR PILING DATE: 2000-07-10

PRIOR PILING DATE: 2000-07-10

PRIOR PILING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 118

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Pred. No. 45;
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Publication No. US20030180749A1
GENERAL INFORMATION:
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US20030180748A1
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; ORGANISM: Homo sapien
US-10-272-665-107
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ORGANISM: Homo sapien
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Best Local Similarity
Matches 22; Conserv
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US-LUCATOR APPLICATION US/10272756

PUBLICATION NO. US20030190644A1
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PO TITLE OF INVENTION: METHODS FOR GENERAL STATES OF INVENTION: METHODS FOR GENERAL STATES OF INVENTION: METHODS FOR GENERAL STATES OF INVENTION: GENERAL SAFE SOCIATION OF STATES OF SOCIATION OF STATES OF SOCIATION OF STATES OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATION OF SOCIATIO
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Sequence 106, Application US/10273228

Publication No. US20030207297A1

GENERAL INFORMATION:

APPLICANT: Braun et al.

ITILE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PG

TITLE OF INVENTION: GENETIC MARKERS

FILE OF INVENTION: GENETIC MARKERS

FILE OF INVENTION: GENETIC MARKERS

FILE OF INVENTION: GENETIC MARKERS

FILE OF INVENTION: GONETIC MARKERS

FILE OF INVENTION: GONETIC MARKER: US/10/273,228

CURRENT APPLICATION NUMBER: US/10/273,228

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR PLING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 60/159,176

PRIOR APPLICATION NUMBER: 60/1217,251

PRIOR APPLICATION NUMBER: 60/217,251

PRIOR PLING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 118

SOFTWARE: PASKER PASKER FOR WINDOWS VERSION 4.0

SEQ ID NO 106

LENGTH: 100
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Pred. No. 45;
0; Mismatches 13; Indels
       13; Indels
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   0; Mismatches
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Best Local Similarity 62.9%;
Matches 22; Conservative
          Matches 22; Conservative
                                                                           1625 TTTTGACCTGCCT
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, ORGANISM: Homo sapien
US-10-273-228-106
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CRGANISM: Homo sapien
US-10-272-756-106
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Sequence 100, Application US/10273321

Sequence 100, Application US/10273321

GENERAL INFORMATION:

APPLICANT: Braun et al.

TITLE OF INVENTION: GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: GENERAL US/10/273,321

CURRENT FILING DATE: 2002-10-15

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

SPIOR FILING DATE: 2000-07-10

SPIOR FILING DATE: 2000-07-10

SPIOR FILING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 118

SOCIENTAL: 100

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LEAGTH: 100
                                                                                                                                                                                                                                                                                                         JENURAL INCOMENTATION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PORTILE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PORTILE OF INVENTION: GENERAL MARKERS

TITLE OF INVENTION: GENERAL MARKERS

FILE REPERENCE: 24736-2033E

CURRENT APPLICATION NUMBER: US/10/272,665

CURRENT FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 118

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 106
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              38 TGTGGGCCTCCACTGTCCCCCTTGCAGGAGTCCTT 4
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62.9%; Pred. No. 45;
tive 0; Mismatches
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Best Local Similarity 62.9
Matches 22; Conservative
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CORGANISM: Homo sapien
US-10-272-665-106
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ORGANISM: Homo sapien
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Best Local Similarity
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GENERAL INFORMATION:
                                                                                                                                                      RESULT 42
US-10-272-665-106/c
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Sequence 23323, Application US/10029386

Sequence 23323, Application US/10029386

Sequence 23323, Application US/10029386

Publication No. US20030134704A1

GENERAL INFORMATION: US0030134704A1

APPLICANT: Penn, Sharron G.

APPLICANT: Pank, David R.

APPLICANT: Hanzel, David R.

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Publication No US20030220247A1
GENERAL INPORMATION:
APPLICANT: The Children's Hospital of Philadelphia
APPLICANT: CAMIRE, RATHERINE A.
APPLICANT: APPLICANT: LARSON, PETER J.
APPLICANT: LARSON, PETER J.
APPLICANT: LARSON, PETER J.
APPLICANT: LARSON, PETER J.
APPLICANT: LARSON, PETER J.
APPLICANT: LARSON, PETER J.
APPLICANT: UNINTION: ENANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT C.
TITLE OF INVENTION: EACTORS
FILE REFERENCE: 018743-0301425
CURRENT APPLICATION NUMBER: 09/526,947
PRIOR APPLICATION NUMBER: 09/526,947
PRIOR APPLICATION NUMBER: 60/124,609
PRIOR APPLICATION NUMBER: 60/124,609
PRIOR FILING DATE: 1999-03-16
; OTHER INFORMATION: Description of Artificial Sequence: Expression; OTHER INFORMATION: cassette for expression of FVII in mammalian cells US-09-782-587B-4
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN BALIN, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: ST HUXAN HIT: AL531777.1, EVALUE 3.000-26
OTHER INFORMATION: SWISSPROT HIT: P08709, EVALUE 3.000-26
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0.6%; Score 12; DB 1; Length 222
Best Local Similarity 58.3%; Pred. No. 2.1e+02;
Matches 21; Conservative 0; Mismatches 15; Indels
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                                                                                                                                                                                     DB 1;
                                                                                                                                                                       Query Match 0.7%; Score 14.2; Est Local Similarity 70.4%; Pred. No. 37; Matches 19; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
FEATURE:
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LENGTH: 222
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0.7%; Score 14.2; DB 1; Length 1338;
Best Local Similarity 70.4%; Pred. No. 38;
Matches 19; Conservative 0; Mismatches 8; Indels 0
                           Score 14.2; DB 1; Length 100;
Pred. No. 45;
0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09782587B

Sequence 2, Application US/09782587B

Publication No. US20030095338A1

Sequence 2, Application US/09782587B

Publication No. US20030095338A1

SEPLICANT: PEDERSEN, ANDERS H.

APPLICANT: ANDERSON, KIN V.

APPLICANT: BORNAES, CLAUS

FILLE OF INVENTION: EACTOR VII OR VIIA-LIKE MOLECULES

FILE REPERMOCE: 31-001100US

CURRENT APPLICATION NUMBER: US/09/782,587B

CURRENT APPLICATION NUMBER: 60/184,036

PRIOR FILING DATE: 2000-02-11

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 2000-02-22

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Publication No. US20030096338A1

FURBEAL INFORMATION:
APPLICANT: PEDERSEN, AUDERS H.
APPLICANT: BORNAES, CLAUS
ITTLE OF INVARIANCE, CLAUS
ITTLE OF INVARIANCE, CLAUS
FILE REFERENCE: 31-001100US
CURRENT FILING DATE: 2002-03-26

PRIOR APPLICATION NUMBER: DA 2000 00218

PRIOR APPLICATION NUMBER: PA 2000 00218

PRIOR APPLICATION NUMBER: 60/184,036

PRIOR FILING DATE: 2000-02-21

PRIOR APPLICATION NUMBER: 60/241,916

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 19

SEPTING DATE: 2000-10-18

NUMBER OF SEQ ID NOS: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               crcricraccracracracadades
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                   1625 TTTTGACCTGCCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) NAME/KEY: CDS
; LOCATION: (115)..(1332)
US-09-782-5878-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                     Similarity
                                                                                                                                                                                                                                                                                       38
                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 2
LENGTH: 1
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Matches ,
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APPLICANT: Nicolaisen, Else Marie
APPLICANT: Nicolaisen, Else Marie
APPLICANT: Nicolaisen, Lars Soegaard
TITLE OF TWENTION: Method for the Production of Vitamin K-Dependent Proteins
FILTE OF TWENTION: Method for the Production of Vitamin K-Dependent FILE REFERENCE: 6270.204-US
CURRENT FILINGO DATE: 2003-09-02
FRIOR PAPLICATION NUMBER: US/10/398,422A
CURRENT FILINGO DATE: 2000-10-02
FRIOR FILING DATE: 2000-10-02
FRIOR FILING DATE: 2001-02-16
FRIOR FILING DATE: 2001-03-14
FRIOR FILING DATE: 2001-03-14
FRIOR FILING DATE: 2001-05-14
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FRIOR FILING DATE: 2001-05-16
FRIOR FILING DATE: 2001-05-16
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                                                                                                                                                               Query Match 0.6%; Score 11.6; DB 1; Length 32; Best Local Similarity 77.8%; Pred. No. 1.4e+02; Matches 14; Conservative 0; Mismatches 4; Indels
   ; ORGANISM: Unknown
; FRATURES:
OTHER INFORMATION: DNA primer for preparation of $314E-FVII
US-10-281-727-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 TAATATATTTTCTTGAAGCCTCTGCTGGC 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/10398422A, Publication No. US20040058413A1, GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 52
US-10-398-422A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-969-357-2
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69.6%; Pred. No. 1.8e+02;
tive 0; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: DNA primer for preparation of S314E-FVII
US-10-281-727-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/10281727
| Publication No. US20030130191A1
| GENERAL INFORMATION:
| APPLICANT: Persson, Egon
| APPLICANT: Persson, Egon
| TITLE OF INVENTION: Human Coagulation Factor VII
| TITLE OF INVENTION: Human Coagulation Factor VII
| TITLE OF INVENTION: Human Coagulation Factor VII
| TITLE OF INVENTION: Human Coagulation Factor VII
| TITLE OF INVENTION: POlypeptides
| FILE REFERENCE: 6410.200-US
| CURRENT APPLICATION NUMBER: US/10/281,727
| CURRENT PILING DATE: 2002-10-28
| PRIOR FILING DATE: 2001-11-02
| PRIOR FILING DATE: 2001-11-15
| NUMBER OF SEQ ID NOS: 7
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO FARMER OF SEQ FOR WINDOWS OF SEQ ID NOS: 7
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Fublication No. US20030130191A1
GENERAL INFORMATION:
APPLICANT: Persson, Egon
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Polypeptides
FILE REPRENCE: 6410.200-US
FURRENT APPLICATION NUMBER: US/10/281,727
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: EA 2001 01627
PRIOR APPLICATION NUMBER: 60/335,383
PRIOR FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 60/335,383
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                          1819 TGAGGTTCCTGTTGGGTTCTTAA 1841
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NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
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                                                                                                                                                                                                                                               Query Match
Best Local Similarity 69.6%
Matches 16; Conservative
                                                                                                                                  TYPE: DNA
CRCANISM: Homo sapiens
US-10-349-858-8
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 50
US-10-281-727-6/c
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LENGTH: 32
TYPE: DNA
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                                                                                                   APPLICANT: Person, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/09/951,121A
CURRENT FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: PA 2000 01361
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR PILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 33
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Publication No. US20030104978A1

GENERAL INFORMATION:
APPLICANT: Persson. Egon
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REPERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/09/951,121A
CURRENT FILING DATE: 2001-09-13
PRIOR PPLICATION NUMBER: 60/236,455
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOOTHWARE: FASUSEQ for Windows Version 4.0
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US-10-295-682-14/c
US-10-295-682-14/c
Sequence 14, Application US/10295682
Publication No. US20030100740A1
GENERAL INFORMATION:
APPLICANT: Persson, Egon
APPLICANT: Olsen, Ole Hvilsted
ITTLE OF INVENTION: Human Coagulation Factor VII Variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; DB 1;
2e+02;
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Best Local Similarity 66.7%; Pred. No. 2e+0
Matches 16; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                       US20030104978A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
COTHER INFORMATION: Synthetic
US-09-951-121A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 56
US-09-951-121A-15
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LENGTH: 33
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PRIOR FILING DATE: 2000-10-02

PRIOR APPLICATION NUMBER: Danish Applicatin No. PA 2001 00262

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00430

PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-05-14

PRIOR FILING DATE: 2001-05-14

PRIOR APPLICATION NUMBER: US 60/238,944

PRIOR APPLICATION NUMBER: US 60/271,581

PRIOR PRIOR APPLICATION NUMBER: US 60/271,581

PRIOR FILING DATE: 2001-02-26

PRIOR FILING DATE: 2001-03-16

NUMBER: OF SEQ ID NOS: 2

SOFTWARE: Patentin version 3.2

FILING DATE: 2001-03-16

NUMBER: PATENT OF SEQ ID NOS: 2

SOFTWARE: PATENT NETSION 3.2
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0.6%; Score 11.4; DB 1; Length 38;
Best Local Similarity 62.1%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 11; Indels
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US-09-951-121A-14/c
; Sequence 14, Application US/09951121A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: Synthetic US-09-969-357-2
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TYPE: DNA ORGANISM: Artificial Sequence
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Publication No. US20030100740A1

GENERAL INFORMATION:
APPLICANT: Persean. Egon
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT APPLICATION NUMBER: DA 2000 01361
PRIOR PLING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: PA 2000 01361
PRIOR PLING DATE: 2000-09-13
PRIOR PLING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18.
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Sequence 8, Application US/09951121A
Publication No. US20030104978A1
Publication No. US20030104978A1
APPLICANT: Persson, Egon
APPLICANT: Olsen, Ole Hvilsted
APPLICANT: Olsen, Ole Hvilsted
APPLICANT: Olsen, Ole Hvilsted
APPLICANT: Olsen, Ole Hvilsted
APPLICANT: Olsen, Ole Hvilsted
APPLICANT: Olsen, Ole Hvilsted
APPLICANT: SITTLE BEFERNES: 6224.200-US
CURRENT APPLICATION NUMBER: US/09/951,121A
PRIOR APPLICATION NUMBER: PA 2000 01361
PRIOR FILING DATE: 2000-09-13
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Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches
FILE REFERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: PA 2000 01361
PRIOR PILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FREUSEQ for Windows Version 4.0
SEQ ID NO 33
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ORGANISM: Artificial Sequence
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, OTHER INFORMATION: Synthetic
US-10-295-682-15
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US-10-295-682-15
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| Sequence 8, Application US/1025532
| Publication No. US20030100075A1
| GENERAL INPORMATION:
| APPLICANT: No. US2033100075A10 No. US20030100075A1disk A/S
| TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
| TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
| PILE REPERRENCE: 6357-W0
| CURRENT APPLICATION NUMBER: US/10/255,032
| CURRENT FILING DATE: 2002-09-24
| PRIOR FILING DATE: 2001-09-27
| NUMBER OF SEQ ID NOS: 9
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 8
| LENGTH: 36
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; Sequence 9, Application US/09951121A
; Publication No. USZ0030104978A1
; Publication No. USZ0030104978A1
; APPLICANT: Olsen, Ole Hvilsted
; APPLICANT: Person, Egon
; TILE OF INVENTION: Human Coagulation Factor VII Variants
; TLE REPERENCE: 6224.200-US
; CURRENT APPLICATION NUMBER: PA 2000 01361
; PRIOR APPLICATION NUMBER: PA 2000 01361
; PRIOR PILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/236,455
; PRIOR PILING DATE: 2000-09-29
; NUMBER: OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 36
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Pred. No. 3.4e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                Score 10.6; DB 1;
Pred. No. 3.4e+02;
0; Mismatches 4;
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 36
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 76.5%;
Matches 13; Conservative (
                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 76,5%;
Matches 13; Conservative
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                                                                                                                                                                                                                    ) OTHER INFORMATION: Synthetic US-09-951-121A-8
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VENCULO 295-682-9; Sequence 9, Application US/10295682; Sequence 9, Application US/10295682; Publication No. US20030100740A1; Publication No. US20030100740A1; APPLICANT: Olsen, Ole Hvilsted; APPLICANT: Olsen, Ole Hvilsted; ILE REFERENCE: 624.200-08; FILE REFERENCE: 624.200-08; CURRENT PILING DATE: 2002-11-15; PRIOR APPLICATION NUMBER: US/10/295,682; PRIOR PILING DATE: 2000-09-13; PRIOR PILING DATE: 2000-09-13; PRIOR FILING DATE: 2000-09-13; PRIOR FILING DATE: 2000-09-29; NUMBER OF SEQ ID NOS: 17.
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; OTHER INFORMATION: Protein C mutagenic oligonucleotide
US-09-803-810-8
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| Publication No. US20010018414A1
| GENERAL INFORMATION:
| APPLICATION NO. US20010018414A1
| TITLE OF INVENTION: POLYPEPTIDES
| TITLE OF INVENTION: POLYPEPTIDES
| FILE REPERENCE: 09531/002001
| CURRENT APPLICATION NUMBER: US/09/803,810
| CURRENT FILING DATE: 2001-03-12
| NUMBER OF SEQ ID NOS: 18
| SOFTWARE: FastSEQ for Windows Version 3.0
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     1896 CACTITCAGGICCTGAA 1912
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-10-298-330-8
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LENGTH: 36
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LENGTH: 42
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                         ; OTHER INFORMATION: DNA primer for preparation of E296V/M298Q-FVII US-10-255-032-8
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                                                                                                                                                                                                                                                                                                                                                          NS-10-255-032-9

Sequence 9, Application US/10255032

Publication No. US20030100075A1

GENERAL INFORMATION:
TILLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES

TILLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES

CURRENT APPLICATION NUMBER: US/10/255,032

CURRENT FILING DATE: 2002-09-24

PRIOR APPLICATION NUMBER: DK PA 2001 01413

PRIOR PILING DATE: 2001-09-27

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PALENTIN VERSION 3.1

SEQ ID NO 9
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Publication No. US20030100740A1
GENERAL INFORMATION:
APPLICANT: Perseson, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REPRENCE: 6224 200-08;
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
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O.5%; Score 10.6; DB 1; Length 36;
Best Local Similarity 76.5%; Pred. No. 3.4e+02;
Matches 13; Conservative 0; Mismatches 4; Indels
                                                                                                    Query Match
0.5%; Score 10.6; DB 1; Length 36;
Best Local Similarity 76.5%; Pred. No. 3.48+02;
Matches 13; Conservative 0; Mismatches 4; Indels
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0.5%; Score 10.6; DB 1; Length 36;
Best Local Similarity 76.5%; Pred. No. 3.4e+02;
Matches 13; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                           1896 CACTTTCAGGTCCTGAA 1912
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COTHER INFORMATION: Synthetic US-10-295-682-8
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LENGTH: 36
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; FEATURE:
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Length 42; Indels

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TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PORTITIE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PORTITIE OF INVENTION: METHODS FOR GENERAL MARKERS
FILE REPERBENCE: 24736-2033B
CURRENT APPLICATION NUMBER: US/10/273,321
CURRENT APPLICATION NUMBER: 09/687,483
PRIOR FILING DATE: 2000-07-10
PRIOR PRIOR FILING DATE: 2000-07-10
PRIOR PRIOR FILING DATE: 2000-07-10
PRIOR PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 2000-07-10
PRIOR PRIOR APPLICATION NUMBER: 60/217,251
PRIOR PRIOR APPLICATION NUMBER: 60/217,251
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
SEQ ID NOS: 118
SEQ ID NO 23
LENGTH: 60
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TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PG

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PG

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PG

TITLE OF INVENTION: METHOD FOR GENERATING DATE: 2002-0-15

CURRENT APPLICATION NUMBER: 60/217,658

PRIOR PILING DATE: 2000-07-10

PRIOR PELING DATE: 2000-07-10

PRIOR PELING DATE: 1999-10-13

PRIOR PELING DATE: 1999-10-13

PRIOR PELING DATE: 1999-10-13

PRIOR PELING DATE: 2000-07-10

PRIOR PELING DATE: 2000-09-10

PRIOR PELING DATE: 2000-09-10

PRIOR PELING DATE: 1999-10-13

PRIOR APPLICATION NUMBER: 60/129,16

PRIOR PELING DATE: 1999-10-13

PRIOR PELING DATE: 1999-10-13

PRIOR PELING DATE: 1999-10-13

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0.5%; Score 10.6; DB 1; Length (
Best Local Similarity 53.7%; Pred. No. 4.4e+02;
Matches 22; Conservative 0; Mismatches 19; Indels
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US20030180749A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapien
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Best Local Similarity
Matches 22; Conserv
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US-10-272-756-23/c
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Pred. No. 4.4e+02;
0; Mismatches 19; Indels
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                           TITLE OF INVENTION: Modified Vitamin K-Dependent TITLE OF INVENTION: Modified Vitamin K-Dependent TITLE OF INVENTION: POlypetides FILE REPERBNCE: 09531-127001 CURRENT FILING DATE: 2002-11-18 PRIOR APPLICATION NUMBER: 09/497,591 PRIOR APPLICATION NUMBER: 09/497,591 PRIOR PILING DATE: 2000-02-03 PRIOR PILING DATE: 1999-04-29 PRIOR PILING DATE: 1999-04-29 PRIOR PILING DATE: 1999-04-29 PRIOR PILING DATE: 1999-04-29 SQUAMBER: 08/985,636 PRIOR FILING DATE: 1997-10-23 NUMBER: OF SEQ ID NOS: 27 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO SEQ ID NOS: 27 LENGTH: 42
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US-10-273-321-23/c
; Sequence 23, Application US/10273321
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Best Local Similarity 53.7%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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COTHER INFORMATION: Primer US-10-298-330-8
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US-10-272-665-23
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Sequence 3, Application US/10281727
Publication No. US20030130191A1
GENERAL INFORMATION
APPLICANT: Persson, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 6410.200-US
FILE REFIGHT APPLICATION NUMBER: US/10/281,727
CURRENT APPLICATION NUMBER: PA 2001 01627
PRIOR PILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 60/335,383
PRIOR PILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 7
SOFFWARE FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 10.4; DB 1;
Pred. No. 3.9e+02;
0; Mismatches 11;
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Best Local Similarity 60.7%
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                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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  Sequence 23, Application US/10273228

Publication No. US2003020729741

GENERAL INCRAMION:

APPLICANT: Braun et al.

TITLE OF INVENTION: GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: GENERAL US/10/273,228

TITLE OF INVENTION: GENERAL US/10/273,228

CURRENT PELICATION NUMBER: US/10/273,228

CURRENT PELING DATE: 2002-10-15

PRIOR PELING DATE: 2000-07-10

PRIOR PILING DATE: 2000-07-10

PRIOR PILING DATE: 2000-07-10-13

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR PELING DATE: 2000-07-10

PRIOR PELING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 118

SOFTWARE: PSELED FEASTED FOR WINDOWS VERSION 4.0
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; OTHER INFORMATION: DNA primer for preparation of S314E/K316H-FVII
US-10-281-727-2
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Pred. No. 4.4e+02;
0; Mismatches 19; Indels
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0.5%; Score 10.4; DB 1; Length 36;
Best Local Similarity 60.7%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 11; Indels
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Person, Egon
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Polypeptides
FILE REPERENCE: 6410.200-US
CURRENT APPLICATION NUMBER: US/10/281,727
CURRENT APPLICATION NUMBER: 0202-10-28
PRIOR FILING DATE: 2001-11-02
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 7-11-15
SEQ ID NOS: 7-11-15
SEQ ID NOS: 7-11-15
SEQ ID NOS: 7-11-15
SEQ ID NOS: 7-11-136
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Best Local Similarity 53.7°
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Homo sapien
US-10-273-228-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Unknown
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DB 1;

0.5%; Score 10.2;

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Query Match 0.5%; Score 10.2; DB 1; Length 38; Best Local Similarity 58.1%; Pred. No. 4.6e+02; Matches 18; Conservative 0; Mismatches 13; Indels
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US-10-109-498-6

Sequence 6, Application US/10109498

Publication No. US20030044908A1

FORDERAL INFORMATION:
APPLICANT: Person

TITLE OF INVENTION: Cagulation Factor VII Derivatives

FILE REFERENCE: 6286.200-US

CURRENT APPLICATION NUMER: US/10/109,498

CURRENT FILING DATE: 2002-03-22

PRIOR FILING DATE: 2002-03-22

PRIOR PELING DATE: 2001-04-03

PRIOR FILING DATE: 2001-03-22

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6

LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/10109498;
Publication No. US20030044908A1
GENERAL INFORMATION:
APPLICANT: Persson. Page 1
TITLE OF INVENTION: Coagulation Factor VII Derivatives
FILE REFERENCE: 6286.200-US
CURRENT FILING DATE: 2002-03.22
PRIOR FILING DATE: 2001-04.03
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 35
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Best Local Similarity 55.9%; Pred. No. 5.1e+02;
Matches 19; Conservative 0; Mismatches 15;
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                                                                                                                                                                                                                                                                                                                                                                                                       35 GAAGCCTCTGCTGGCAATACTTCTGGGGCTG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 gcaccrccrccaggaagcgrrrragcgccg 4
; SCPTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 2; LENGTH: 38
7: TYPE: DNA ORGANISM: Artificial Sequence FRATURE: OS-10-254-394-2
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OTHER INFORMATION: Nucleotide Primer
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ORCANISM: Artificial Sequence
FEATURE:
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US-10-109-498-5/c
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                                                Gaps
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APPLICANT: Pingel, Hans K
APPLICANT: Riausen, Mals K
TITLE OF INVENTION: Factor VII Glycoforms
FILE REPERENCE: 6207.510-02
CURRENT APPLICATION NUMBER: US/09/969,357
CURRENT FILING DATE: 2002-10-02
PRIOR PELICATION NUMBER: Danish Application No. PA 2001 00262
PRIOR FLING DATE: 2001-02-16
PRIOR FLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-03-14
PRIOR PLILING DATE: 2001-03-14
PRIOR PLILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-05-14
PRIOR FILING DATE: 2001-05-14
PRIOR PLILING DATE: 2001-05-14
PRIOR PLILING DATE: 2001-05-14
PRIOR PLILING DATE: 2001-01-06
PRIOR APPLICATION NUMBER: US 60/236,944
PRIOR PLILING DATE: 2001-02-16
PRIOR PLILING DATE: 2001-01-06
PRIOR PLILING DATE: 2001-01-06
PRIOR PLILING DATE: 2001-03-16
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Publication No. US2030096366A1

GENERAL INFORMATION:

APPLICANT: Knudsen, Ida Molgaard

TITLE OF INVENTION: Method for Production of Recombinant

TITLE OF INVENTION: Proteins in Eukaryote Cells

TITLE OF INVENTION: Proteins in Eukaryote Cells

FILE REFERENCE: 6480.500-US

CURRENT FILING DATE: 2002-09-25

PRIOR APPLICATION NUMBER: PCT/DK01/00632

PRIOR PLING DATE: 2001-10-02

PRIOR APPLICATION NUMBER: PCT/DK01/00634

PRIOR PLING DATE: 2001-10-02

PRIOR PLING DATE: 2001-10-02

PRIOR PLING DATE: 2001-10-02

PRIOR PLING DATE: 2002-03-26

PRIOR PLING DATE: 2002-03-26

PRIOR PLING DATE: 2002-03-26

PRIOR PLING DATE: 2002-03-26

PRIOR PLING DATE: 2002-10-04

PRIOR PLING DATE: 2002-10-04

PRIOR PLING DATE: 2002-10-04
                ilarity 58.1%; Pred. No. 4.6e+02;
Conservative 0; Mismatches 13; Indels
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                                                                                                         35 GAAGCCTCTGCTGCCAATACTTCTGGGGCTG 65
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                                                                                                                                                                                                                                                      RESULT 74
US-09-969-357-2/c
US-09-969-357-2/c
; Sequence 2, Application US/09969357
; Paulication No. US20020137673A1
; GENERAL INFORMATION:
; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
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                Best Local Similarity
Matches 18; Conserv
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US-10-254-394-2/c
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Sequence 22, Application US/1027256

Sequence 22, Application US/1027256

Sequence 22, Application US/1027256

Sequence 22, Application US/1027256

Sequence 22, Application US/10272766

Sequence 22, Application US/10272766

TITLE OF INVENTION: BETHODS FOR GENERATING DATABASES FOR IDENTIFYING PC TITLE OF INVENTION: GENERAL SUBJECT OF INVENTION: GENERAL SUBJECT OF INVENTION: GENERAL SUBJECT OF INVENTION: GENERAL SUBJECT OF INVENTION: GENERAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INVERSAL SUBJECT OF INTERPRETARIATION SUBJECT OF INVERSAL SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT OF INTERPRETARIATION SUBJECT
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US-10-273-228-22
US-10-273-228-22
Sequence 22, Application US/1027328
Publication No. US20030207297A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PRITTIES OF INVENTION: GENETIC MARKERS
TITLE OF INVENTION: GENETIC MARKERS
TITLE OF INVENTION: GENETIC MARKERS
UNRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 09/687,483
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR APPLICATION NUMBER: 60/217,658
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 60
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                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: Probe
US-10-273-321-22
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ORGANISM: Homo Sapien
                                                                                                  TYPE: DNA
ORGANISM: Homo Sapien
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                                                                      Query Match 0.5%; Score 10; DB 1; Length 35; Best Local Similarity 55.9%; Pred. No. 5.1e+02; Matches 19; Conservative 0; Mismatches 15; Indels
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; Sequence 22, Application US/10273321
; Publication No. US20030180749A1
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/10272665 Publication No. US20030180748A1 GENERAL INFORMATION:
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US-10-272-665-22
                  US-10-109-498-6
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US-LW-Z(LZ-)DS-LU)

Sequence 107, Application US/10272756

Publication No. US200319064441

GENERAL INFORMATION:

APPLICANT: Braun et al.

TITLE OF INVENTION:

FILE PERFERNCE: 24736-2033C

CURRENT FILING DATE: 2002-10-15

PRIOR PLICATION NUMBER: US/10/272,756

CURRENT FILING DATE: 2000-07-10

PRIOR PLICATION NUMBER: 60/217,658

PRIOR PLING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR PLING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 1990-10-13

PRIOR FILING DATE: 1990-10-13

PRIOR FILING DATE: 1990-10-13

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 1990-10-13

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: PRIOR DATE: PRIOR PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILI
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, TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PO
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0.5%; Score 10; DB 1; Length 100;
Best Local Similarity 72.2%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 5; Indels
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 09/687,483
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/1217,658
PRIOR FILING DATE: 2000-07-10
PRIOR PELING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PSESSEQ for Windows Version 4.0
SEQ ID NO 107
LENGTH: 100
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; Publication No. US20030207297A1
; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 GGGCCAGGGTAGGGGCAC 156
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ORGANISM: Homo sapien
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Matches 13; Conserv
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US-10-273-228-107
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Sequence 107, Application US/10272665

Publication No. US20030180748A1

GENERAL INFORMATION:

APPLICANT: Braun et al.

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: GENERIC MARKERS

FILE REFERENCE: 24736-2033E

CURRENT FILING DATE: 2002-10-15

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 09/687,483

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

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PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 09/663,968

PRIOR FILING DATE: 2000-09-19
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PUDIcation No. US20030180749A1
GENERAL INFORMATION:
APPLICANT: Braun et al.
ITILE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING ITILE OF INVENTION: GENERALIC MARKERS
FILE REPERENCE: 24736-2033B
CURRENT APPLICATION NUMBER: US/10/273,321
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0.5%; Score 10; DB 1; Length 100;
Best Local Similarity 72.2%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.5%; Score 10; DB 1; Length 60; Best Local Similarity 72.2%; Pred. No. 5.9e+02; Matches 13; Conservative 0; Mismatches 5; Indels
        PRIOR APPLICATION NUMBER: 60/159,176
PRIOR FLING DATE: 1999-10-13
PRIOR FLLING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR PILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO. 22
LENGTH: 60
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 107
LENGTH: 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ), OTHER INFORMATION: Probe US-10-273-228-22
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapien
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JOHENTAL INTEGRATE Braun et al.
APPLICANT: Braun et al.
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PR.
TITLE OF INVENTION: GENETIC MARKERS
FILE REFERENCE: 24736-20338
CURRENT APPLICATION NUMBER: U$/10/273,321
CURRENT APPLICATION NUMBER: 09/67,483
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/159,176
PRIOR APPLICATION NUMBER: 60/159,176
PRIOR APPLICATION NUMBER: 60/17,251
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
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### Sequence 106, Application US/10272756

### Sequence 106, Application US/10272756

### Sequence 106, Application US/10272756

### Sequence 106, Application No. US20030190644A1

### Sequence 106, Application No. US2003019064A1

### SPECIAL INFORMATION:

### TITLE OF INVENTION: GENETIC MARKERS

### TITLE OF INVENTION: GENETIC MARKERS

### TITLE OF INVENTION: GENETIC MARKERS

### TITLE OF INVENTION: GENETIC MARKERS

### CURRENT APPLICATION NUMBER: US/10/272,756

### CURRENT FILING DATE: 2000-07-10

### PRIOR APPLICATION NUMBER: 60/129,176

### PRIOR APPLICATION NUMBER: 60/129,176

### PRIOR APPLICATION NUMBER: 60/129,176

### PRIOR PILING DATE: 2000-07-10

### PRIOR PILING DATE: 2000-07-10

### PRIOR PILING DATE: 2000-09-19

### PRIOR PILING DATE: 2000-09-19

### MUMBER: OF SEQ ID NOS: 118

### MUMBER: OF SEQ ID NOS: 118

### MUMBER: DE NO 106

### ID NO 106

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Best Local Similarity 72,29
Matches 13, Conservative
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Matches 13; Conservative
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CORGANISM: Homo sapien
US-10-273-321-106
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CORGANISM: Homo sapien
US-10-272-756-106
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FILE REPERENCE: 24736-2033E
CURRENT APPLICATION NUMBER: US/10/272,665
CURRENT APPLICATION NUMBER: US/10/210-15
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 1999-10-33
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/159,176
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-09-19
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PRIOR PILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR PILING DATE: 2000-09-19
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0.5%; Score 10; DB 1; Length 100;
Best Local Similarity 72.2%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 5; Indels
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TITLE OF INVENTION: GENETIC MARKERS
FILE REPERENCE: 2479-2033)
CURRENT APPLICATION NUMBER: US/10/273,228
CURRENT FILING DATE: 2002-10-15
PRIOR FILING DATE: 2000-07-10
PRIOR PLING DATE: 2000-07-10
PRIOR PLING DATE: 2000-07-10
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PRIOR PLING DATE: 1999-10-13
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PRIOR PLING DATE: 1999-10-13
PRIOR PLING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/12/1/21
PRIOR PLING DATE: 2000-07-10
PRIOR PLING DATE: 2000-07-10
PRIOR PRIOR DATE: 2000-07-10
PRIOR PRIOR DATE: 2000-07-10
PRIOR PRIOR DATE: 2000-09-19
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; Publication No. US20030180749A1
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ORGANISM: Homo sapien
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; OTHER INFORMATION: DNA primer for preparation of E296V/M298Q-FVII
US-10-255-032-8
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TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
FILE REPERENCE: 635-W0
CURRENT APPLICATION NUMBER: US/10/255,032
CURRENT FILING DATE: 2002-09-24
PRIOR FILING DATE: 2001-09-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 8
LENGTH: 36
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                                                                              APPLICANT: Person, Bgon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/09/951,121A
CURRENT APPLICATION NUMBER: BA 2000 01361
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SEQ ID NOS: 17
SEQ ID NO 9
SEQ ID NO 9
LENGTH: 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.5%; Score 9.8; DB 1; Length 36; 58.6%; Pred. No. 5.9e+02; tive 0; Mismatches 12; Indels
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Sequence 9, Application US/09951121A Publication No. US20030104978A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/10255032; Publication No. US20030100075A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 58.64
Matches 17, Conservative
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                                                                                                      APPLICANT: Brain et al.

APPLICANT: Brain et al.

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: GENERIC MARKERS

FILE REPRENCE: 24736-2033D

CURRENT APPLICATION NUMBER: US/10/273,228

CURRENT APPLICATION NUMBER: 09/687,483

PRIOR APPLICATION NUMBER: 09/687,483

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-09-19

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Publication No. US20030104978A1
GENERAL INFORMATION:
APPLICANT: Persson,
TITLE OF INVENTION: Human Coagulation Factor VII Variants
TITLE PERSENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/09/951,121A
CURRENT APPLICATION NUMBER: PA 2000 01361
PRIOR APPLICATION NUMBER: PA 2000 01361
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR FILING DATE: 2000-09-13
PRIOR PELLING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.5%; Score 10; DB 1; Length 100; 72.2%; Pred. No. 4.8e+02; tive 0; Mismatches 5; Indels
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      US-10-273-228-106

"Sequence 106, Application US/10273228
; Publication No. US20030207297A1
; GENERAL INFORMATION:
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Best Local Similarity 72.24
Matches 13; Conservative
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CORGANISM: Homo sapien
US-10-273-228-106
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US-09-951-121A-9/c
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LENGTH: 100
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LENGIH: 36
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Publication No. US20030220247A1
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                  TYPE: DNA ORGANISM: Artificial Sequence
                                                          FEATURE:
; OTHER INFORMATION: Synchetic
US-10-295-682-9
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US-10-349-858-8
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Best Local Similarity
Matches 11, Conserv
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; Sequence 8, Application US/10295682
; Publication No. US2030100740A1
; Publication No. US2030100740A1
; Publicant: Person, Egon
; APPLICANT: Olsen, Ole Hvilsted
; TILE REFERENCE: 6224.200-US
; FILE REFERENCE: 6224.200-US
; CURRENT FILING DATE: 2002-11-15
; PRIOR PILING DATE: 2002-09-13
; PRIOR PILING DATE: 2000-09-13
; PRIOR PILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 17
; SOFTMARE: FastSEQ for Windows Version 4.0
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APPLICANT: Olsen, Ole Hvilsted
APPLICANT: Olsen, Ole Hvilsted
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REPERENCE: 6.244.200-US
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT FILING DATE: 2002-11-15
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
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0.5%; Score 9.8; DB 1; Length 36;
Best Local Similarity 58.6%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 12; Indels
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PRIOR APPLICATION NUMBER: DK PA 2001 01413
PRIOR FILING DATE: 2001-09-27
NUMBER OF SEQ ID NOS: 9
SEQTYARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Synthetic US-10-295-682-8
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Best Local Similarity 58.69
Matches 17; Conservative
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LENGTH: 36
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GENERAL INFORMATION:

APPLICANT: HIGH KATHERINE A.

APPLICANT: HIGH KATHERINE A.

APPLICANT: HIGH KATHERINE A.

APPLICANT: HIGH KATHERINE A.

APPLICANT: HIGH KATHERINE A.

APPLICANT: ARROW, PETER J.

APPLICANT: STAFFORD. DARREL W.

TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT (

TITLE OF INVENTION: FACTORS

TITLE OF INVENTION: FACTORS

FILE REFERENCE: 108749-03146

CURRENT FILING DATE: 2000-03-16

PRIOR PRILING DATE: 2000-03-16

PRIOR FILING DATE: 1999-03-16

PRIOR FILING DATE: 1999-03-16

PRIOR FILING DATE: 1999-03-16

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PATENTIN VEREION 3.1

SEC ID NO 9

LEVING DATE: 1000-03-16

SEC ID NO 9

LEVING DATE: 1000-03-16

SEC ID NO 9
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1 Sequence 23, Application US/10272665

1 Sequence 23, Application US/10272665

2 Publication No. US20030180748A1

3 Publication No. US20030180748A1

4 APPLICANT: Braun et al.

1 TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PRITILE OF INVENTION: GENETIC MARKERS

7 TITLE OF INVENTION: GENETIC MARKERS

7 TITLE OF INVENTION: GENETIC MARKERS

7 TILL REPERENCE: 24736-2033E

7 TITLE OF DATE: 2002-10-15

7 FILE REPERENCE: 24736-2034E

7 TITLE OF DATE: 2000-07-10

7 FILE REPERENCE: 2000-07-10

7 FILE REPERENCE: 1999-10-13

7 FRIOR PILING DATE: 2000-07-10

7 FRIOR PILING DATE: 1999-10-13

7 FRIOR PILING DATE: 1999-10-13

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Length 36;
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Query Match

0.5%; Score 9.8; DB 1;
Best Local Similarity 58.6%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 12
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Sequence 23, Application US/10273228
| Publication No. US20030207297A1 |
| GENERAL INFORMATION: |
| APPLICANT: Braun et al. |
| TITLE OF INVENTION: | METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PORTITIES OF INVENTION: | GENERATING DATABASES FOR IDENTIFYING PORTITIES OF INVENTION: | GENERATING DATABASES FOR IDENTIFYING PORTITIES OF DATE: 2002-10-15 |
| CURRENT APPLICATION NUMBER: 09/687,483 |
| PRIOR APPLICATION NUMBER: 60/159,176 |
| PRIOR FILING DATE: 2000-07-10 |
| PRIOR FILING DATE: 2000-07-10 |
| PRIOR FILING DATE: 2000-07-10 |
| PRIOR FILING DATE: 2000-07-10 |
| PRIOR FILING DATE: 2000-07-10 |
| PRIOR FILING DATE: 2000-07-10 |
| PRIOR FILING DATE: 2000-07-10 |
| PRIOR FILING DATE: 2000-07-10 |
| PRIOR FILING DATE: 2000-07-10 |
| PRIOR FILING DATE: 2000-09-19 |
| NUMBER OF SEQ ID NOS: 118 |
| SOSTWARE: FRESEQ for Windows Version 4.0
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; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Person. Egon
; TITLE OF INVENTION: Cogulation Factor VII Derivatives
; FILE REFERENCE: 6286.200-US
; CURRENT FILING DATE: 2002-03-22
; PRIOR FILING DATE: 2001-04-03
; PRIOR FILING DATE: 2001-04-03
; PRIOR FILING DATE: 2001-04-03
; PRIOR FILING DATE: 2001-04-03
; PRIOR FILING DATE: 2001-04-03
; PRIOR FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 20
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66.7%; Pred. No: 6.4e+02;
tive 0; Mismatches 7;
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66.7%; Pred. No. 6.4e+02;
tive 0; Mismatches 7;
   PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PASLSEQ for Windows Version 4.0
SEQ ID NO.
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Matches 14; Conservative
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CORGANISM: Homo sapien
US-10-272-756-23
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CORGANISM: Homo sapien
US-10-273-228-23
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Best Local Similarity
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US-10-109-498-5
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GENERAL INFORMATION:
FULLICATION NO. US2003018074941
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
TITLE OF INVENTION: GENERATION MARKERS
FILE REPERENCE: 24736-2033B
CURRENT APPLICATION NUMBER: US/0/213,321.
CURRENT FILING DATE: 2000-10-15
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR FILING DATE: 2000-07-10
FRICK APPLICATION NUMBER: 60/217,551
PRIOR PLILOM DATE: 1999-10-13
PRIOR PLILOM DATE: 2000-07-10
FRICK APPLICATION NUMBER: 60/217,251
PRIOR PLILOM DATE: 2000-07-10
FRICK APPLICATION NUMBER: 60/217,251
PRIOR PLILOM DATE: 2000-09-10
FRICK APPLICATION NUMBER: 60/217,251
PRIOR PLILOM DATE: 2000-09-10
FRICK APPLICATION NUMBER: 09/663,968
FRICK FILING DATE: 2000-09-19
FRICK PLILOM DATE: 2000-09-19
FRICK FILING DATE: 2000-09-19
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Requence 23, Application US/10272756

Publication No. US200301906441

REMEMBLI INFORMATION:
APPLICANT: Braun et al.
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC
TITLE OF INVENTION: GENETIC MARKERS
TITLE OF INVENTION: GENETIC MARKERS
TITLE OF INVENTION: GENETIC MARKERS
TITLE OF PRICE APPLICATION NUMBER: US/10/272,756
CURRENT APPLICATION NUMBER: 09/687,483
PRIOR PELLING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
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NUMBER OF SEQ ID NOS: 118
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
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                                                                                                                        TYPE: DNA,
ORGANISM: Homo sapien
US-10-272-665-23
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; ORGANISM: Homo sapien
US-10-273-321-23
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Matches 14; Conserv
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Publication No. US20030087244A1
Sequence 1. INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL THE REPERBUCE: MAI-007
CURRENT APPLICATION NUMBER: US/10/017,122
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/327,487
PRIOR FILING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 4
SOPTWARE: PatentIn Ver. 2.0
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Pred. No. 7.4e+02;
0; Mismatches 6
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5 LENGTH: 35
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                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 68.4%;
Matches 13; Conservative
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Matches 13; Conserv
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Best Local Similarity
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US-10-109-498-6/c
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APPLICANT: Olsen, Egon
TITLE OF INVENTION: Human Coagulation Factor VII Variants; FILE REFERENCE: 6224-200-US; CURRENT PILING DATE: 2001-09-13; PRIOR APPLICATION NUMBER: US/09/951,121A; PRIOR APPLICATION NUMBER: PA 2000 01361; PRIOR PILING DATE: 2000-09-13; PRIOR PILING DATE: 2000-09-13; PRIOR FILING DATE: 2000-09-13; PRIOR FILING DATE: 2000-09-13
Sequence 2, Application US/09951121A
Sequence 2, Application US/09951121A
Publication No. US20030104978A1
GENERAL INFORMATION:
APPLICANT:
TITLE PETSON. BGON
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224.200-05;
CURRENT APPLICATION NUMBER: US/09/951,121A
CURRENT FILING DATE: 2000-09-13
FRIOR FILING DATE: 2000-09-13
FRIOR FILING DATE: 2000-09-13
FRIOR FILING DATE: 2000-09-13
SOFTWARE: FELICATION NUMBER: 60/236,455
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2:
LENGTH: 34
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0.5%; Score 9.2; DB 1; Length 34;
Best Local Similarity 63.6%; Pred. No. 8.2e+02;
Matches 14; Conservative 0; Mismatches 8; Indels
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Pred. No. 8.2e+02;
0; Mismatches 8;
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SOFTWARE: RaskSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 34
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ilarity 63.6%;
Conservative (
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ORGANISM: Artificial Sequence
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: DNA primer for preparation of S314E/K316H-FVII
US-10-281-727-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ), OTHER INFORMATION: DNA primer for preparation of $314E/K316H-FVII US-10-281-727-3
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           GENERAL INFORMATION:
APPLICANT: Persson, Egon
APPLICANT: Olsen, Ole Hvisted
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 6410.200-US
CURRENT APPLICATION NUMBER: 9202-10-28
PRIOR PILING DATE: 2002-10-28
PRIOR PILING DATE: 2001-11-02
PRIOR PILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO SEQ ID NOS: 7
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/10281727
Publication No. US20030130191A1
GENERAL INFORMATION:
APPLICANT: Person, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 6410.200-US
CURRENT APPLICATION NUMBER: US/10/281,727
CURRENT APPLICATION NUMBER: BA.2001 01627
FRIOR APPLICATION NUMBER: E0.02-10-28
FRIOR APPLICATION NUMBER: E0.0335,383
FRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 7
SEQ ID NOS: 7
SEQ ID NOS: 7
LEDICHARY OF SEQ ID NOS: 7
SEQ ID NOS: 7
LEDICHARY SECTION NUMBER: 10.301
SEQ ID NOS: 7
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US20030130191A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 78.6%;
Matches 11; Conservative
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ORGANISM: Unknown
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ORGANISM: Unknown
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US-09-951-121A-14
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                                                                                  Sequence 2, Application US/10295682
| Publication No. US20030100740A1
| GENERAL INFORMATION:
| APPLICANT: Persson. Egon
| TITLE OF INVENTION: Human Cosqulation Factor VII Variants
| FILE REPERBNCE: 6224.200-115
| CURRENT PAPLICATION NUMBER: US/10/295,682
| CURRENT FILING DATE: 2002-11-15
| PRIOR PAPLICATION NUMBER: 60/236,455
| PRIOR FILING DATE: 2000-09-13
| PRIOR FILING DATE: 2000-09-29
| NUMBER OF SEQ ID NOS: 17
| SOFTWARE: PastSEQ for Windows Version 4.0
| SEQ ID NO 2: LENTH: 34
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APPLICANT: Olem, Ole Hvilsted
TILLE OP INVENTION: Human Coagulation Factor VII Variants
FILE REPERENCE: 624.200-US
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: PA 2000 01361
PRIOR APPLICATION NUMBER: PA 2000 01361
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO : BASE OF ID NOS: 17
MANDER OF SEQ ID NOS: 17
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Publication No. US20030100740A1
GENERAL INFORMATION:
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US-10-281-727-2
; Sequence 2, Application US/10281727
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Synthetic
US-10-295-682-2
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US-10-295-682-3/c
                                                                 US-10-295-682-2
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Sequence 15, Application US/10295682

Publication No. US20030100740A1

GENERAL INCORMATION:
APPLICANT: Persson. Bgon
ITILE OF INVENTION: Human Coagulation Factor VII Variants
FILE FEFENCE: 6224.200-US
CURRENT FILING DATE: 200-11-15
PRIOR FILING DATE: 200-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
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Publication No. US20010018414A1;
GENERAL INFORMATION: WOLDSTED VITAMIN K-DEPENDENT;
ITILE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT;
ITILE OF INVENTION: MOLFFEED VITAMIN K-DEPENDENT;
ITILE OF INVENTION: MOLFFEED VITAMIN K-DEPENDENT;
ITILE OF INVENTION: MOLFFEED VITAMIN K-DEPENDENT;
ITILE OF INVENTION: MOLFFEED VITAMIN K-DEPENDENT;
ICREMIT APPLICATION NUMBER: US/09/803,810;
CURRENT APPLICATION NUMBER: US/09/803,810;
CURRENT APPLICATION NUMBER: 05.001-03-12;
NUMBER OF SEQ ID NOS: 18;
SOFTWARE: FactSEQ for Windows Version 3.0;
ILBUGHH 42;
TYPE: DNA
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PRIOR APPLICATION NUMBER: PA 2000 01361
PRIOR FILLING DATE: 2000-09-13
PRIOR FILLING DATE: 2000-09-13
PRIOR FILLING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
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                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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Best Local Similarity 60.09
Matches 15; Conservative
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US-09-803-810-8/c
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    APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224.200-0.951,121A
CURRENT APPLICATION NUMBER: US/09/951,121A
CURRENT FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 33
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APPLICANT: Olsen, Ole Hvilsted
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REPERSING: 6224.200-US
CURRENT PILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: 00/296,455
PRIOR FILING DATE: 2000-09-13
PRIOR PLING DATE: 2000-09-13
PRIOR PRILICATION NUMBER: 60/236,455
PRIOR PLING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
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0.4%; Score 9; DB 1; Length 33;
Best Local Similarity 60.0%; Pred. No. 9.1e+02;
Matches 15; Conservative 0; Mismatches 10; Indels
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Publication No. US20030100740A1
GENERAL INFORMATION:
APPLICANT: Person, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 624.200.US
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT FILING DATE: 2002-11-15
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0.4%; Score 9; DB 1; Length 33;
Best Local Similarity 60.0%; Pred. No. 9.1e+02;
Matches 15; Conservative 0; Mismatches 10; Indels
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Sequence 15, Application US/09951121A
Publication No. US20030104978A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Synthetic US-09-951-121A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 112
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Sequence 4, Application US/10017122
| Publication No. US20030087244A1
| GENERAL INFORMATION NO. US20030087244A1
| GENERAL INFORMATION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
| TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
| FILE REFERENCE: MM. 007
| CURRENT FILING DATE: 2001-12-14
| PRIOR PILING DATE: 2001-12-14
| PRIOR PILING DATE: 2001-10-09
| NUMBER OF SEQ ID NOS: 4
| SOFTWARE: PATENTIN OF: 2.0
| SEQ ID NO 4
| LENGTH: 31
; OTHER INFORMATION: DNA primer for preparation of S314E-FVII
US-10-281-727-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: DNA primer for preparation of S314E-FVII
US-10-281-727-7
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0.4%; Score 8.2; DB 1; Length 31;
Best Local Similarity 61.9%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 8; Indels
                                                               Length 32;
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                                                          Score 8.4; DB 1; Length 32
Pred. No. 1.2e+03;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                     Sequence 7, Application US/10281727
; Sequence 7, Application US/10281727
; Publication No. US20030130191A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; APPLICANT: Persson, Ole Hyilsted
; TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Human Coagulation Factor VII
; TITLE OF INVENTION: Human Coagulation Factor VII
; TITLE OF INVENTION: Human Coagulation Factor VII
; TITLE OF PRICATION NUMBER: US/10/281,727
; CURRENT FILING DATE: 2002-10-28
; PRIOR FILING DATE: 2001-11-02
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 7
; SEQIID NO 7
; TENGTH. 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 8.4; DB 1;
Pred. No. 1.2e+03;
0; Mismatches 1;
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                                                               Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                            866 TGCAGCAGTA 875
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ORGANISM: Unknown
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US-10-017-122-4/c
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                                                                                                       Length 42;
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                                                                                                                                            Indels
                       FEATURE:
; OTHER INFORMATION: Protein C mutagenic oligonucleotide
US-09-803-810-8
                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/10281727
Publication No. US20030130191A1
GENERAL INFORMATION:
APPLICANT: Persson, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 6410.200-US
CURRENT APPLICATION NUMBER: US/10/281,727
CURRENT FILING DATE: 2002-10-28
PRIOR FILING DATE: 2001-11-02
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: FastSEQ for Windows Version 32
                                                                                                    0.4%; Score 8.8; DB 1; L
52.8%; Pred. No. 9.8e+02;
tive 0; Mismatches 17;
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      ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                Ouery Match
Best Local Similarity 52.81
Matches 19, Conservative
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ORGANISM: Unknown
FEATURE:
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US-10-281-727-6
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US-10-295-682-3
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                                                                                                                                                  US-09-951-121A-2/C

Sequence 2, Application US/09951121A

Publication No. US20030104978A1

GENERAL INFORMATION:
APPLICANT: Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen, Olsen
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Publication No. US20030104978A1

GENERAL INFORMATION:
APPLICANT: Persson. Egon
APFLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REPERENCE: 6224, 200-08

CURRENT APPLICATION NUMBER: US/09/951,121A
CURRENT FILING DATE: 2001-09-13

PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-29

NUMBER OF SEQ ID NOS: 17

SOFFWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7.8; DB 1; Length 34; Pred. No. 1.4e+03;
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0.4%; Score 7.8; DB 1; Length 34;
Best Local Similarity 81.8%; Pred. No. 1.4e+03;
Matches 9; Conservative 0; Mismatches 2; Indels
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31 CAGAGAGTACCCCTCATGGCA 11
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 81.8%;
Matches 9; Conservative
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Synthetic US-09-951-121A-2
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LENGTH: 34
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RESULT 121 US-10-295-682-2/c

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Sequence 2, Application US/10295682
Publication No. US20030100740A1
GENERAL INFORMATION:
APPLICANT: Persenon. Egon
APPLICANT: Olsen, Ole Hvilsted
ITILE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: EA 2000 01361
PRIOR PILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO : SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10295682
| Sequence 3, Application US/10295682
| Publication No. US2030100740A1
| GENERAL INFORMATION:
| APPLICANT: Persson. Egon
| TITLE OF INVENTION: Human Coagulation Factor VII Variants
| TITLE OF INVENTION: Human Coagulation Factor VII Variants
| FILE REPERENCE: 6224.200-US
| CURRENT APPLICATION NUMBER: US/10/295,682
| CURRENT FILING DATE: 2002-11-15
| PRIOR APPLICATION NUMBER: PA 2000
| PRIOR APPLICATION NUMBER: 60/236,455
| PRIOR APPLICATION NUMBER: 60/236,455
| NUMBER OF SEQ ID NOS: 17
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 3
| IEMNOTH: 34
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0.4%; Score 7.8; DB 1; Length 34;
Best Local Similarity 81.8%; Pred. No. 1.4e+03;
Matches 9; Conservative 0; Mismatches 2; Indels
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Pred. No. 1.4e+03;
0; Mismatches 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: August 9, 2004, 16:50:07 Job time : 27 secs
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; CTHER INFORMATION: Synthetic US-10-295-682-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-295-682-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      640 TTTGGTGCATA 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         640 TITGGTGCATA 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 TTTGGGGCACA 21
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

August 9, 2004, 16:50:27; Search time 3 Seconds (without alignments) 3.679 Million cell updates/sec Run on:

Title:

1 agctttccagagagacttca......tcaaggaccttttatgaatt 2003 us-10-664-775-3 2003 Perfect score: Sequence:

Scoring table:

IDENTITY\_NUC Gapop 10.0 , Gapext 0.5

4 seqs, 2755 residues Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 250 summaries

rstdb:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

•	Description	ACCESSION: AL531727	ACCESSION: AI116939	ACCESSION: AL531727	ACCESSION: AU099140	ACCESSION: AI099321	ACCESSION: AI099321	ACCESSION: AU099140	ACCESSION: AI116939
	ID	AL531727	AI116939	AL531727	AU099140	AI099321	AI099321	AU099140	AI116939
	. BB	Н	Н	-1	Н	Н	Н	Н	н
	core Match Length DB ID	1201	645	1201	300	609	609	300	645
Query	Match	1.0	1.0	6.0	0.8	0.8	0.7	0.7	0.7
	Score	20.6	19.8	18	17	16.3	14.4	13.6	13.6
1t	No.	Н	N	m	4	ហ	9	^	œ
Result	2 :	υ	υ			υ		υ	

AL531727/c AL531727 AL531727 Homo sapiens FETAL LIVER Homo sapiens CDNA CSODMO03Y101 5-PRIME, mRNA sequence.  ACCESSION AL531727 Homo sapiens FETAL LIVER Homo sapiens CDNA Clone CSODMO03Y101 5-PRIME, mRNA sequence.  AL531727 GI:31069559 KEYMORDS AL531727 GI:31069559 SOURCE Homo sapiens (human) CRGANISM Homo sapiens (human) Mammalla: Extheria; Primates; Craniata; Vertebrata; Buteleostomi; Mammalla: Extheria; Primates; Catarrhini; Hominidae; Homo.  AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D. TITLE Full-length CDNA libraries and normalization JOURNAL On Feb 13, 2001 this sequence version replaced gi:12795220.  COMMENT Contact: Genoscope
--

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:930178

Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu

/organism="Mus musculus"

source

FEATURES

/mol\_type="mRNA" /strain="C57BL"

/db\_xref="taxon:10090" /clone="IMAGE:1481822"

Seg primer: custom primer used High quality sequence stop: 483 Location/Qualifiers

Contact: Marra M/Mouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Waterston, R. The WashU-HHMI Mouse EST Project Unpublished (1996)

TITLE JOURNAL COMMENT

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AI116939 645 bp mRNA linear EST 02-SEF-1998 ue29908.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1481822 5'. similar to gb:M13232 COAGULATION PACTOR VII PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Mammalia, Butherlai, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
I (bases 1 to 645)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Galsal, S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="FETAL LIVER"
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/clone_lib="Homo salens FETAL LIVER"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 ITCAAIIGICITITAICIGICGAGACIIGCIIIGIIITIGAAAIAIGIAIICAAIITIIGG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                648 TITGCIGGCATITCTTTTTTTTAGAATAGGTATTTTTCCACATGGATATICAACTGIGG 590
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7252.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODW003AE0IQPL&cluster=7252.f. Contact :
ferg Liang Email : fliangelifeetch.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODW003AE0IQPl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.0%; Score 20.6; DB 1; Length 1201; 59.3%; Pred. No. 0.32; vative 0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODM003Y101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
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Best Local Similarity
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AI116939/c
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
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0

Gaps

.. 0

13; Indels

7; Mismatches

10664775-3.rst

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22; Conservative
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AI099321/c
LOCUS
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
  Matches
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AU099140
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KEYWORDS
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                                                                                                    셤
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                                                                     /done liber Sugano mouse liver mlia"
/done liber Sugano mouse liver mlia"
/note="Organ: liver; Vector: pWB185-FL3; Site_1: DrallI
(CACTGTGTG); Site_2: DrallI
(CACCATGTGG); 1st strand cDNA
was primed with an oligo(dT) primer
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DrallI adaptor [TGTTGGCTACTGG], digested
and cloned into distinct DrallI sites of the pWB185-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the CDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGAAAAGCTGCG and 3' end
primer CGACCTGCAGCACAA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/dollow="conditions"
/tissue_type="FETAL LIVER"
/tissue_type="FETAL LIVER"
/dev stage="fetal"
/clone lib="Homo sapiens FETAL LIVER"
/note="Organ: liver; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a Not1-oliga(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 19 1006 EVRY cedex - France
Email: seqretégenoscope.ons.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7252.f For
more information about this cluster, see
http://www.genoscope.ons.fr/
cgilbin/cluster.cgiPseq=CSODM03AE01QP1&cluster=7252.f. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODM003AE01QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL531727 AL000 sapiens FETAL LIVER Homo sapiens CDNA clone CSODM003Y101 5-PRIME, MRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
11 (Dases 1 to 1201)
11 M. B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Feb 13, 2001 this sequence version replaced gi:12795220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
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1.0%; Score 19.8; DB 1; Length 645;
Best Local Similarity 69.2%; Pred. No. 0.88;
Matches 27; Conservative 0; Mismatches 12; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1766 CIGCCIGAGAINCTCICITCIAICTCITGIAITCIGICA 1804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         586 CIGCIGGAGITICITITITICIACAACAGGIATICICCCA 548
                              dev_stage="adult"
lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL531727.2 GI:31069559
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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JOURNAL
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AL531727
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KEYWORDS
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Score 18; DB 1; Length 1201; Pred. No. 1.1;

0.9%;

Query Match Best Local Similarity

```
Contact: Yutuka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,''. Yoshitokono-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.
                                                                                                                                                                                                       AU099140
AU099140 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP20983 similar to Human factor VII serine protease precursor mRNA
clone lambda-HVII2463, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 300).

Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S.

In silico mapping of the 5'-ends of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries constructed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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ue37b03.yl Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1482509 5' similar to gb:M13232 COAGULATION FACTOR VII
PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 TCCTCTGCCTTCTGCTTCAGGGCTGCCTGGCTGCAGTCTTCGT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.8%; Score 17; DB 1; Length 300; ilarity 59.2%; Pred. No. 6.6; Conservative 0; Mismatches 20; Indels
1571 TCTCAAGGTTAGGAAATTTTTCTTTTTTGGTTTTTCTTGAAA 1612
                                                            1148 TCCCAAAWHAGGAKAAATTTTTTKCGGTWWTYGAWGGAAA 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                    AU099140.1 GI:13550269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI099321.1 GI:3448846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligo-capping method
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149-156 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                AU099140
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Mon Aug

TITLE JOURNAL COMMENT

source

FEATURES

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/dev stage="adult"
//dev stage="adult"
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/clone lib="Sugano mouse liver mlia"
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/ATGTGGCTTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a Draill adaptor [TGTTGGCTACTGG], digested and cloned into distinct Draill sites of the pME18S-FL3 vector (5' site CACTGTGG, 3' site CACTGTGG, 3' site CACTGTGG, Site CACTGTGG, Site CACTGTGG, Site CACTGTGG, Site CACTGTGG, Site CACTGTGG, Site CACTGTGG, Site CACTGTGG, Site CACTGTGG, Site CACTGTGG, Site Selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU099140
AU099140 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HER20983 aimilar to Human factor VII serine protease precursor mRNA clone lambda-HVII2463, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKATYCE, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 300)
Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Taira,H., Mizushima-Sugano,J., Sese,J., Okubo,K., Suyama,A. and Sugano,S.
In silico mapping of the 5'-ends of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries constructed by Oligo-capping method
Unpublished (2001)
                                                                                           444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
Fnis clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:930865
Seq primer: custom primer used
High quality sequence stop: 289.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Institute of Medical Science, University of Tokyo Afel, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yeuzukiejms.u-tokyo.ac.jp Suzukiejms.u-tokyo.ac.jp Suzuki;'., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14.4; DB 1; Length 6
Pred. No. 7.3;
0; Mismatches 11; Indels
   Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAGAAGGTACAGTCTTTGTGTTTTGGTGAAA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 caagaargaacagtrgarcrgrgcaaargaaa 391
                                                                                                                                                                                                                                                                                                                                                                                                                                      'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
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Department of Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 65.6
Matches 21; Conservative
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AU099140/c
LOCUS
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KEYWORDS
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         COMMENT
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/lab_host="adult"
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/note="Organ: liver; Vector: pWE18S-FL3; Site_1: Brand cDNA
was primed with an oligo(dT) primer
[ATGTGGCTTTTTTTTTTTTTTT] double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCTAGTGG], digested
and cloned into distinct DraIII sites of the pWE18S-FL3
vector (5' site CACTGTGT, 3' site CACTGTGG]. XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGATAAAGCTGCG and 3' end
primer CGACCTGCAGGCACA."
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ۲;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 GGGCTGCTGCCTTTCTCCCTGTCTGATTCCTAGGGTGAGGGTTAC-CACTGCTCTCTCTCTC 118
The WashU-HHMI Mouse EST Project Unpublished (1956)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
This ollone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:930865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 GGGCTCTTGAAGATCTCCGGGCCTCCTCAAAGGAGCACTCTTCCTCATTGCACTCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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ue37b03.yl Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1482509 5' similar to gb:M13232 COAGULATION FACTOR VII
PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.8%; Score 16.3; DB 1; Length 609; 63.5%; Pred. No. 4.3; ive 0; Mismatches 22; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
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/db xref="taxon:10090"
/clone="IMAGE:1482509"
                                                                                                                                                                                                                                                                                                                                                                           Seg primer: custom primer used
High quality sequence stop: 289.
Location/Qualifiers
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI099321.1 GI:3448846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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hes 40; Conserv
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Query Match

Matches

ò g DEFINITION

RESULT 6 AI099321

δ a ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

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Gaps

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and

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/lab_host="bHlog"
/lab_host="bHlog"
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/lone="lorgan: liver; Vector: pME185-FL3; Site 1: DraIII
/note="Organ: liver; Vector: pME185-FL3; Site 1: BraIII
(CACTGTGTG); Site 2: DraIII (CACCATGTG); lst strand cDNA-
was primed with an oligo(dT) primer
/was primed with an oligo(dT) primer
/latgredctrartrartrartrart]; double-stranded cDNA-
was ligated to a braIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct braIII sites of the pME185-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI116939 645 bp mRNA linear BST 02-SEP-1998 ue29908.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1481822 5' similar to gb:M13232 COAGULATION FACTOR VII PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                               ·.
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gaelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Morris,M., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Sugano, S. Construction and characterization of a full length-enriched and a S'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:930178
                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
Contact: Marra M/Mouse EST Project
Contact: Marsh Mouse EST Project
WashIngton University School of MedicineP
4444 Porset Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                     0.7%; Score 13.6; DB 1; Length 300; 61.1%; Pred. No. 17; tive 0; Mismatches 14; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 AGAAATCCAGAACAGCTTCGTCCTCTCCGCGTCCTT 242
                                                                                                                                                                                                                                                                                                                                                                                                                      650 AGACATTAAGAATTGCAATGTCCTCTTGGTGGATTT 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seg primer: custom primer used
High quality sequence stop: 483.
Location/Qualifiers
1. 645
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                                                                                                                 1. .300
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "mol_type="mRNA"
'strain="C57BL"
db_xref="taxon:10090"
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sex="female"
                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI116939
AI116939.1 GI:3517263
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 61.1
Matches 22; Conservative
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AI116939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
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constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCACCAA."
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Gaps ô Length 645; 19; Indels DB 1; Query Match
0.7%; Score 13.6; Di
Best Local Similarity 56.8%; Pred. No. 7.8;
Matches 25; Conservative 0; Mismatches

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1437 CCTTGCATCTTTAATATTCTTTCTTTGTTCTATACTTTTAGTG 1480 333 CATCTCAAGTCTTACGTCTGCTTCTGCCTCCTAGACTTTGAGGG 376 ò

Search completed: August 9, 2004, 16:50:30 Job time : 3 secs

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